	424259	AK001776	Hs.143954	hypothetical protein FLI10914	8.3
			Hs.132578	ESTs	8.3 8.3
	410391		Hs.15043	Homo sapiens clone FLB5227 PRO1367 mRNA, complete cds ESTs	8.3
5	407989 410536	AW135208 N39533	Hs.256092	gb:yv27d04.s1 Soares fetal liver spieen 1NFLS Homo sa	8.3
•	452273		Hs.231022	ESTs	8.3
	454297	A1223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	8.3
	45371B	AL119317	Hs.120360	phospholipase A2, group Vt (cytosolic, caldum-Indepe NM_007242:Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) b	8.3 8.3
10	401654 432891	AF161483	Hs.279761	HSPC134 protein	8.3
10		AW081455	Hs.120219	ESTs	8.2
	433627	AF078866	Hs.284298	Homo saplens cDNA: FLJ22993 fis, clone KAT11914	8.2
	435452	AA831004	Hs.124874	ESTS	8.2 8.2
15	418683 440065	U90908 W03476	Hs.87241 Hs.266331	hypothetical protein from clones 23549 and 23762 hypothetical protein MGC4595	8.2
13	439752	178968	Hs.14411	ESTs	8.2
	447983	AW812726	Hs.282113	ESTs, Weakly similar to 138022 hypothetical protein [8,2
	441966	AA568689	Hs.16131	hypothetical protein FLJ12876	8.2 8.2
20	408182	AA047654 Y18418	Hs.272822	gb:z#49g04.r1 Soares relina N2b4HR Homo saplens cDNA RuvB (E coll homolog)-like 1	B.2
20	432180 436005	BE551650	Hs.158126	Homo saplens cDNA FLH13350 ffs, clone OVARC1002143	8.2
	414962	AF273304	Hs.235376	XPMC2 protein	8.2
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), soluble	8.2
25	408175	W29089	Hs.19066	hypothelical protein DKFZp667O2416 ESTs, Weakly similar to 178885 serine/thremine-speci	8.2 8.2
23	413940 437277	A1633205 AA748016	Hs.159914 Hs.123370	ESTs	8.2
	431445	AA505135	Hs.44037	ESTs	8.1
	418927	BE349635	Hs.190284	ESTs	8.1
20	452446	AA086123	Hs.297856	ESTs	8.1 8.1
30	445380 421174	Al222019 AW969058	Hs.144838 Hs.291974	ESTs ESTs, Moderately similar to A45010 X-linked retinopat	8.1
	444374	AA009841	Hs.11039	hypothetical protein MGC2722	8.1
	417247	N5B024		gb:yv63c01.s1 Soeres fetal liver spieen 1NFLS Homo sa	8.1
35	439335	AJ498421	Hs.243168	ESTs	8.1 8.1
33	445235 422585	AL564022 NM 016186	Hs.138207 Hs.118620	ESTs protein Z-dependent protease inhibitor precursor	8.1
	442522	A1087038	Hs.146592	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	8.1
	430684	Al808979	Hs.293193	ESTs	8.1
40	446442	BE221533	Hs.257858	ESTs	8.1 8.0
40	441410 419485	AA932689 AA489023	Hs.233304 Hs.99807	ESTs, Wealdy similar to 138022 hypothetical protein (ESTs, Wealdy similar to urmemed protein product (H.sa	8.0
	449539	W80363	Hs.58446	ESTs	B.0
	4068B3	U24683	Hs.302063	insmuscoglobulin heavy constant mu	8.0
AE	423767	H18283	Hs.132753	F-box only protein 2	8.0 8.0
45	450937 430977	R49131 AA490069	Hs.26267 Hs.306676	ATP-dependant interieron response protein 1 Homo sapiens cDNA FLI14302 fis, clone PLACE2000003	B.0
	455677		Hs.8867	cystelne-rich, angiogenic inducer, 61	8.0
	436706		Hs.194609	ESTs	8.0
50	459407			gb:za22h11.r1 Soares letal liver spieen 1NFLS Homo sa	8,0 6,0
50	444132 437149		Hs.10340 Hs.202234	hypothetica) protein FLJ20445 ESTs, Weekly similar to ALU4_HUMAN ALU SUBFAMILY SB2	8.0
	418499		Hs.302023	hypothetical protein FKSG25	8.0
	411298			gb:PMO-LT0017-031299-001-h07 LT0017 Homo saplens cDNA	8.0
55	432571		Hs.278429	hapatocallular carcinoma-associated antigen 59	8.0 8.0
55	416295 427485		Hs,193385 Hs.178655	EGTs ribonucieses H1	8.0
	409857			gb:UI-HF-BR0p-ajp-c-12-0-UI.r1 NIH_MGC_52 Homo sapica	7.9
	433854			ESTs	7.9
60	4580B0			gb:MR0-HT0157-021299-004-008 HT0157 Homo saplens cDNA	7.9 7.9
60	423573 404495			gb:EST31993 Embryo, 12 week I Homo saplens cDNA 5' en C8001441"::ji)8923061 kef NP_060114.1 hypothetical pr	7.9
	443135		Hs.156103	ESIB	7.9
	448939	BE267795	Hs,22595	hypothetical protein FLJ10637	7.9
65	413283		Hs.23756	hypothetical protein similar to swine acylinetraminate	7.9 7.9
65	443987 434197			seven transmembrane protein TM7SF3 gb:ng63b04.s1 NCI_CGAP_Ov6 Homo saplens cDNA clone si	7.9
	436882			SH2 domain-containing phosphatase anchor protein 1	7.9
	434502			ESTs	7.9
70	43550	7 Al143579	Hs 26510	vacuoler protein sorting 33B (yeast homolog)	7.9
70	444B9		Hs.144856	ESTs	7.9 7.9
	41932 44626		Hs.6137 5 Hs.14559	ESTs hypothetical protein FLJ10540	7.9
	42556			Homo saplens cDNA FLJ12073 fis, clone HEM891002387	7.9
~ ~	44520	9 AW29423	0 Hs.80988	collagen, type VI, alpha 3	7,9
75	44919		Hs.195653	ESTS	7.9 7.9
	44739 45503			E-1 enzyme gb:MRO-HT0167-081199-001-e02 HT0167 Homo sepiens cDNA	7.9 7.9
	45336			PKCL1-related HTT protein	7.8
00	43931	7 AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothetical protein D	7.8
80	42400		Hs.137548	CD84 antigen (laukocyte antigen)	7.8 7.8
	40856 43519		9 Hs.4835	NM_004520°Homo saplens kineste heavy chain member 2 eukaryotic translation initiation factor 3, subunit 8	7.8
	43515			gb;CM3-HT0183-181099-023-b05 HT0183 Homo saplens cDNA	7.8
				-	

	436216	AA380887	Hs.5085	dolichyl-phosphate mannosyltransfarese polypeptide 1,	7.8
	418623	AW194757	Hs.266804	ESTs	7.8
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo saplens cDNA	7.8 7.8
5	430146 441841	AW815330 AA971819	Hs.176083	gb;QV0-ST0215-060100-083-209 ST0215 Homo sepiens cDNA ESTs	7.8
,	457677	AA628890	Hs.158701	ESTS	7.8
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),	7.8
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	7.B
10	434407 406410	AW815933		gb:QV0-ST0215-060100-083-g01 ST0215 Homo septens cDNA C5000010*:gi[10440464[db][BAB15765.1] (AK024475) FLJ0	7,B 7.8
10	453579	A1204463	Hs.61857	ESTs	7.8
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis vinal oncegene homolog-lik	7.7
	452139	AA099969	Hs.16331	Homo saplens cDNA: FLJ21482 fis, clone COL05135	7.7
15	405510	******	11. 420EE2	ENSP00000233779*:Hypothelical 68.0 kDa protein.	7.7 7.7
13	440777 446424	AA994020 AW134529	Hs.128553 Hs.244647	ESTs ESTs	7.7
	448004	AW451477	Hs.257456	ESTs	7.7
	430610	AJ821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	7.7
20	427080	AW068287	Hs.173466	res-related C3 botulinum todn substrate 2 (the famil	7.7 7.7
20	451693 417558	BE220445 AF045229	Hs.279635 Hs.82280	ESTs regulator of G-protein signalling 10	7.7
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	7.7
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (polypyrlmklin	7.7
25	425423	NM_005897		Intracistemal A particle-promoted polypeptide	7.7
25	450663	H43540	Hs.25292	ribonudease HI, large subunit	7.7 7.7
	432585 402682	AA705591	Hs.190209	ESTs Target Exon	7.7
	400247			Eos Control	7.7
••	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	7.7
30	426761	AJ015709	Hs.172089	Homo sepiens mRNA; cDNA DKFZp586/2022 (from clone DKF	7.7
	405514	A2281 4 D 4 T 7		ENSP0000241075:TRRAP PROTEIN. gb:RC0-MT0013-280300-021-b08 MT0013 Homo sapiens cDNA	7.7 7.7
	412406 440226	AW948172 AA873387	Hs.207330	EST8	7.7
	435625	H50654	Hs.113999	ESTs	7.7
35	418529	AW005695	Hs.250897	TRK-fused gene	7.6
	407758	D50915	Hs.38365	KIAA0125 gene product	7.6
	447276	AL049795	Hs.17987	hypothešical protein MGC1203 Homo saplens cDNA; FLJ21367 tis, clone CCL03051	7.6 7.6
	449938 422893	AW970512 X98411	Hs.172635 Hs.121555	myosh IF	7.6
40	451593	AF151879	Hs.26706	CGI-121 protein	7.6
	424148	BE242274	Hs.1741	integrin, beta 7	7.6
	447519	U46258	Hs,339665	ESTs	7.6
	409361 436279	NM_005982 AW900372	2 Hs,54416 Hs.180793	sine oculis homeobox (Orosophila) homolog 1 ESTs, Weekly similar to S65657 alpha-1C-adrenergic re	7,6 7.6
45	428523		Hs.170222	solute earlier family 9 (sodium/hydrogen exchanger).	7.6
	456926		Hs.158688	KIAA0741 gene product	7.6
	416294		Hs.79170	KIAA0227 protein	7.6
	409206			gb:QV3-DT0044-221269-045-c03 DT0044 Homo sapiens cDNA ESTs, Weakly similar to S55024 nebulin, skeletal musc	7.6 7.6
50	417086 418181		Hs.73451 Hs.83727	cleavage and polyadenylation specific factor 1, 160kD	7.5
-	436910		12,0012.	gb:om68g01.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3'	7.5
	401008			Target Exon	7.5
	413245		Hs.75249	ADP-ribosylation factor-like 6 Interacting protein	7.5 7.5
55	446820 439279		' Hs.254986 Hs.130636	ESTS ESTS	7.5
-	426116		Hs.144694	ESTs	7.5
	410098		Hs.17433	hypothetical protein FL120967	7.5
	422326		Hs.78592	eukaryotic translation initiation factor 2B, subtrait	7.5
60	435513 421629		i Hs.42785 Hs.4983	DC11 protein ESTs	7.5 7.4
00	434663			ESTs	7,4
	452461		Hs.108106	transcription factor	7.4
	418811		Hs.88663	hypothetical protein FLJ10545	7.4
65	405417			CX001144*gij7242973jdbj BAA92547.1 (AB037730) KIAA1 gb:nc74e05.s1 NCL_CGAP_P/2 Homo septens cDNA clone, m	7.4 7.4
UJ	414076 435014			milochondrial ribosomal protein L17	7.4
	44961		Hs.14044	ESTs	7.4
	40339	7		Target Exon	7.4
70	43687		Hs.50477	RAB27A, member RAS oncogene femily	7.4
70	45138 40491		Hs.26334	spastic paraplegia 4 (autosomal dominant; spastin) NM_004046*:Homo sapiens ATP synthese, H+ transporting	7.4 7.4
	41983		Hs.93304	phospholipase A2, group VII (platelet-activating fact	7.4
	43282	0 Al554057	Hs.152477	ESTs	7.4
m c	41897	8 T85295	Hs.260606	ESTs .	7.4
75	44683			citron (rho-interacting, serine/threonine kinase 21)	7.A 7.4
	45463 43452			gb:RC2-ST0158-091099-011-d05 ST0158 Homo sapiens cDNA gamma-aminobulyric acid (GABA) receptor, theta	7.4
	45823			ESTs, Weakly similar to A47234 homeobox protein H6 [H	7.4
00	44104	3 AA913422	2 Hs.192104	ESTs	7.4
80	42283			Homo sepiens cDNA: FLi22664 fis, clone HSt08202	7.3
	45509 44230			gb:RC1-CT0279-070100-021-a06 CT0279 Homo saplens cDNA ESTs	7.3 7.3
	42545			Homo sapiens chromosome 19, cosmid R26894	7.3

	AEE997	AW896238	() - 224DAC	Homo saplens cDNA FLJ14604 ffs, clone NT2RP1000363, m	7.3
		AW578160	Hs.334805 Hs.100729	KIAA0692 protein	7.3
	424563	AA446932	Hs.151428	re! finger protein 2	7.3
_		AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein 1	7.3
5	453902	BE502341	Hs.3402	ESTs COTo	7.3 7.3
	446842 454128	A1343510 AL031259	Hs.176992 Hs.41639	ESTs programmed cell deeth 2	7.3
	427011	BE302729	Hs.173162	neighbor of COX4	7.3
10	450872	AI742594		gb:wg55h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	7.3
10	451512	AI800236	Hs.207080	ESTS	7.3
	406708 432576	Al282759 AW157424	Hs.165954	gb:qt84z01.x1 NCt_CGAP_Co14 Homo saplens cDNA done i ESTs, Waskly similar to t38022 hypothetical protein (7.3 7.3
	459304	AW005809	Hs.281076	ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELIC	7.3
	401375			NM_020999*:Romo sapiens neurogenin 3 (NEUROG3), mRNA.	7.3
15	413258	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo septens cDNA	7.3
	406016	DE202708	Hs.105097	Target Exon ihymidine khase 1, soluble	7.3 7.3
	421506 422742	BE302796 AA316117	Hs.337128	ESTs	7.3
••	440031	BE045970	Hs.244746	ESTs	7.3
20	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PLACE1005111	7.3
	449656	AA002008	Hs.188633	E8Ts	7.3
	444310 459274	A1140432 AA382590	Hs.175936 Hs.170980	ESTs KIAA0946 protein	7.3 7.3
	425404	BE048060	Hs.133494	Homo sapiens clone TCCCIA00164 mRNA sequence	7.3
25	431150	T63857	101100101	gb:yc16e01.s1 Stratagene lung (937210) Homo saptens c	7.3
	443217	NM_001545		immature colon carcinoma transcript 1	7.2
	413405	AW022253	Hs.215976	ESTs	7.2 7.2
	447653 414704	BE327277 NM_014757	Hs.161145	ESTs mastermind (Drosophita), homolog of	7.2
30	424046	AF027866	Hs.138202	sertne (or cysteine) proteinase Inhibitor, dade 9 (o	7.2
	409188	AW3632B4	Hs.32553	EST8	7.2
	453493	AL039478	Hs.304447	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	456111	AK000150	Hs.78185	MAX-like bHLHZIP protein	7.2 7.2
35	400297 446364	A1127076 AB006624	Hs.334473 Hs.14912	hypothetical protein OKFZp564O1278 KIAA0286 protein	7.2
55	432216	AU078609	Hs.2934	ribonuclegilde reduciase M1 polypeptide	7.2
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine protease	7,2
	446936	AWB16036	Hs.151251	ESTs	7.2
40	418469 414907	U34879 X90725	Hs.85279 Hs.77597	hydroxysteroid (17-beta) dehydrogenase 1 polo (Drosophia)-like kinase	7.2 7.2
70	429065	A1753247	Hs.29643	Homo sagions cDNA FLJ13103 Es, clone NT2RP3002304	7.2
	424568	AF005418	Hs.150595	cytochrome P450, subtamily XXVIA, polypeptide 1	7.2
	416450	AA180467		gbzp14g08.s1 Stratagene felal refina 937202 Homo sap	7.2
45	449714	AB033015	Hs.23941	KIAA1189 protein	7.2 7.2
45	455447 437154	AW947507 AI023133	Hs.10739	gb:RC0-MT0002-140300-011-a12 MT0002 Homo sapiens cONA ESTs	7.2
	423059	AW378445	Hs.123080	Homo sapiens unknown protein mRNA, partial cds	7.2
	419092	J05581	Hs.89603	mucin 1, transmembrane	7.2
50	426736	AA431615	Hs.130722	ESTs	7.2
20	417748 434748	Z43011 A1862604	Hs.21169 Hs.211884	ESTs ESTs, Weskly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2 7.2
	438929			ESTs	7.2
	452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	7.1
55	446416		Hs.163959	EST8	7.1
55	415023 434766		Hs.133494 Hs.120634	Homo saplens clone TCCCIA00164 mRNA sequence ESTs	7.1 7.1
	432566			ESTs, Weakly similar to 2109260A B cell growth fector	7.1
	420252			ESTs	7.1
<i>6</i> 0	435403		Hs.269658	EST ₅	7.1
60	430151	AW968203 AA417272		gb:EST380398 MAGE resequences, MAGJ Homo saplens cDNA	7.1 7.1
	427908 417758		Hs.24122 Hs.82535	ESTs solute carrier territy 6 (neurotransmitter transporter	7.1
	40009B		12.0200	Eos Control	7.1
CF	412647			gb:EST387196 MAGE resequences, MAGN Homo saplens cDNA	7.1
65	437234		Hs.247711	hypothetical protein FLJ20557	7.1 7.1
	453366 425803		Hs.28921 Hs.211408	zinc finger protein ESTs	7.1
	447383		HOLETTOD	gb:yx22a11.r1 Soares melanocyte 2NbHM Homo saplens cD	7.1
	423864		Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	7.1
70	450799			gh: UF HF-BM0-edit-g-12-0-UI.r1 NIH_MGC_38 Homo sapiens	7.1
	409592			EH-domain containing 4 activating transcription factor 1	7.1 7.1
	453945 425196			carbonic anhydrase il	7.0
	439776			putative transmembrane protein	7.0
75	417662	R07478	Hs.268845	ESTs	7.0
	438087		Hs.190422	ESTS	7.0
	452724 448633		Hs.30464 Hs.21635	cyclin E2 ໂປວນນຶກ, gamma 1	7.0 7.0
	433154			ESTs	7.0
80	440094	A1651558	Hs.270372	ESTS, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.0
	409253		Hs.52002	CD5 antigen-like (scavenger receptor cystelne rich fa	7.0
	431270 407629			gb:hn41e11.x1 NCL_OGAP_RDF2 Homo saptens cDNA clone 3 ESTs	7.0 7.0
	-rv+ u2:			-415	

5 10 15	445439 427106 408623 426561 408492 428894 419102 429067 422684 424701	AL117452 Hs.4: BE243084 Hs.1: AA398193 Hs.9: AA398193 Hs.2: AA391661 Hs.1: AA437066 Hs.4: AA446019 Hs.1: BE561617 Hs.1: AA322599 Hs.1: AA322599 Hs.1: AA322599 Hs.1: AW449233 Hs.1: W26276 Hs.1: NM 006410 Hs.9:	regulator of nonsense transcripts 1 7.0	
20	439575 407027	W79259 U63312	gbzd/75c06.r1 Soares_fetal_heart_NbRH19vV Homo septens 7.0 gb:Human cosmid LL12NC01-242E1, ETV6 gene, exons 1B a 7.0	
	Table 15	В		
25	Pkey: CAT num Accessio	iber: Gene cluster n	et identifier number er n numbers	
	Pkey	CAT Number	occessions	
30	_		AND THE AND TH	
35	409113	104479_1 110079_2	\adatasa aadstoo aadssa41 \adatasa aadtasa aadtasa \adatasa aattasa aadtasa aadtas \adatasa aadtasa aadtas \adatasa aadtasa aa	AA083070 AA079209 AA070053 AA071110
40	409206 409857 410146 410536 41129B	1108161_1 1156298_1 1178974_1 1207322_1 1237955_1	AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929 AW384844 AW364847 AW937534 AW937593 AW937659 AW591908 AW502999 AW502540 AW592655 ROS927 RO6916 N39533 AW753084 AW753093 AW838586 AW835886 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW	
45	412406	1293055_1	AW835848 AW835851 AW835852 AW835862 AW835855 AW835855 AW835847 AW835838 AW948172 AW948178 AW848169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW	
50	412647 413258 413314 413500 414076 416450	1317804_1 1355998_1 1360034_1 1373933_1 141490_1 159561_1	AW948177 AW948171 AW948183 AW948173 AW975090 N44182 BE076514 BE075283 BE076518 BE081585 BE081717 BE081863 BE081794 BE081659 BE144914 BE994989 AA457735 AA135210 AW968166 AA457804 AA180467 AA449184 AA464831 AA505048	
	417247 417739	1660859_1 1696198_1	N58024 T58194 T11693 N64222 T05B48 Z43B95 R12357 R34740	
55	417081 418347	170544_1	A1879117 AW161351 Z45765 BE003661 AA206949 AA476541 AA216419 F03238 AA229517	
60	422429 423573 426561 428294 430145	229714_1 269158_1 269365_1 313562_1	AA310527 AW962205 Z44865 H08641 AA328504 AA327783 AW982370 AA381437 AA628833 AW407275 AA425488 AA495895 F23221 AW816330 AW968170 Al732687 Al732725 AA468343 AA467817 AW063961	
65	430151 430709 430848 431150 431270 432363 434197	322338_1 324621_1 328626_1 330676_1 345469_1	AW968203 AT732757 AA470353 AA468025 AA468479 A1734161 R34356 AW969880 AA484613 AW021726 AA487752 AA488065 T63857 AW971220 AA493469 T63699 BE046609 BE046118 AA501604 AA534489 AW970240 AW970323 AA6324223 AA643443 AA650619 AA543463 AA643453 AA643438 AW802964 AW821585 AW821684 AA643431 AA6434	132
70	434407 434410 436910	385744_1 385798_1	AW827513 AW815333 AW815409 AA632563 AA632644 AA635376 AA664188 AA926944 AA767974 AA737237	
	437056	3 432282_1	A1147061 AA743380 AA765223 AW976398 AI803927	
75	439354 439573 444314 447197 447383	4 47146_1 5 47400_1 4 600667_1 7 711623_1 3 71990_1	AF086174 W31798 W04694 W79259 AF086396 W73927 A1140497 AW749625 AW749626 AW749644 R36075 A1386548 R35167 N24231 BE617964 N36313	
80	450794 450872 454354 454634 454764	2 849959_1 6 1130264_1 9 1227728_1	AW407504 W31274 AI738877 AI742594 AI761397 R31198 AI819332 R31257 AW812535 AW812536 AW380307 AW811633 AW811652 AW811898 AW819529 AW854320	
			227	

	455037 455098	1249783_1 1253078_1	BE144549 AW851677 AW851643 AW851711 AW851719
	455161	1256167_1	AW856718 AW855740 AW855748 BE145900 AW859906 BE145895 BE145831 BE145914 BE145820 BE145817 BE145890 BE145908
5	455410	1288380_1	AW936678 AW936637 AW936882 AW936685 AW936817 AW936811 AW936762 AW936653 AW936815 AW936812 AW936683 AW936822 AW936823 AW936821 AW936732 AW936730 AW936781
	455447 455855	1292444_1 1375834_1	AW947507 AW947509 AW947791 BE008335
	455994	1398737_1	BE147440 BE147708 BE147563 BE147456 BE179190 BE179206 BE179162 BE179185 BE179186 BE179194
10	457892 458080	432926_1 471050_1	AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698 BE142728 AA834047 AW837124
	458115	47705_29	9E091597 8E091730 8E091577 BE091655 BE091728 RE091640 RE091578 RE091777 RE091803 RE091608 RE091731 RE091777 RE091803 RE091777 RE09177 RE0917
			AVV992912 BEUBB/91 BEBB/955 BEOB3504 BEDB3455 AW997967 AW997991 BE166595 AW843686 AW84334 BE079091 AW603391 BE081427 BE079514 BE184580 BE009962 BEDB9722 AW579912 AW866561 AW890184 AW705776 AW967410 AW804314 AW814334 AW705776 AW967410 AW804314 AW814334 AW705776 AW967410 AW804314 AW814334 AW805776 AW967410 AW804314 AW814334 AW805776 AW967410 AW804314 AW814334 AW805776 AW967410 AW804334 BE081427
15			AYY0020 IS DEU/0924 DEUROBA HER/0957 HER/0921 AW774106 HERI1060 AW768100 AR76927 AW769240 AM067796 DEGGG449 AM769290
15			AI547161 AW844767 AW393596 AW579444 BE083334 AI547158 AW799883 AASB5179 AW982792 AW882215 BE011913 AW997894 AI547159 AW992772 AW581778 AAQ922A7 AW843916 BE079190 AW878478 BE083648 BE066454 AI469937 AW393594 AW579696 AW939276 BE173265
			AW878631 AW878638 AW992802 BE079913 AA633638 AW369008 BE076590 AW843456 AW992791 BE173247 AW843921 AW843333 AW678934 BE090236 BE078240 BE066325 AW603276 BE169310 AW817299 BE091841 BE000160 AW898164 AW994624 AW998991 AW862797 AW889438
20			AW/0000/ AW93000 AW94001/ AI200402 BE167391 AW939319 AW799837 AW939983 AW990881 DE6794 98 AMADED DE679666 AMDD 264
20			BEU70544 AW80372 BE061223 AW939237 BE064239 A1774202 BE077604 BE078026 AA512912 A1124908 A1147524 A1884882 AW939962 AW939254 BE171687 AW998400 AW998348 AW998353 AW998383 AW998393 AW998393 AW998392 AW998392 AW998393
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25		•	AW8000859 AW801017 AWS81371 BE098300 AW995341 BE098233 AW663788 BE191739 BE080113 AW678162 AW799799 AW992396 AW994673 BE186170 AW792778 AW663225 BE076590 BE080111 AA662934 BE090227 Al475441 BE086884 BE090222 AW681366 BE010705 AW898740
			DEBROTO AW9923/5 HEU/7833 HEUR3557 HEDIGER AW999450 AWR03434 REGROODE AAEGGGG DEGGGGG DEGGGGG REGGGGG
20			BEOUTING ARTHUR BEOTINGS BEOUGSES BEOUGSES AA973929 BE185724 MORSACES BE185743 BED1342 BED15476 AD00289 AM789056 BEOGRAFIA AWRATING AM7601410 BED101542 BED101544 BED10154 BED10154 BED101544 BED10154 BED10154 BED10154 BED101544
30			AVVIUUT 14 SEUBD/57 A4480195 AA491145 AA772914 AA632730 AA53R388 REDRINGS RE186440 DECODARG AMBAGA92 DECODARG A
			AW839003 BE006145 BE085405 BE008880 BE081428 AW581373 AW507246 BE034328 BE001338 AW886170 BE074119 AW884149 BE091734 BE009744 AI540867 BE185808 BE080183 BE185858 AA476398 BE081040 BE074724 BE085426 BE074725 AW998297 AW867608 BE185788
			AW898734 BE078389 BE081672 BE088178 AA610284 BE088118 AA284217 AW578085 BE074518 BE001358 BE001328 AW820227 AW608196 AW868190 AW8045848 BE008526 BE012037 BE075061 BE005870 AW867804 AW878433 BE008751 BE005876 BE008748 BE093440 BE183050
35			ANDICOTO DELUTIZA BELLERIA MELIKITIZA HERRIKAT BIXARIARRA DIVIDARRA BIXADARRA BIXADARDA ALBADARDA REPORTADA BIXADARDA BIXADA BIXADARDA BIXADA BI
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40			AW842067 BE008678 BE008670 BE551820 AW838974 BE081637 BE048696 BE003673 BE010328 BE003250 BE089514 BE082052 BE081424 BE001678 AW581363 AA503194 AW883721 AW883522 BE08564 AW888771 BE171078 BE078249 BE078194 AA565255 BE083486 AW942081
			AMO42090 AMO60204 BEU00/17 AA484369 AB31719 AM997365 BED79327 AA503956 BED91999 AM793852 BED80251 BED78086 BED92515 BE170364 AW866183 AW067958 BE008042 BE008761 BE0081671 AW867400 BE082003 BE082033 BED824470 BED84480 BE084480
			AYYOUUUU AADU1//X AWSSSSI/ BEDSS/SS HETRISIS AAAGIIISI AWRGSYGG ANATRIBOS RESEALAD DEGGEED DEGDAGGA ANADGSSIG DEGGAGGA
45			AW866792 AW753605 BE082045 BE081106 BE008373 BE075399 AW958828 AW578707 BE084305 AW753604 BE185916 AW842220 BE185222 BE008192 BE008795 AW578706 BE080256 BE183984 AI934532 AA449648 AW578699 BE150514 AW883680 AA493568 BE085748 AW753601
			BE150562 AW892677 BE091797 AW899123 BE081679 BE080121 AW506787 AW603410 BE001317 AW805789 BE150513 BE092206 AW898343 BE068922 BE008805 AW844759 AW600009 BE160487 AW750728 BE150491 BE160515 AW806010 BE160508 BE008718 AW578702 BE150509
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55			BEU/34/I AWB339/2 AWB0/923 AWB020I AW/39//2 AWB2462 AWB02451 BE505041 BE161537 AW802206 AWB50404 AWB6055 BE007843 AWB0332 AW80247 AWB90419 AWR60405 EMB2042 AWS70201 BE183386 AWB50140 BETFEET FETTERED AWB50404 BE1850 AWB5040
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60			BE082513 BE183342 AW789806 AA442935 BE092268 AA580022 AW843219 BE093306 BE092275 BE087111 BE183392 AW842976 BE183697 BE183895 BE185276 BE082343 AW846219 BE079199 BE092272 AA586687 AW946109 AW946175 AW946184 BE008365 BE078172 BE085673
			050/0240 0500199 050/0004 050/9196 AW8/6636 AW799803 REMITSER REMITSER REMAINS AMADOSOD DEDOLOGO DERICAGE ALABOSOD
			BE003407 BE008410 AW842670 AW603738 BE088661 AA484571 AT799184 BE174545 BE001405 AA436967 AW99584 AW995785 AW896598 AW883999 BE075967 AA503938 BE092281 BE092279 BE087460 BE087569 BE081542 AI375386 AW843886 BE080115 BE171517 BE079898
65			AW882382 BE001450 BE076430 AW579377 BE008412 BE008790 BE182298 BE182297 BE078805 AW899132 BE078810 BE185867 BE087790 AA84928 AW578955 BE008400 BE074080 AW805101 BE076110 AW799904 AI205084 BE008370 BE182345 BE182373 BE008401 AA84441
			##102902 BE1023/2 BE008414 BE078185 BE010185 RE010187 RE010167 RE014008 BE072338 BE403370 AMPRASE AFACOS AT
			DEUTITUU AAASAO (9 BENZEISE BETISSIS) BENZEIST AASTSUST AWBEZST 9 EEXST AAATRAT AASSIG13 BE182365 AW821838 AW028827 BE008413 AW82605 AASTG658 AATG672 BENZEISE AASTG658 AASTG658 PENSARS AASTG672 BENZEIST AW82705 AW82705 AASTG658 AW82705 AW
70			Al241060 AW802041 AW802005 BED11244 BE087051 AAS84758 AA452997 AW892786 AW797500 BE077829 BED38402 AW881760 BE083516 AW802084 AW369007 BE185123 BE087775 AW801018 BE093443 AW867978 AW843271 BE173850 AW997859 BED10620 AW982516 AW843908
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			AACO/100 AW93C913 AW13C931 BEDV1453 AW841903 BEDV17613 AW5/T/500 BED81473 AW932558 BED11065 AW843187 AW867390 AW898296 BED74333 AASO1697 AW745997 PRI767629 AW8A7501 PEDRST48 AWR04879 DED746743 AW93C90 A ABSTED AMSTED A ABSTED AMSTED AM
			AW997932 AW899099 AW842706 AW890727 AW843175 BE075428 AW843155 AW842679 AW842708 BE069915 AW842721 AW438792 AI251478 BE069911 BE087054 BE079889 BE075453 BE069927 AA491920 BE170506 BE182305 BE060052 AW843406 BE011076 BE075869 AA525261
80			ANNOUN O DEUTYZIZ ARCONIO BEGTONIO ARAGONIO ARAGONIO ARAGONIO ARAGONIO DEUTZECO A A SEGURA DEUTZECO A SEGURA DEUTZECO A DEUTZE
G.			ECUCRY 19 A-7-13988 BI-D75376 AAR84500 AVISBUSSS BED77372 AAS03571 AVR84724 AVR861124 AVR86454 AVR77502 AVR77489 AVY79829 AVS92545 BID75806 AVR9468108 BI-SEXSIER AAST75818 BID177582 AVR846724 AVR860124 AVR8
			PSV(*) 12 (*) 12 (*) 14 (*) 27 (*) 15 (*) 15 (*) 17 (*) 17 (*) 17 (*) 17 (*) 18
			AW842868 AW868310 BED11071 BED75429 AW843152 AW905848 BED75397 AW842762 BED75402 BED7590 AW837810 BED75998 BE183965
			/38

BE075431 AW815917 AW998359 AW799883 AW603782 AA557480 AW841444 BE075915 AA548034 AW843393 AW391559 BE083265 AW939721 AW800857 AW079109 AW364901 Al435993 AA985526 AW799848 BE182463 AA776111 AW799916 BE008399 BE075377 AW577809 BE010272 BE182443 BE010295 AW577806 BE008415 BE184036 BE076597 Al817413 AW795053 AW896761 AW841433 BE182458 AW603796 AW842676 BE085455 AW888879 BE075414 AW838836 AW878273 AW999088 AW799778 AW899125 BE08247 AA714670 BE001401 BE001408 AW817297 AW796670 AW394063 BE001396 AW384070 AW603797 BE182447 AW562483 AW843283 AW749520 AW867449 AW899274 AW578232 AW603765 AW843919 AW578235 BE184139 AW897742 BE183923 BE084210 AW802033 AW748724 AW39018 AW997459 AW842742 AA213697 5 BE182308 BE011078 AW807702 AW882623 BE080016 AW580994 BE076531 AA443462 AW607407 AW883382 AW939399 AW606627 AW844615 BE18230B BE31107B AW007102 AW03223 BEIDBUT 10 AV930335 BEJ07031 AW339724 AW01697 MC03306 AV5935359 AW003627 AV644616
AW039724 AW815931 AW883765 AA287421 BE075626 AW946171 AW841445 BW737994 AW815957 AA683300 AW369004 BE075586 BE081560
AW005626 AW939398 AA507280 AA506317 AW941230 AW992519 AA466332 AA425246 BE090234 BE090236 AA483259 AA451961 AA535566
AA506406 AA888571 AA503588 AA507130 AA532944 AA501672 BE168634 AA492022 AA507662 AW842286 AA494226 AA776038 AA442419
AW579900 BE171816 AA683065 AA491916 AA447490 AA461423 AA434543 AA243279 AW997466 AW603740 BE000295 AA658571 10 15 TABLE 15C Unique number corresponding to an Eos probeset Pkey: Sequence source. The 7 digit numbers in this column are Genbank klentiller (Gi) numbers. "Dunham I. et al." refers to the publication entitled "The DNA Ref: sequence of human chromosome 22.* Dunham I. et al., Nature (1999) 402-489-495. Indicates DNA strand from which exons were predicted. 20 Strand: Nt_position: Indicates nucleofide positions of predicted exons. Strand Nt_position Pkey Ref 25 400715 8118885 Minus 80151-80297 149447-143851 400736 8118985 Plus 81421-81551,82354-82512,82862-82938 401008 8117391 Minus 401069 3927852 Minus 45682-45B31 6121-6766 401375 7417809 Minus 30 401405 69276-69452,69548-69958 7768126 Minus 62028-62608 112785-112924 401539 B072433 Minus 401557 2099966 Minus 64695-64797 9097132 Minus 401854 153460-153592 401940 3738108 Plus 35 173835-173998 141714-141842,142010-142122 402025 7547159 9796503 B13B477 402442 Plus 402832 147522-147795 Minus 6128-6265,6416-6689 402796 3646083 Minus 33518-34546 290021-290284 109532-110225 402967 5360987 Mirus 40 403038 403055 7717439 8748904 Minus Minus 183883-184026 403310 8139936 Minus 84481-84655 21201-22223 403397 943836B Minus 403939 4176355 Plus 45 404110 9212839 18344-18510 Minus 404495 8151634 59449-60477 Minus 404534 8247909 Minus 147853-148086 404630 404649 9796665 Plus 74495-74715 100027-100399 9796926 Minus 50 159810-159979,160213-160321,161023-161304,162862-163140,164490-164644,166404-168530,166936-167083,167392-167522 404880 9797204 Minus 404914 7341760 92603-92827 Plus 50704-51499 133807-134053 4753290 7656675 405417 Mimus 405454 Plus 405510 7630909 101028-101174 Minus 55 405514 9454624 164091-164162,164397-164516,166720-186790,167785-167935 41341-41940 85953-36151 405536 9795661 Plus 406016 8272861 Plus 115806-116104 406410 9256394 Minus 406464 9789674 Pius 72161-72562 60 406562 7711584 Plus 37316-37426 TABLE 16A: 200 GENES DOWN-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX 65 Table 16A shows 200 genes down-regulated in corvical cancer compered to normal adult cervix. These were selected as for Table 15A, except that the numerator and denominator were switched, the median value emongst normal centres was greater than or equal 40 units, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in turnor vs. normal cervis). 70 Pkey: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number UnigeneiD: Unigene number Unigene Title: Unigene gene title RI: Retio of cervical cancer to normal cervix 75 R1 Pkey ExAcon UnigenelD Unigene Title Hs.62905 453596 AA441838 hypothetical protein FLJ14834 443912 R37257 Hs.184780 ESTS 80 AF097021 13.6 13.1 420923 Hs.273321 differentially expressed in hematopoletic lineages 414422 AA147224 Hs.337232 Homeo box A13 Hs.94694 Homo sepiens cDNA FLI10561 fis, clone NT2RP2002672 420058 AK001423 412639 AW961284 Hs.296235

	418994	AA296520	Hs.89546	selectin E (endothelia) adhesion molecula 1)	12.4
	407938	AA906097	Hs.85050	phospholamban	11.3
	410544	AI446543	Hs.95511	ESTs	11.3
5	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	11.1
3	423690 420874	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 protein [H.saplens]	11.0
	453060	NM_000055 AW294092	Hs.1327 Hs.21594	butyrylcholinesterase hypothetical protein MGC15754	10.9 10.6
	424765	AA428211	Hs.284256	hypothetical protein FLJ 14033 similar to hypoxia induci	10.5
10	452106	Al141031	Hs.21342	ESTB	9.5
10	428780	A1478578	Hs.60636	ESTs	9.5
	431706 419589	A1816086 AW973708	Hs.296341 Hs.201925	edenyiyi cyclase-associated protein 2 Homo sapiens cDNA FLJ13446 fis, clone PLACE1002968	9,2 9,0
	430468	NML,004673	Hs.241519	angiopoletin-like 1	9.0
1.5	443790	NM_003500	Hs.9795	acyl-Coenzyme A exidase 2, branched chain	8.7
15	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activit receptor inte	8.6
	401486 417511	NA At 040476	13- paggs	C4000647*:gi[4758508]ref]NP_004253.1[airway trypsin-li	8.4
	429900	AL049176 AA460421	Hs.82223 Hs.30875	chordin-like ESTs	8.3 8.2
	411908	L27943	Hs.72924	cylidine deamhase	8.0
20	408134	AK000184	Hs.42945	acid sphingomyskasse like phosphodiesterase	8.0
	448543	AWB97741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp588P1124 (from clone DKFZp	8.0
	437846 421666	AA773866 AL035250	Hs.244569 Hs.1408	esophagus cancer-related gene-2 endothelin 3	8,0 7.9
	450164	At239923	Hs.30098	ESTs	7.9
25	412642	BE244598	Hs.809	hepatocyte growth factor (hepepoletin A; scatter factor	7.7
	425608	AA360486	Hs.92448	ESTa	7.6
	442748	AI016713	Hs.135787	ESTS	7.3
	415672 414175	N53097 Al308876	Hs.193579 Hs.103849	ESTs hypothetical protein DKFZp761D112	7.2 7.2
30	409601	AF237621	Hs.B082B	keretin 1 (epidermolytic hyperkeratosis)	7.0
:	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nucleotide pyroph	6.7
	414214	D49958	Hs.75819	glycoprotein M6A	6.5
	436637 408621	A)783629 A)970672	Hs.26766 Hs.46638	ESTs chromosome 11 open reading frame 8	6.5 6.5
35	432101	AI918950	Hs.123642	EphA3	6.3
	45B440	A1095468	Hs.135254	Horno sapiens clone 1 thrombospondin mRNA, complete cds	6.3
	424153	AA451737	Ha.141496	MAGE-like 2	6.3
	420228 418390	R25023	Hs.12369	ESTs	6.2
40	444931	AF133820 AV652066	Hs.84665 Hs.75113	titin immunoglobulin domain protein (myotilin) general transcription factor IIIA	6.1 6.1
	449394	AA004368	Hs.18160	Homo saplens cDNA FLJ11550 fis, clone HEMBA1002970	6.1
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	6.1
	410425 410765	BE278367 Al694972	Hs,63510 Hs,66180	KIAA0141 gene product nucleosome assembly protein 1-like 2	6.0 6.0
45	424973	X92521	Hs.154057	matrix metalloproteinase 19	6.0
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like 1	5.9
	429414	A1783656	Hs.202095	empty spiracles (Drosophita) homolog 2	5.9
	440594 45276B	AW445167 AW069459	Hs.126036 Hs.61539	ESTs ESTs	5.9 5.9
50	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 protein [H.sapiens	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
	425010	T16837	Hs.4241	ESTs	5.9
	426342 437980	AF093419 R50393	Hs.169378 Hs.278436	multiple POZ domein protein KRAA1474 protein	5.8 5.8
55	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	- 5.7
	404097	NA		C5000242*:gf 9369379 gb AAF87128.1 AC006434_24 (AC00643	5.7
	422546	AB007989	Hs.301478	KIAA0500 protein	5.7
	445872 429999	Al681573 Al761902	Hs.288671 Hs.99597	Homo sepiens cDNA FLJ11997 fis, clone HEM881001458 ESTs	5.7 5.6
60	453354	W55946	Hs.234863	Homo sapiena cDNA FLJ12082 fis, close HEMBB1002492	5.6 5.6
	442082	R41823	Hs.7413	ESTs	5.5
	452073	AA625150	Hs.82098	ESTs	5.4
	430032 408767	AW936136 AA057279	Hs.99610 Hs.211928	ESTs ESTs	5.4 5.4
65	433234	AB040928	Hs,65366	KIAA1495 protein	5.3
	431708	A1698136	Hs.108873	ESTS	5.3
	421200	AA284811	Hs.264433	ESTs	5.2
	435133 409643	AJ010482	Hs.31412	Homo saplens cDNA FLJ11422 fls, clone HEMBA1001008	5.2
70	416676	AW450866 AW392022	Hs.257359 Hs.79507	ESTs KIAAQ582 prolein	5.1 5.1
	420357	U94333	Hs.97199	complement component C1q receptor	5.0
	417355	D13168	Hs.82002	endothelin receptor type B	5.0
	423448	AK000778	Hs.128753		5.0
75	430965 419958	AA489732 X04430	Hs.154918 Hs.93913	ESTs Interieukin 6 (mierieron, beta 2)	4.9 4.9
. —	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	4.8
	404485	NA		Target Exon	4.8
	429594	AK001128	Hs,210297	Homo sepiens cDNA FLJ10266 fis, clone HEMBB1001024	4.B
80	417692 432304	R09338 AA932186	Hs.50724 Hs.69297	Homo saplens cDNA FLJ10934 fis, clone OVARC1000640 ESTs	4.B 4.7
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.7
	448851	A\$582207	Hs.177166	ESTs	4.7
	405523			CB001409*:gl[7441226 pirl[S31212 collagen alpha 1(XIV)	4.7

	450656	AA010539	Hs.18912	ESTs	4.6
	422942	AF054839	Hs.122540	tetraspan 2	4.6
	401479	T49304	Hs.110950	Rag C protein	4.6
5	444192 439648	AW469413 AW780192	Hs.161145 Hs.267696	ESTs ESTs	4.6 4.5
J	41037B	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4	4.5
	444702	AJ220122	Ha.326560	hypothetical protein MGC2780	4.5
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALUB_HUMAN ALU SUBFAMILY SX	4.5
10	452249 430376	BE394412 AW292053	Hs.202095 Hs.12532	empty spiracles (Drosophila) homolog 2 chromosome 1 open reading frame 21	4.5 4.5
10	411037	BE145915	Hs.99472	ESTs	4.4
	442B03	AJ675298	Hs.199917	ESTs	4.4
	414831	M3115B	Hs.77439	protein kinase, cAMP-dependent, regulatory, type il, be	4.4
15	400628	NA NA	II- TECOO	C10001871:gi 1705533 sp P32018 CA1E_CHICK COLLAGEN ALP	4.3
13	414629 437110	AA345824 ALD49240	Hs.76668 Hs.144995	carboxylesterase 1 (monocyte/macrophage serine esterase ESTs	4.3 4.2
	410646	W7940B	Hs.50745	ESTs	4.2
	456304	AI820973		gbtnc21c02.y5 NCI_CGAP_Pr1 Homo septens cDNA clone, mRN	4.2
20	401270			Target Exon	4.2
20	419447 414807	BE092696 A)738616	Hs.75928 Hs.77348	ESTs hydroxyprosteglandin dehydrogenase 15-(NAD)	4.2 4.2
	427019	AA001732	Hs.173233	hypothetical protein FLJ 10970	4.2
	434469	AA634806		gbtab28c02.rt Stratagene lung (937210) Homo saptena cDN	4.1
25	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR	4.1
25	418947	W52990	Hs.22860	ESTs	4.1
	416434 454736	AW163045 BE184348	Hs.79334	nuclear factor, interieukin 3 regulated gb:CM0-HT0676-010500-355-e11 HT0676 Homo saptens cDNA,	4.0 4.0
	407945	X69208	Hs.606	ATPase, Or transporting, alpha polypeptide (Menkes synd	4.0
	447499	AW262580	Hs.147674	protocadherin beta 16	4.0
30	430686	NM_001942	Hs.2633	desmoglein 1	4.0
	409882	AJ243191	Hs.66874	heat shock 27kD protein family, member 7 (cardlovascula	3.9
	419047 414272	AW952771 Al651603	Hs.90043 Hs.46988	ESTs ESTs	3.9 3.9
	443808	AW377736	Hs.12420	ESTS	3.9
35	426883	H21520	Hs.35088	EST6	3.9
	410659	AI080175	Hs.68826	ESTs	3.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.9
	432181 422890	AA527650 Z43784	Hs.156037 Hs.75893	ESTs ankyrin 3, node of Ranvier (ankyrin G)	3.9 3.8
40	453296	AA034413	Hs.62560	ESTs	3.8
	400878	NA		Target Exon	3.8
	401103	NA		C12001233:gij7305361 ref NP_038652.1 ctogelin [Mus mus	3.8
	436670	A1690021	Hs.201536	ESTs	3.7
45	432251 408793	AW972983 BE258371	Hs.232165 Hs.254660	polycythemia rubra vera 1; cell surface receptor ESTs	3.7 3.7
	419093	At804054	Hs.112885	spinal cord-derived growth factor-B	3.7
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.7
	450776	NM_007250	Hs.320861	Kruppel-like factor 8	3.7
50	437140	AA312799	Hs.283689	activator of CREM in testis	3.6
50	418421 443476	R58620 AW068594	Hs.85050 Hs.133878	phospholamban ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN	3.6 3.6
	417194	N53793	*13.1000,0	gb:yz07a01.r1 Soares_multiple_sclerosis_2NbHMSP Homo sa	3.6
	443567	AI077540	Ks.134090	ESTs	3.6
55	451879	Al821030	11. 40.44	gbryb52f11.y5 Stratagene overy (937217) Homo sapiens cD	3.6
22	421013 451896	M62397	Hs.1345	mutated in colorectal cancers	3.5
	413237	AF196304 AJ468574	Hs.27197 Hs.171965	SUMO-1-specific protezse ESTs	3.5 3.5
	424636	AA453734	Hs.10198	ESTs	3.5
co	43266D	A128B430	Hs.64004	ESTs	3.5
60	414681	AL079440	Hs.74002	nuclear receptor coectivator 1	3.5
	400802 430015	NA AW768399	Hs.112157	Target Exon ESTs	3.5 3.5
	45197B	AW813747	Hs.27371	Homo saptens mRNA; cDNA DKFZpS66J123 (from clone DKFZp5	3.5
~~	449088	AI654048	Hs.198556	ESTa	3.5
65	425113	A1936992	Hs.154658	plackskin and Sec7 domain protein	3.5
	458459	AJ124553	Hz,48965	Home saplens cDNA: FLI21693 fis, clone COL09609	3,5
	420249 401159	BE262895 NA	Hs.276916	nuclear receptor subfamily 1, group D, member 1 Target Exon	3.5 3.5
	442789	AW904361	Hs.131191	ESTS, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQ	3.5
70	426083	AW982712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5 [H.saplens]	3.4
	407118	AA156790	Hs.262036		3.4
	423587	AA328074	Hs. 284256		3.4
	443178 430694	AI631241 AA810624	Hs.47312 Hs.30936	ESTs ESTs, Weakly shriber to H2BH_HUMAN HISTONE H2B H [H.sap	3.4 3.4
75	423073	BE252922	Hs.123119		3.4
	437950	U79244	Hs.112642		3.3
	419368	AI753518	Hs.209464	KIAA1604 protein	3.3
	447335	BE617695	Hs.286192		3.3
80	451398 452814	A1793124 A1092790	Hs.144479 Hs.334703		3.3 3.3
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, expressed in pro	3.3
	412295	AWCB8B26	Hs.117176		3.3
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	3.3

	444216	DOE303	II. Opp	total of the b	
	418771	D25303 AA807881	Hs.222	integrin, alpha 9	3.3
		AA574091	Hs.25329	ESTs	3.3
	404584	AA3/4091	Hs.105964	ESTs	3.2
5	404195			Target Exon	3.2
_		AL135623	11- 100014	NM_015718*:Homo saplens NADPH oxidese 3 (NOX3), mRNA, V	3.2
		AA352090	Hs.193914	KIAA0575 gene product	3.2
		R47948	Hs.128003 Hs.188732	hypothetical protein FLJ21213 ESTs	3.1
		AA127133	18.1001-02		3.1
10	413607	T64741		gb:zl87e03.r1 Stratagene coton (937204) Homo sapiens cD	3.1
		A1093577	Hs.255416	gb:yc48f11.r1 Stratagene liver (937224) Homo sapiens cD	3.1
		AF023456	Hs.193558	hypothetical protein FLJ21986 protein phosphatase, EF hand cabium-binding domain 2	3.1
		AA205273	Hs.177011	hypothetical protain	3.1
		AA531287	Hs.105805	ESTs	3.1
15		AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-adrenergic race	3.1 3.1
		AC005013	Hs.149	cAMP response element-blading protein CRE-BPa	3.1
	433546	A1075877	Hs.125461	hypothetical protein FLJ11539	3.0
	430317	AB020645	Hs.239189	glutarinase	3.0
00	425130	AA448208	Hs.99163	ESTs	3,0
20		AB002351	Hs.10587	KIAAD353 protein	3.0
		AL122107	Hs.49599	Homo saplens mRNA; cDNA DKFZp434G0827 (from clone DKFZp	3.0
		AL133761		gb:DKFZp761C1413_r1761 (synonym; hamy2) Homo seplens c	3.0
		AI02567Q	Hs.109308	ESTs, Weakly similar to leucine-rich glioma-inactivated	3.0
25		H10207	Hs.47314	ES is	3.0
25		AW885909	Ks.6975	PRO1073 protein	3.0
		AI954365	Hs.42892	ESTs	3.0
		AA687415	Hs.28107	ESTs	3.0
	445175	AV652851	Hs.20255	ESTs .	3.0
30	T4011* 400				
50	TABLE 168				
	Pkev:	Informa Engl	probeset ident	for wimhor	
		r: Gene chuster	mumber	one remade	
	Accession:	Genbank acc	ession numbe	ire	
35		- white an	COOLDINATION IN THE COLD	no	
	' Pkey	CAT Number	Accessions		
	-				
	413156	135116_1	AA127133 A	A384396 AW958912 T72119	
40	413607	1379911_1		58393 BE152805	
40	417194	1657323_1	N53793 N53	716 N53739	
	434469	3B7447_1	AA634806 C	18732 AA729161 AA729860	1
	451879	888642_1	AI821030 T4	7128 Al821318	•
	453773	880699_1	AL133761 A		
45	454738	1232235_1	BE184348 A	W817453 BE01106B	
7.7	456304	176820_1	AJ820973 AJ	734077 A1B209B4 AA225796 AA225060 AA225101	
	TABLE 16C				
	Wiber 100				
	Pkey:	Unione numb	er comesnend	ling to an Eos probeset	
50	Ref:	Sequence so	eirce. The 7 d	igit numbers in this column are Genbank identifier (GI) numbers. "Dunha	em I of all a major to the major and a major and a
		SOUTH OF THE	нинан акоп	USOING 22. CUMBAM LET BL. NAMED A 1999 I 407-489-496	IN I SELECT TENSIS IN THE DUDICATION BUSINESS . LIVE DIVIN
	Strand;	moiceles DN	A strand from	which exons were predicted.	
	Nt_position:	Indicates nuc	lootide positio	ns of predicted exons.	
55	Diene	m.d	04-1	Alt As	
<i></i>	Pkey	Ref	Strand	Nt_position	-
	400628	3818355	Plus	41851-41984	
	400802	8567867	Minus	174571-174858	
	400878	9B64757	Plus	31493-32842	
60	401103	8568122	Minus	98330-98449	
	401159	6087118	Miras	3180-3953	
	401270	9797168	Minus	141659-141813	
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179	
	404097	7770701	Plus	55512-55781	
65	404195	3805917	Minus	39185-39332	
	404485	8096921	Plus	75166-75264,124038-124232	
	404584	9857511	Plus	138651-139153	
	405523	8454643	Plus	114550-114688,117255-117407,119490-119599,123237-123395,13114	IQ-131217
70				· · · · · · · · · · · · · · · · · · ·	·- ·-···
70					

TABLE 17A: 605 genes upregulated in testicular cancer retailve to normal body tissues

Table 17A lists about 605 genes upregulated in cervicel cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this enalysis was expressed as average intensity (Ai), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have encogenic function or of transducing intercellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or lon_transporter). Certain predicted protein domains are noted. 75

80 Pkey: ExAccn: UniGenelD: Pred.Prot.Domains:

Unique Eos probeset identifier number Exemplar accession number, Gentlank accession number UniGene number Certain predicted protein domains. Abbreviations used; TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M,

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likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
                                                           UniGene Title:
                                                                                                                                                                               UniGena gene title
                                                                                                                                                                             95th percentile of cervical cancer Als divided by the 50th percentile of normal tissue Als, where the 10th percentile of all normal tissue Als was subtracted from
                                                                                                                                                                             both the numerator and denominator
           5
                                                           Pkey; ExAcon; Unigenel D; Unigene Title; Pred. Prot. Domains; R1
                                                            408522; A/541214; Hs. 46320; Small proline-rich protein SPRK (human, ; none, Cornifir; 33.942)
                                                         408522; Al541214; Hs.46320; Small proline-rich protein SFRK [human.; none, Cornifin; 33.942
422166; AA586894; Hs.112408; S100 calclum-binding protein A7 (pscrias; efhand, S_100;TM=M;SS=N; 33.05
424098; AF077374; Hs.19322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 22.856
422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.604
433091; Y12642; Hs.3195; brighocyte antigen 6 complex, locus D; UPAR_LY6; toxkn,Activin_secp;TM=M;SS=Y; 27.95054945
433091; Y12642; Hs.3195; brighocyte antigen 6 complex, locus D; UPAR_LY6; toxkn,Activin_secp;TM=M;SS=Y; 27.95054945
431948; L42583; Hs.334309; keratin 6x; filament,RhoGAP,DUF286,bzIP, Tropomyosin,lubulin,DUF164,TBCA, Collagen;TM=M;SS=N; 26.778
445292; AF081497; Hs.279682; Rt type C glycoprotein; Arumonium_transp.FecCD;TM=Y;SS=M; 26.1133829
407242; M16728; gb:Human nonspectic crossreacting antig; lg:TM=M;SS=M; 23.382
424687; J05070; Hs.151736; matrix metafloproteinses 9 (galatinese B; fin2,hemopexin,Peptidase_M10;; 22.622
412718; AW016610; Hs.816; ESTs; pone.none; 21.198
  10
  15
                                                        412719; AW016610; Hs.816; ESTs; none,none; 21.198
406690; M29540; Hs.220529; carcinosmbryonic antigen-related cell ad; ig;TM=M;SS=M; 20.028
402075; ;ENSP00000251056*;Plasms membrane calcium; none;; 19.038
431950; X83629; Hs.2877; cacherin 3, type 1, P-cadherin (placents; cadherin,Cadherin_C_term;TM=Y;SS=M; 17.92061281
412471; M63193; Hs.73946; endothefal cell growth factor 1 (platet; Glycos_transf_3,Glycos_trans_3N;TM=M;SS=M; 17.8978979
417308; H60720; Hs.81892; KIAA0101 gene product; none;TM=M;SS=N; 17.08333333
429259; AA420450; Hs.81034; interteukin 1 receptor antagonist; II.1;; 16.91668628
419709; U6599t; Hs.81134; interteukin 1 receptor antagonist; II.1;; 16.91668628
419926; AW014875; Hs.137007; ESTS; none,none; 16.69
419693; AA133749; Hs.301350; FXYD domain-containing lon transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 16.365
413763; U17760; Hs.75517; laminin, beta 3 (nicela (125kD), kallaln; terminin_EGF; laminin_Nierm;; 15.75294118
413276; BE563085; Hs.833; Interferon-stimulated protein, 15 kDs; ublquttn;; 15.48600509
401781;; Target Exon; filament; TM=M;SS=N; 15.43668831
420440; NM_002407; Hs.97644; memmeglobin 2; Uteroglobin;; 15.394
                                                            412718; AW016610; Hs.816; ESTs; none,none; 21.198
20
 25
                                                         401781; ;; Target Exon; fisament; TM=M;SS=N; 15,43668831
420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobin; 15,394
441633; AW955544; Hs. 112242; normal mucosa of esophagus specific 1; none; TM=M;SS=M; 15.12264151
452240; Al591147; Hs.61232; ESTs; none,none; 14.63
428957; NM_003881; Hs.194679; WNIT1 inducible signaling pathway protein; tsp_1,vwc,IGFBP;TM=M;SS=M; 14.49772727
414987; AA524394; Hs.294022; hypothe5cal protein FLJ14950; SH2;TM=M;SS=N; 14.4399313
432374; W66816; Hs.301885; Homo seplens cDNA FLJ11346 fis, clone PL; none, none; 14.0090901
400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin,Peptidase_M10,Astacin;; 13.824
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8,TM=M;SS=Y; 13.7754386
421552; AF025692; Hs.105700; secreted frizzled-risted protein 4; F2,NTR;; 13,37459834
400284; :: NM_000128*: Homo seolens estonen recentic homone; ms.z5C4.Qest_neecoTM=M;SS=M; 13.31578947
  30
  35
                                                         421552; AF025692; Hs. 105700; secreted frizzled-related protein 4; Fz,NTR;; 13.74596843
400284; ;; NM, 0001257; Homo septems estrogen recepto; hormone_reo,zt,C4,Oest_recep;TM=M;88=M; 13.31576947
428227; AA321648; Hs. 2249; small inducible cytokine subfamily B (Cy; ILB;TM=M;8S=Y; 13.05294118
411274; NM_002776; Hs. 69423; kallikrein 10; trypsin;TM=M;SS=N; 13.038
406687; M31126; Hs. 352054; matrix metalloproteinase 11 (stromalysin; hemoperin,Peptidese_M10;; 13.00311527
427656; AI791495; Hs. 180142; csimodulin-like skin protein (CLSP); efinand;TM=M;SS=N; 12.79
400301; X03635; Hs. 1857; estrogen receptor 1; F-box, hormone_reo,zf-C4,Oest_recep.edh_zinc,ketoecyl-synt,pp-binding,Acyl_transf,Thioesterase,ketoecyl-synt_CAAA,E7,RFX_DNA_binding;TM=M;SS=N; 12.47
400301; AB041036; Hs. 67771; keillikrein 11; trypsin;TM=M;SS=M; 12.47
422310; AA316822; Hs.98370; cytochrome P460, subfamily liSp, polypept; none,pkinase,fn3/g; 12.28597122
430830; AW269920; Hs.2621; cystefin A (stefin A); cystefin;TM=M;SS=N; 12.13379205
437044; AL033684; Hs.69517; differentially expressed in Fanconi's an; none;TM=M;SS=M; 12.04945055
418462; EB001598; Hs.98266; integrin, beta 4; fn3,Integrin_B,Cabx-beta,EGF;TM=M;SS=M; 11.95538462
443859; NM_013409; Hs.9914; follistatin; leareth; 11.95467422
    40
    45
                                                        437044; AL035664; Hs. 69517; differentially expressed in Fanconi's arr, none; TM-M:SS-M; 12.04945055
418462 BE001598; Hs. 69566; integrin, beta 4; fin3, Integrin, B.Caix-beta, EGF; TM-M; SS-M; 11.95538462
43895; NM, 013409; Hs. 9914; foliatabic; lezarg; 11, 95467422
428355; NM, 013409; Hs. 9914; foliatabic; lezarg; 11, 95467422
428355; NM, 013409; Hs. 914; foliatabic; lezarg; 11, 95467422
428355; NM, 013409; Hs. 914; foliatabic; lezarg; 11, 95467422
428355; NM, 013409; Hs. 914; foliatabic as a property of the control of the c
    50
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                                                              424441; X14850; Hs.147097; HZA histone tamity, member Z; historie, Lahr L B, Liber; B AS 16050 44
438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group 1, m; hormona_rec_2f-C<sub>1</sub>, conce, 9.840720222
413859; AW393366; Hs.8364; Horno sapieras pyruvala deltydrogenase king; SAM_PHT, none; 9.823170732
408000; L11690; Hs.198689; butlous pemphigold antigen 1 (230/240kD); efhand, spectrin, GAS2, SH3, Plectin, RA, Xylose_jsom, FilD, bZIP, Tropomyosin, Myo-LZ, MJdt_C, CH, AIP3; TM=M;SS=N; 9.812
    80
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409893; AW247090; Hs.57101; minichromosome meintenance deficient (S.; MCM,aldo_ket_red;TM=M;SS=N; 9.787878788 442599; AF078037; Hs.324051; RefA-associated imhibitor; SH3,ank;TM=M;SS=N; 9.637037037 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgeris entigen; cadherin;TM=M;SS=N; 9.596 417900; BE250127; Hs.62906; CDC20 (cell division cycle 20, S. carevi; WD40;TM=M;SS=N; 9.558 444946; AW139205; Hs.156457; hypothetical protein FLJ22409; abhydrollese_2;TM=Y;SS=M; 9.55 421481; AW391972; Hs.104696; KQA41324 protein; none;TM=M;SS=M; 9.529085873 408591; AF015224; Hs.46452; mammaglobin 1; Uteroglobin;TM=M;SS=M; 9.506 444381; BE387335; Hs.233713; hypothetical protein BC014245; Collegen;TM=M;SS=M; 9.477981433 444006; BE395085; Hs.334762; hype I transmembrane protein Fn14; kd_recept_a,PKD,MHC_J;TM=M;SS=Y; 9.415151615 413719; BE435680; Hs.75498; small inducible cytokine subfamily A (Cr. II 8 * 9 406
                5
                                                                                                        4137(9; BE439580; Hs.75498; small inducible cylokine subfamily A (Cy; IL8;; 9.408 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 sitrophin-; ras;TM=M:SS=N; 9.36 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;SS=N; 9.315693431 421379; Y15221; Hs.103982; small inducible cylokine subfamily B (Cy; IL8;TM=M;SS=Y; 9.31 418004; U37519; Hs.87539; aldehyde dehydrogenses 3 family, member; aldehyt TM=M;SS=M; 9.29 418004; U37519; Hs.87539; aldehyde dehydrogenses 3 family, member; aldehyt M:SS=M; 9.29 418004; U37519; Hs.87539; aldehyde dehydrogenses 3 family, member; aldehyt Aldehyde dehydrogenses 3 family, member; aldehyde dehydrogenses 3 family, member; aldehyde dehydrogenses 3 family aldehyde dehydrogenses 3 family aldehyde dehydrogenses 3 family member; aldehyde dehydrogenses 3 famil
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                                                                                             470005; ILS-5105; 260005; 163505; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 260005; 2600
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417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 9.241561181
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 28 (p1; ank;; 9.207272727
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428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.2984375
422203; AWA11307; Hs.114311; CDC45 (cell division cycle 45, S.cerets); CDC45;TM=M;SS=N; 7.2984375
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418819; U77735; Hs.80205; pim-2 oncogene; pkinase;; 7.234455959
421817; AF146074; Hs.108660; ATP-binding cessette, sub-tamily C (CFTR; Fascictin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 7.162534435
451035; AU076788; Hs.430; plastin 1 (I Isoform); effizand,CH_Adaptin_N;; 7.14546546
424008; R02740; Hs.137655; putative chemokine receptor; GTP-binding, 7m_1;TM=Y;SS=M; 7.126
414482; SS7498; Hs.76252; endothelin receptor type A; 7m_1;TM=Y;SS=M; 7.122413793
425003; AF119046; Hs.154143; aputinic/apyrintillinde endocuclease(APEX; Troponlin,Exo_endo_phos,IQ;TM=M;SS=N; 7.106719368
430890; XS4232; Hs.2695; glypizen 1; Clypican;TM=M;SS=M; 7.089937053
407772; AU077715; Hs.38938; putative secreted figand homologous to f; none;TM=M;SS=Y; 7.052
426514; BEB16633; Hs.170195; bone morphogenetic protein 7 (osteogenic; TGF-bets,TGFb_propeptide;; 7.042
43124; AA498799; Hs.36958; ESTe; SH2,RasGEF;none; 7.03
437139; W73686; Hs.118513; ESTe, Weedly similar to RTA RAT PROBABLE; 7m_1;TM=Y;SS=M; 7.03
420311; AW445044; Hs.36207; Human DNA sequence from clone RP4-530115; none,none; 7.028
439979; AW600291; Hs.6823; hypothetical protein FL/10430; none;TM=M;SS=N; 7.008
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422846; BE513934; Hs.1583; neutrophil cytosofic factor 1 (47kO, chr. SH3,PX,TM=M;SS=N; 6.991626794 416250; AA581398; Hs.73452; Kremen 2; kringle,CUB,WSC;; 6.972 430770; AA765694; Hs.123296; ESTs; none,none; 6.95 418869; AW516565; ; gb:xq01d05.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,WW,IC; 6.948
                                                                   430770; AA765694; Hs. 123296; ESTs; none,none; 6.95
418368; AWS16565; gb:nglhod105.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,WW,IQ; 6.948
428953; AA306510; Hs. 348183; tumor necrosis fector receptor superfami; 60s_ntbosomal_k1bosomal_L10,TNFR_c6,DEAD;; 8.914
418283; S79895; Hs. 83942; carthepsin K (pycnodysostosis); Peptidase_C1;; 6.876190476
419667; AU077005; Hs. 92200; a disinlegrin and metalloproteltase doma; disinlegrin,Reprolysin,Pep_M12B_propep;TM=M;SS=M; 6.862970711
421143; AB024536; Hs. 102171; Immunoglobulin superfamity containing its; ig_LPR,LRRNT,LRRCT;TM=M;SS=M; 6.849056604
456181; L36463; Hs. 1030; ras infubitor; RA,SH2,VPS9;TM=M;SS=N; 6.762
43686; Al469355; Hs. 127310; ESTs; pkinase,mr;TM=M;SS=N; 6.762
43686; Al469355; Hs. 168877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 6.720348837
439750; AL350053; Hs. 57664; Homo sepiens mRNA full length insert cDN; IMPDH_D,CIMPDH_D,CISS_integrin_B,Ricin_B_lectin; 6.717307692
450334; AF03595; Hs. 189895; ubdqutfin-conjugeting enzyme E21; 6, Armačilo_seg_UO_son_none; 6,688194444
439738; BE246502; Hs. 9598; serna domain, immunoglobulin domain (g); Sema_PSI,Integrin_B;TM=Y;SS=N; 6,670553936
428365; AF112213; Hs. 184062; putartive Rab5-interacting protein; 542,SH3; 6,669291349
425289; AW139342; Hs. 155530; Interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN; 6,852671756
42630; NM_014638; Hs. 170156; KIAA0466 gene product; C2PI+PL-Y;TM=M;SS=N; 6,633713299
425289; AW139342; Hs. 155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN; 6,852671756
44689; NM_000676; Hs. 45743; adianosine A2b receptor; 7Im_1;TM=Y;SS=N; 6,584146148
410929; AA402307; Hs. 322844; hypothetical protein DKFZp564A176; Sema_PSi,ITG,Integrin_B;TM=Y;SS=M; 6,532763533
414609; AA402307; Hs. 3274679; ESTs; none,none; 6,447658402
421445; AA913059; Hs. 150433; Hono seplens clone IMAGE:4054868, mRNA; Ion_trans,K_tetra.asp; 6,426666667
433933; A7764399; Hs. 375597; Homo seplens clone IMAGE:4054868, mRNA; Ion_trans,K_tetra.asp; 6,426666667
433933; A7764399; Hs. 355937; Homo seplens 
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427640; APOSB293; Hs. 180015; D-dopachrome tautomerase; COX8,6HMT,MIF,GST_C,EF1G_domain,GST_N,81,Fz,Frizzied,calceliculin,7tm_2,mm,PAP_assoc;TM=Y;SS=M;
                                                                                     435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 6.269720102
                                                                                 435232, NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 6.268720102
418203; X54942; Hs.83758; CDC28 protein kinase 2; CXS;; 6.219031272
418203; BE297902; Hs.89360; kinesin-like 6 (mibbit centromere-assoc; kinesin;TM=M;SS=N; 6.19
409512; AW978187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARC;TM=M;SS=N; 6.18888888
449230; BE613348; Hs.356392; melanoma cell adhesion mulecule; ig.isodh,Ribosomal_L6,F-bor;TM=Y;SS=M; 6.188886888
449230; BE613348; Hs.356392; melanoma cell adhesion mulecule; ig.isodh,Ribosomal_L6,F-bor;TM=Y;SS=M; 6.188886888
449230; BE613348; Hs.2595; TGF-beita 4; TGF-beita, TGFb propeptide; 6.162
430681; AF081513; Hs.25195; TGF-beita 4; TGF-beita, TGFb propeptide; 6.162
432314; AA533447; Hs.285173; ESTs; Xlink,none; 6.123040762
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421733; AL19671; Hs.1420; fibroblast growth factor receptor 3 (ach; ip.pkinase;TM=Y;SS=kt; 6.095758365
422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial i mito_carr;TM=M;SS=N; 6.089164786
452683; Al099576; Hs.374574; progesterone membrane binding protein; homeobox,none; 6.06284153
444309; U83236; Hs.10803; calcium and integrin binding protein (DN; effiend); 5.04015644
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414166; AW(689941; Hs.75789; N-myc downstream regulated; DEAD, helicase_C,mm,Ndr,Cys_l,not,TiL,vwa,vwc,vwd,KQ,Rilia,abhydrolase,TGF-beta_DUF139;TPR_DSPe,tsp_1,Ribosomat_S21,rvyTiM=M,89=4; 6,009562942
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413369; NM, Q00878; Hs.75596; interleukin 2 receptor, beta; none; TM=Y;SS=N; 5.984536083
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405484; ;; C30021244; gijl 2737280 [ref]VP_006682.2 | k; none; TM=Y;SS=N; 5.984536083
414907; X90725; Hs.7597; poto (Drocophila)-kite kinase; Ribosomal_L37ae,pklinsse,POLO_box,IRNA-synt_fb,dynamin_dynamin_2,GED,bZIP,M;; 5.978431373
419216; AU076718; Hs.164021; small inducible cytokine strifamity 8 (Cy; ILis; 5.978
414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Ribodanese,DSPc,Y_phosphatase;TM=M;SS=N; 5.98367755
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424291; AL120051; Hs.144700; ephin-81; Ephin;TM=Y;SS=M; 5.951550388
453459; BE047032; Hs.257789; ESTs; none,none; 5.95
456373; BE247706; Hs.66593; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 5.938
429359; W00482; Hs.2399; metrix metalloproteinase 14 (membrane-in; hemopexin, Peptidase_M10;TM=M;SS=M; 5.917857143
414703; BE243077; Hs.380063; ATTease, Na7 transporting, heta 3 polyper; Na_K-ATTease;TM=Y;SS=M; 5.910465487
448775; AB022537; Hs.3396; nucles (aphosphatabe, receptor t; none,none; 5.868362832
            50
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                                                                                         448775; AB025237; Hs.388; nudix (nucleoside diphosphate tinked mol; NUDIX;TM=M;SS=M; 5.901886793
452238; AW379376; Hs.356289; protein tyrosine phosphates, receptor t; none,none; 5.959362832
418345; AU01688; Hs.241407; serine (or cysteine) proteinses inhibito; serpin;TM=Y;SS=M; 5.842
452875; BE276760; Hs.30928; DNA segment on chromosome 18 (unique) 11; Eut., porin;TM=M;SS=M; 5.816363636
439525; AP066453; Hs.58611; ESTs; Fork, head,glycolytic_snzy,Ma_sulph_symp; 5.811594203
447343; AA256841; Hs.236894; ESTs; Highly similar to 502392 slphs-2-m; none,none; 5.811594203
447343; AA409701; Hs. 1578; beculovits! IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.806
415198; AW409480; Hs.943; natural killer cell transcript 4; none;TM=M;SS=N; 5.804137931
431941; AK000106; Hs.272227; Homo septens cDNA FLI20099 fis., clone CO; pkinese;Furin-like,Recep_i_domain,none; 5.8
457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; homone, rec.2f-C4,Metalkothio_5;TM=M;SS=N; 5.794
439335; AA742697; Hs.62492; NM_052863;Homo septens secretoglobin, fa; none; 5.778588808
439248; A498072; Hs.361474; membrane-associated tyrusine- and threon; ank,pkinase,UFF0073; 5.763492064
452461; N78223; Hs.108106; transcription factor; zf-C3HC4µubquilin,PHD;YDG_SRA;TM=M;SS=N; 5.728
414983; AA926960; Hs.348666; CDC28 protein kinase 1; CKS;; 5.714634146
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424517; AK599443; Hs. 137447; Horno sepiens cDNA FLJ12169 fis, cbne MA; SH2;STAT,STAT_bind,STAT_prot,none; 5.701666667
419056; M89957; Hs. 89575; CD798 antigen (immunoglobulin-associated; ig,ITAM;TM=Y;SS=M; 5.692
432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (o-met; pklmase,Sama,PSI,TIG,A4_EXTRA;TM=M;SS=M; 5.686
45269p; Al826645; Hs. 211534; ESTs; ArfGap,PH,ank,Guarnylate_kin,PDZ,SH3; 5.693673469
411030; BE397193; Hs.67696; 7-60 probein; none;TM=H\SS=N; 5.6767676777
447131; NM_004685; Hs. 17468; retinoic actid receptor responder (tzzaro; none;TM=Y;SS=N; 5.672977625
426227; U67056; Hs. 154299; Human proteinese activated receptor-2 mR; 7km_1;TM=Y;SS=M; 5.656
407722; BE252241; Hs.38041; pyrkloxati (pyrkloxine, vilamin B6) kinas; pfkB;TM=M;SS=N; 5.656616943
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427490; Z95152; Hs. 176695; milogen-activated protain kinase 13; pkinase; TM=Mt;SS=N; 5.6486823
415010; NM_004203; Hs. 77783; membrane-associated tyrosine- and threon; ank pkinase, LPF0073;; 5.648
45290; Al538070; Hs. 15085; ESTs; pru;homeobox, Ig., chan, ANF_receptor; 5.646
424321; W74048; Hs. 1766; lymphocyte-specific protein fyrosine kin; SH2, SH3, pkinase; TM=Mt;SS=N; 5.642405063
418703; NM_014448; Hs. 87435; Rho guanine exchange factor (GEF) 16; SH3, PH, RhoGEF, Bima_VP3; TM=Mt;SS=N; 5.636
426108; AA622037; Hs. 166466; programmed cell death 5; DUF122; TM=Mt;SS=N; 5.635087719
424490; AJ278016; Hs. 55565; ankyrin repeat domain 3; ank, pkinase; TM=Mt;SS=N; 5.635087719
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417018; M16033; Hs. 2003; protein phosphetises 4 (formerty X), cata; Matallophos; TM=Mt;SS=N; 5.608352145
417018; M16033; Hs. 80887; v-yes-1 Yamaguchi sarcoma viral related; SH2,SH3, pkinase; TM=Mt;SS=N; 5.608352145
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435017; AA336522; Hs. 15959; ESTs; pkinase, PP2C, none; 5.575112108
435017; AA336522; Hs. 1793; p-arc tyrosina kinase; SH2,SH3, pkinase; TM=Mt;SS=N; 5.55610569
439963; AW2475229; Hs. 6793; platelel-scrivating factor acetylhydrola; PAF-AH_In, Lipase_GDSL; TM=Mt;SS=N; 5.558195955
415012; NM_004383; Hs. 77793; o-arc tyrosina kinase; SH2,SH3, pkinase; TM=Mt;SS=N; 5.55621687
424909; S76187; Hs. 153752; cell division cycle 258; Rhodanese; S-549751244
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417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.514964789
447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fin3.[g,Y_phosphatase,MAM;TM=Y;SS=M]; 5.494202899
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448633; AA311426; Hs.21635; lubulin, garvina 1; tubulin;TM=M;SS=N; 5.460078046
408716; A1557639; Hs.161714; Homo saptens miRNA for KIAAT789 protein, ; UvrD-helicase,RNB,Runt;TM=M;SS=N; 5.450413223
426410; RE998446; Hs. 935800; RGJ 2 Jilies 1; Rel-2 RNA come; 5.44657856
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48633; ASS11405; Nat. 165087; ESTs; utduptini, niterpitu. B.UBA, none; 3.48334814]
48633; ASS11405; Nat. 165744; Hono sopiens mRNA for KAA1759 public, i. UmD-balicase, RNB, Runt, TM=M;SS=N; 5.450413223
42610; EE26446; Na. 305809; DCL.2 Nat. 1; babba, TM=M;SS=N; 5.44495185
457619; AA057494; Na. 35406; FL.20522 Hypotholical proble PL.20522; none, none; 5.444281625
426579; EE24699; Na. 116834, ATP-binding casebs, sub-family B (MDN; AA6C, tran, ABC, membrane, PRK, TM=Y;SS=N; 5.437931005
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436466; AK001455; Hs.5196; Down syndrome critical region game 2; none;; 5.209259259
421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospha; Ribosomal_120,Na_PL_cotrans;TM=Y;SS=N; 5.202
425365; BE244477; Hs.155939; mosfiol polyphosphate-6-phosphatases, 14; Exo_endo_phos,SH2;TM=M;SS=N; 5.19979716
437412; BE09528B; Hs.34744; Homo sepiene mRNA; cDNA DKFZp647C136 ft; APC_tran,GTP_EFTU,ABC_membrane,none; 5.199074074
416602; NM_006159; Hs.367895; Protein Kinase C-binding protein NELL2; EGF,vvc;TSPN;; 5.198224952
42556; AM139399; Hs.314807; ESTs; none;TM=M;SS=N; 5.192439863
427857; AL133017; Hs.288679; hypothetical protein FL122865; myosin_head,IO,zf-MYND;TM=M;SS=M; 5.190251572
400517; ; Hengstin; none;TM=M;SS=N; 5.18
413438; Rs.28803; Hs.69861; synthonosine klosse 1: DAGKe-TM=M;SS=M; 5.17281358
                    65
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                                                                                                                        400517; ;; lengstn; none;TM=M;SS=N; 5.18
413436; AF238063; Hs.68061; sphingosine kinese 1; DAGKc;TM=M;SS=N; 5.172881356
423527; Al205865; Hs.105861; hypothetical protein FIJ13824; none;TM=M;SS=N; 5.165060241
419136; U48508; Hs.89631; ryanodine receptor 1 (skeletal); lon_trans;SPRY,PYDR_TPR,RyR,MIR;TM=Y;SS=N; 5.166976744
437809; AL137723; Hs.5956; Horno septens mRNA; cBNA DIKTZp43400818 (f; none,none; 5.154676259
452069; AB028949; Hs.183994; KIAA1025 protein; Metatlophos;TM=N;SS=N; 5.152360515
409340; BE174629; Hs.321130; hypothetical protein MGC27711;
aa_permesses,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_Kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 5.144859313
442875; BE623003; Hs.23625; Horno septens clone TCCCTA00142 mRNA sequ; K_Jetra,DUF-51,none; 6.142
434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;; 5.141534392
434808; AF155106; Hs.256150; NY-REN-41 antigen; none;TM=M;SS=N; 5.14
431341; AA307211; Hs.251531; proteasome (prosome, macropein) subunit; proteasome;TM=M;SS=N; 6.13968254
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### 1008. AND/06/16 http://www.com.com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/com/oc/
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41295B; BE391579; Ha. 25087; Fao-activated earline/theronine kinase; none;: 4.738781619
414443. AUIVT26B; Ha. 576144; pictuled-derived growth factor receptor; in phinase; The Y;SS=N; A.733
41925D; AWT710B; Ha. 55080; Lib anRNP-specific protein, 116 for; Thr. 1_BRIA_EC/COC,OMA_methylase; 4.72545456
41925D; AWT710B; Ha. 57830; willine mornohosphaging protein, 116 for; Thr. 1_BRIA_EC/COC,OMA_methylase; 4.72545456
41930; MM, B02342; Ha. 116; lymphotoxin belar receptor (TINR superfam; TINF; Lef; IM=M<sub>2</sub>SS=N; 4.718858132
41476B; Y78324; Ha. 77313; cyclide mornohosphaging kinase; PKE, Cocie_F, 2-718836565
42655B; BE292842; Na. 56120; Inharison regulatory factor; 1; RFT; 4-718543046
41476B; Y78324; Ha. 77313; cyclide opendant lines (DCD2-like) by Cybasse; FIM=M<sub>2</sub>SS=N; 4.70B
40760; ACD02300; Ha. 37129; sodium channel, anonologa-gaded 1, beta; ASCTIM=Y;SS=N; 4.70B
40760; ACD02300; Ha. 37129; sodium channel, anonologa-gaded 1, beta; ASCTIM=Y;SS=N; 4.70B
40760; ACD02300; Ha. 37129; sodium channel, anonologa-gaded 1, beta; ASCTIM=Y;SS=N; 4.70F1653
407146; C.14076; Ha. 33232; EST; none; TIM=Y;SS=N; 4.680E75815
407146; C.14076; Ha. 33232; EST; none; TIM=Y;SS=N; 4.680E75815
407810; AND 47814; Ha. 75000; Horno sepions cDNN: ELVITSS2 fb., clone; C. SIR,PDZ, Garanylata, Irin, none; 4.68040771
408309; AND 47814; Ha. 75000; Horno sepions cDNN: ELVITSS2 fb., clone; C. SIR,PDZ, Garanylata, Irin, none; 4.68040771
410312; AND 47814; Ha. 7780; Cybol brecoplor 1 (aclosify; Foida; pre-Maryl-TiM=M<sub>2</sub>ASS=N; 4.575941897
410312; AND 47814; Ha. 77816; Cybol brecoplor 1 (aclosify; Foida; pre-MirT-MaxSS=N; 4.57594189)
410323; AND 47814; Ha. 77814; Cybol brecoplor 1 (aclosify; Foida; pre-MirT-MaxSS=N; 4.57594189)
410323; AND 47814; Ha. 77814; Cybol brecoplor 1 (aclosify; Foida; pre-MirT-MaxSS=N; 4.57518048)
410323; AND 47814; AND 47814; AND 478148887
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426125; X3724; Hs.168994; FAT tranor suppressor (Drosophile) homoto; EGF,cadherin,laminin_G;TM=Y;SS=M; 4.529710145
402330; ;; Target Evon; pkinase,none; 4.528070175
439238; N47305; Hs.302161; EDG-8 (endothellal differentiation, sph; 7tm_1;TM=Y;SS=M; 4.524
433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20; 4.523715415
413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenas; CBS,IMPDH_C,NPD;TM=M;SS=N; 4.522900763
431429; AFU72813; Hs.252831; reticulon 3; Raticulon,F2jg,Ixtingle,pkinase;TM=Y;SS=N; 4.512
424076; AB006525; Hs.139033; paternally expressed 3; zf-C2H2,K7AB,none; 4.512
425002; AFC00207; Hs.92036; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 4.51
449101; AA206847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.50
440101; AA206847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.50
440101; AA206847; Hs.52306; ESTs; none,pionase; 4.504
440291; BE397753; Hs.14623; Interferon, garmma-hiducible protein 30; GILT;TM=M;SS=Y; 4.50215208
431326; AW970580; Hs.198689; KIAA0728 protein; none,none; 4.501
428072; BE256602; Hs.182366; hast shock protein 75; HATPasa_c,HSP90;TM=M;SS=N; 4.48828125
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431326; AW970580; Hs. 182366; Nast shock protein 75; RATPasa_c, HSP90; TM=M;SS=N; 4.48828125
415149; X12451; Hs.78056; cathepsin t; Peptidasa_C1; 4.484375
421959; AW751497; Hs.98370; cytochroma P450, subtantly IIS, polyept; p450; TM=Y;SS=M; 4.488
421959; AW751497; Hs.378918; caseln kinase 1, delig zI-C3HC4, Filamin, zI-B, box, NH-B, kinase, zi-MiZ;TM=M;SS=N; 4.476092784
421071; Al311236; Hs.104476; ESTs, Weddy similar to CGHU1E collagen; none; TM=Y;SS=M; 4.477337111
410590; BE615216; Hs.84746; chloride intracellular channel 3; none; TM=M;SS=N; 4.478
438774; AA31620; Hs.379034; hypothetical protein MGCZ746; none, none; 4.47874372
410726; A623859; Hs.16936; ESTs; pkinase, pro Jeomerase, none; 4.47
429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory au; CDK5_activetor, none; 4.468
426485; NM, 006207; Hs.170040; plateleit-derived growth factor receptor; 3;;; 4.46944649
433446; A6603319; Hs.155195; ESTs; pou, homeobox, Ig_chem, AMF_eceptor; 3;; 4.46944649
433446; A6803319; Hs.155195; ESTs; pou, homeobox, Ig_chem, AMF_eceptor; 4.488
410293; AK000047; Hs.61960; hypothetical protein; K, latra; TM=M;SS=N; 4.45020134
453464; A6804911; Hs.32989; receptor (calcitonin) activity modifying; none; TM=Y;SS=N; 4.448198198
410583; AW770280; Hs.36256; ESTs, Moderately similar to JCS238 galac; SH3;PDZ, Grenylate, Mn, none; 4.446927374
441456; AJ271671; Hs.7854; zinc/ison regulated transporter-like; Zip; TM=Y;SS=M; 4.44510183
453064; R40334; Hs.99463; potassium large conductance calcium-eti; none, none; 4.47868=N; 4.489411215
411825; AK000334; Hs.39463; potassium large conductance calcium-eti; none, none; 4.4868=N; 4.489
419314; U94905; Hs.29646; KAA1118 protein; Troponin, Evo, endo, phos, JCTTM=Y;SS=N; 4.432765152
428376; AF119665; Hs.184011; pyrophosphatase (incrpanic); Pyrophosphatase; TM=M;SS=N; 4.48271429
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419344; U94905; Hs.
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427138; N77624; Hs.173717; phosphatidic acid phosphatase type 2B; PAP2,none; 4.4234375
414496; W73653; Hs.355424; EST's; pkinase,F5_F8_type_C,adh_short,none; 4.42114094
429432; Al678069; Hs.202676; synaptonemal complex protein 2; none;TM=M;SS=N; 4.42
429922; Z97630; Hs.228117; H1 histone familty, member 0; linker_histone;TM=M;SS=N; 4.419207317
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446700; AW206257; Hs. 156325; Human DNA sequence from clone RP11-145L2; none; TM=M;SS=N; 4.418181818
435411; AW2444519; Hs. 138211; ESTs; none, pkinase; 4.414
414581; AA256213; Hs. 72010; ESTs; none, pkinase; Av14
414581; AA256213; Hs. 72010; ESTs; none, pkinase; Choline_kinase, SCO1-SenC, Glycos_trans_3N; 4.41
418558; AW082266; Hs. 86131; Fas (TNFRSF6)-associated via death domei; death, DED;; 4.408523909
442259; Al690259; Hs. 201345; ESTs; Acayltransf, RhocAP, FCH, SH3, Kelch, fn3; 4.408
415860; DS6051; Hs. 78889; dlazepam binding Inhibitor (GAP) receptor, ACBP; TM=M;SS=N; 4.404678363
434419; ALD40506; Hs. 296308; dual specificity phosphatase 7; DSPc; TM=M;SS=N; 4.404
404440; ;; NM, U21048:Home septens metanoma artigen; MACE; TM=M;SS=N; A.404
435642; AA687376; Hs. 351226; ESTs; SH3;g, pkinase, PH, spectrin, RhocEF, none; 4.394
413367; NM, D0657; Hs. 75317; sotrta carrier family 16 (monocarboxylic; sugar_tr; TM=Y;SS=N; 4.39028777
435732; AF229176; Hs. 123136; leucine rich repeat and death domain con; none, none; 4.38490566
427359; AW020702; Hs. 79881; Home saptens cDNA; FLJ23006 fts, clone L; 7tm_1, none; 4.382129278
42749; AW322587; Hs. 159448; surfeit 2; none; 4.382
417874; BE518160; Hs. 2823; profein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y;SS=N; 4.381422925
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                                                                        425749; AW328587; Hs. 159448; surfeit 2; none;; 4.382
417874; BE618160; Hs. 82629; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y;SS=N; 4.381422926
414808; D14694; Hs. 77329; phosphatidytserine synthese 1; PSS;TM=Y;SS=M; 4.380681818
431837; T79326; Hs. 331967; olfactory receptor, family 2, subtamily; none, 7tm_3,sushl,ANF_receptor; 4.376
417115; AW9S2792; Hs. 334612; small nuclear ribonucleoprotein polypept; Sm.pkinase; 4.370247934
434876; AF160477; Hs. 51460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 4.37
430379; AF134149; Hs. 240395; potassium channel, subfamily K, member 6; fon_frans;TM=Y;SS=M; 4.367777778
403912; ;; CS000394*:gl]12737280[rs]XP_006682.2] k; none;TM=M;SS=N; 4.367684478
426268; AF063420; Hs. 166913; serine/threonine kinase 24 (Ste20, yeast; pkinasec; 4.366348449
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25
                                                                            420205; NFL03420; PS. 100913; Selfmentreonline hiteste 24 (36224, yeas); policises, 4.300340449
434263; N34895; Hs.79187; ESTs; (g.none; 4.358527132
404760; ; Target Exon; cadhetin;TM=MtSS=Mt, 4.356
413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=MtSS=N; 4.35472973
420757; X78592; Hs.99915; androgen receptor (dihydrotestoslerone r; hormone_rec,zf-C4,Androgen_recep;TM=M;SS=N; 4.354
428812; AF105365; Hs.172613; solute cerrier family 12 (polassium/chlo; none;TM=Y;SS=N; 4.353244838
                                                                       420757; X78592; Hs. 199916; androgen receptor (dihydrotestosteroner; hormone_rec.zf-C4_Androgen_recept*TM=M;SS=N; 4.354
426812; AF105365; Hs. 172613; solube certier family 12 (potassiburbidity, none;TM=P;SS=N; 4.35244638
431674; And98901; Hs. 301642; G-protein coupled receptor, none,GCV_H; 4.35
431866; L77964; Hs. 271900; mitogen-activated protein kinase 6; pidmses;TM=M;SS=N; 4.347693916
437719; BE387402; Hs. 19333; hypothetical protein FLJ10349; adenytistekinase,ATP-bind;TM=M;SS=N; 4.346007605
424837; BE276113; Hs. 333034; N-acchyltransferase, homolog of S. cerey; Acetyltransf;TM=M;SS=N; 4.3444
449437; A702038; Hs. 100057; Homo septems ctil/N; FLJ22902 file, close k; none,none; 4.334722222
417569; Mb, 01337; Hs. 171979; Inhetiation 19; L10; 4.322
445360; AF052112; Hs. 12540; hysophosphoRpase I; abhydrolase_2,TM=M;SS=N; 4.320339281
425964; AW788992; Hs. 9071; projectionen emortranse binding protein; homeobox.none; 4.33867925
425964; BE387614; Hs. 25797; splicing factor 3b, stourt 4, 49kD; mm;TM=M;SS=N; 4.316873557
408908; BE2386714; Hs. 25797; splicing factor 3b, stourt 4, 49kD; mm;TM=M;SS=N; 4.316873557
408908; BE2386714; Hs. 25797; splicing factor 3b, stourt 4, 49kD; mm;TM=M;SS=N; 4.316873557
408908; BE2386714; Hs. 25797; splicing protein Publish Alloydrif; none, Cyc., Binch 4, 434724682
438999; AF085833; Hs. 136824; ESTE; none,Pl3_Pl4_kinase,Pj3K-a,Pj3K_a,Pj3K_C2,Pj3K_rbd_Pj3K_p858; 4.314084507
418883; BE33861; Hs. 105824; ESTE; none,Pl3_Pl4_kinase,Pj3K-a,Pj3K_a,Pj3K_C2,Pj3K_rbd_Pj3K_p858; 4.314084507
418883; BE33807; Hs. 146770; pbc10464647; Nill_MGC_65 Hormo septems c, none,NANA; 4.304
419507; RS2557; Hs. 95757; Hs. 951044 file647; Nill_MGC_65 Hormo septems c, none,NANA; 4.302
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44524; NB_004864; Hs. 157199; ELKL motif Mrsse; planses_UBA/k171Melk_SS=N; 4.301639344
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436012; A4393254; Hs.43619; ESTs; Armadilo_seg,none; 4.273134328
409619; AK001015; Hs.55220; BCL2-essociated athanogene 2; BAG;TM=M;6S=N; 4.273109244
418529; AW005695; Hs.250897; TRK-tused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;SS=N;
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                                                                                                                                  4.272123894
                                                                                    41:212.12394
41:5214; Al445236; Hs. 125124; EphB2; fn3.pkinase,SAM_EPH_lbd;TM=Y;SS=M; 4.268
438233; W52448; Hs. 66147; ESTs; Neur_chan_LBD,Neur_chan_memb,MAGE; 4.26284586
429019; AA443280; Hs. 279907; myosin illA; myosin_head,pkinase,PRK,IQ;TM=M;SS=N; 4.262
424959; NM_005781; Hs. 153937; activated p21cdc/2Hs kinase; kth,Idth_C,6H3,pkinase,UBA;TM=M;SS=N; 4.266695652
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                                                                                  24955; NM_00576f; Hs. 153937; acfiveled p21cdo42hs kinase; kh.j.dh_C.S.H3,kinase, UBA;TM=M;SS=N; 4.256695652
453656; AW860427; Hs. 342874; transforming growth factor, beta recepto; zona pelludda,none; 4.257208766
417414; AA34689; Hs. 36766; LUTP prophosphiratase; dUTP pses,KRAB; 4.251785714
453905; NM_002314; Hs. 36566; LM domain kinase 1; pkinase,LMA,PDZ_ZFPARF_TM=M;SS=N; 4.249116608
424232; AB015982; Hs. 143460; protein kinase C, mi; pkinase,DAG_PE-bind,PH;TM=M;SS=N; 4.247692308
404883; ;; ENSP00000216009: Soldium-glucose cotrarspo; SSF;TM=Y;SS=N; 4.242424242
412507; L3664s; Hs. 27396; EphA4; fina,pkinase,SAM,EPH_Ibd;TM=Y;SS=N; 4.242424242
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411089; AA456454; Hs. 355702; ceit diviston cycle 2-like 1 (PITSLRE p; none,none; 4.237313433
436957; AA902488; Hs. 122952; ESTs; none,DAGKc,DAGKs,RA,DAG_PE-bind; 4.235
452568; AA805634; Hs. 300870; Horno sapiens mRNA; cDNA DKFZp547M072 (fir, PI3_P14_kinase; TM=M;SS=M; 4.234793187
432728; NM_005979; Hs. 276721; HLA class II region expressed gene KE4; ZIp,Ig_chart,TM=Y;SS=M; 4.2345945455
41650; AF188025; Hs. 189507; phospholipese A, regulatory subunit HEAT;TM=M;SS=N; 4.234793187
409539; AW969543; Hs. 144602; mitogen-activated protein kinase kinase; Peptidase_C48,none; 4.230666667
427127; AW802282; Hs. 22265; pyruvate dehydrogenase phosphatase; PP2C_none; 4.22609259
403362; ;; NM_0016157:Horno sapiens actin, gamma 2; actin; 4.22680478
417866; AW067903; Hs. 82772; collagen, typa XI, sipha 1; Collagen, COLFI, TSPN, laminin_G, CorA; 4.22638889
             70
                75
                80
```

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428897; AJ245719; Hs.194385; hypothetical protein FLJ20234; SH2;TM=M;SS=N; 4.224731183
425771; BE561776; Hs.194345; Bruton agammaglobulinamia tyrosine kinas; SH2,SH3,pklnase,PH,BTK;TM=M;SS=N; 4.223684211
418566; C21220; Hs.321717; hypothetical protein FLJ10875; zf-C2H2,BTB,K_tatra,7tm_1; 4.222807018
454098; W27953; Hs.217493; Piskophilitr, none,none; 4.22
424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); pkinase,FHA,Dnat;TM=M;SS=N; 4.21875
419222; X60111; Hs.1244; CD3 antigen (p24); transmembrane4;TM=Y;SS=M; 4.217130215
436756; Z18364; Hs.198298; v-src avian sercoma (Scholid-Ruppin A-2); none,none; 4.216
450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 4.215163934
416724; MM, 002007; Mc 7008; Printiplocalibo; 2 EFsband relation binding effect of 2 120041885
    5
                           416224; NM_002902; Hs.79088; reficulocalbin 2, EF-hand calcium bindin; efhand;; 4.212041885
                          41624; NM_U02902; Hs./3068; Rencinocation 2, EF-hand calculut biblin; etirals., 4.21204-hydro_38; 4.207407407
432539; AL138169; Hs.278378; keryopherin beta 2b, brusportin; none,DS,UPF0139;Glyco_hydro_38; 4.207407407
416661; AA634543; Hs.79440; KSF-II mRNA-binding protein 3; KH-domain,mm;TM=M;SS=N; 4.205
432284; AA532807; Hs.287740; ESTs; pkinase,none; 4.205454546
418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 4.204142012
10
                          415735; AVVISSSS11; hs.172012; hypotheridal protein Unit-Epi-SAUOT; phriase, NOT; twi-Nt, SS=N; A.204142012
450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran, ABC_membrane, lg.MHC_II_beta, SRP54, proteasome, ABC_membrane, ABC_tran; 4.202572347
412817; AL037159; Hs.74619; proteasome (prosome, mecropain) 25S subt; PC_rep; TM=Nt; SS=N; 4.202061863
425394; AA356730; Hs.323949; kangei 1 (suppression of tumorigenicity; transmembrane4, none; 4.195014663
445335; AW150717; Hs.345728; STAT induced STAT inhibitor 3; SH2;TM=Mt;SS=N; 4.192248062
15
                          449305; AV9150/17; 18.343726; STAT bidded STAT timbobid 5; 612; fW=Vi,35=N; 4.1922402
415023; AA932146; Hs.355397; Homo seplens clone TCCCIAD0164 mRNA sequ; none; NA;NA; 4.192
449907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none; TM=M;SS=Y; 4.191870961
445330; R52656; Hs.21691; ESTs; 7tm, 1,none; 4.189922481
430016; NM_004736; Hs.227656; xenctropic and polytropic retrovirus rec; SPX,EXS;TM=Y;SS=N; 4.188333333
434633; A1189587; Hs.120916; ESTs; SH3,PH,RhoGAP,none; 4.187106918
20
                           452908; AB001451; Hs.30955; neuronal She adaptor homolog; SH2,PID,Zn_cerbOpept;TM=M;SS=N; 4.186885246
439318; AW837046; Hs.5527; G protein-coupled receptor 56; 7tm_2,CytC_sem,GPS;TM=Y;SS=M; 3.930957684
439201; AL538613; Hs.298241; Transmembrane protesse, serine 3; IdL_recept_a,trypsin;TM=Y;SS=M; 3.893103448
 25
                            428969; AF120274; Hs.194689; artemin; TGF-beta;; 3.8B4030418
                           44633; AF111713; Hs.12940; arctivit; 101-0816; 3.88400418
44633; AF111713; Hs.12284; junctional adhesion molecule 1; ig;TM=Y;SS=M; 3.831669044
432305; M62402; Hs.274313; insulin-Tike growth factor binding prote; thyroglobulin_1,IGFBP,A2M_N;TM=M;SS=N; 3.742995346
405547; ;; NM_018833*:Homo septems transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.676
407853; AA335797; Hs.40499; dickkopf (Xenopus laevis) hornolog 1; none;TM=M;SS=Y; 3.634
 30
                           407855; AA335797; Hs. 40495; dickkopf (kanopus leavis) hornofog 1; none;TM=M;SS=Y; 3.634
425427; M66599; Hs.169840; TTK protein kinase; pkinase; 3.662
427585; D31152; Hs.179729; collegen, type X, atpha 1 (Schmid metaph; C1q, Collegen;; 3.49
405546; ;; NM_018833*:Homo sepiens transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.422661871
433820; AL360204; Hs.26363; Homo sepiens mRNA full length insert cDN; none,none; 3.402
404210; ;; NM_005936:Homo sepiens myebid/lymphold ; FHA,PDZ,RA,Dit,TM=M;SS=N; 3.368807339
424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase_pkinase_C;; 3.213402062
418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); none;TM=M;SS=N; 3.084
451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M;SS=N; 1.55
  35
  40
                             TABLE 17B
                                                              Unique Eos probaset identifier number
                            Pkey: Unique Eos proteset
CAT number: Gene cluster number
                             Accession:
                                                            Gerbank accession numbers
   45
                             Pkey
                                                              CAT Number Accession
                             418869
                                                              12789_14 AA229762 AA230035
   50
                             TABLE 17C
                                                             Unique number corresponding to an Eos probaset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dumham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22."

Dumham I. et al., Nature (1999) 402:489-495.
                              Pkey:
                              Ref:
   55
                                                               Indicates DNA strand from which exons were predicted.
                              Nt_position:
                                                             Indicates nuclectide positions of predicted exons.
                              Pkey
                                                               Ref
                                                                                                                               Nt_posttion
                                                                                               Strand
    60
                                                                                                                               121907-122035,122804-122921,124019-12416
83215-83435,83531-83656,83740-83901,8423
                              402075
                                                               8117407
                                                               7249190
                              401781
                                                                                              Minus
                               405484
                                                                                                                                199214-199579, 199672-199920, 200262-20049
                                                               5922025
                                                                                              Plus
                               405932
                                                                                                                                123525-123713
                                                               7767812
                                                                                               Minus
                                                               9796686
4464283
                                                                                                                                49996-50346
13758-13922,14558-14752
                               400517
                                                                                               Minus
    65
                               402328
                                                                                               Minus
                                                                                                                                118677-118807,119091-119296,121826-12182
                               405545
                                                               1054740
                                                                                               Plus
                                                               4464283
                                                                                                                                15325-15380,15484-15588,15842-15915
                                 402330
                                                                                               Minus
                                                                                                                                80430-81581
72000-72290,72431-72700,72929-73199
223286-223352,224472-224585
                                404440
                                                                7528051
                                                               7710730
7767724
                                403912
                                                                                               Minus
    70
                                404760
                                                                                               Plus
                                 4048B3
                                                                5101762
                                                                                                 Minus
                                                                                                                                94626-94730,96998-97069
                                403362
                                                                8571772
                                                                                                                                64099-84260
124361-124520,124914-125050
                                405547
                                                                 1054740
                                                                                                Plus
                                 405546
                                                                 1054740
                                                                                                                                124010-124183
                                                                                                Plus
      75
                                 404210
                                                                 5006248
                                                                                                Plus
                                                                                                                                  169926-170121
```

Table 18A: 194 Up-Regulated Genes in Uterine Center Versus Normal Adult Tissues

Table 18A lists about 194 genes up-regulated in utenine cancer compared to normal adult tissues. These were selected from 59660 probesets on the Affymetrix/Eos-Ha03 GeneChip erray such that the ratio of "everage" uterine cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" uterine cancer level was set to the 2nd highest amongst uterine cancers. The "average" normal adult tissue level was set to the 90th percentife value amongst non-malignant tissues. In order to remove gene-specific background

levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the railo was evaluated.

5

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
Unigeneitic: Unigene number
Unigene Title: Unigene gene title
R1: Raflo of turnor vs. normal tissue

	R1:	Rallo of tun	ROF V3. NORMAI G	SSUB	
10	Pkey	ЕхАссп	UnigeneID	Unigene Title	RI
	449034	A1624049		gb:ts41a09x1 NCt_CGAP_Utf Homo seplens cDNA	55.7
	435094	Al560129	Hs.277523	EST	45.2
1 =	438817	Al023799	Hs.163242	ESTs	42.6
15	421478 450000	A\683243	Hs.97258	ESTS	35.2 27.3
	45283B 450451	U65011 AW59152B	Hs.30743 Hs.202072	Preferentially expressed antigen in metanoma EST's	26.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252	24.8
	428187	A1687303	Ha.285529	G protein-coupled receptor 49 (GPR49) (HG38)	24.2
20	438993	AA828995	Hs.52620	integrin; beta 8	16.7
	436775	AA731111	Hs.291891	ESTs	14.3
	430491	AL109791	Ha.241559	Homo sapiens mRNA full length insert cDNA do	13.5
	441377	BE218239	Hs.202656	ESTS	13.5
25	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	12.3 10.7
25	400292	AA250737	Hs.72472	BMPR-lb;bone morphogenatic protein receptor lb	10.7 10.1
	403899 44243B	AA995998		predicted exon gb;os26b03.s1 NCL_CGAP_Kid5 Homo saptens cDNA	10.0
	447350	Al375572	Hs.1939	HER4 (c-erh-B4)	9.8
	453964	Al961486	Hs.12744	ESTs	9,7
30	443830	Al142095	Hs.143273	ESTs	9.1
	459325	AW088369	Hs.282184	ESTs	9.0
/	415245	N59650	Hs.27252	ESTs	8.9
	446608	N75217	Hs.257846	ESTs	8.9
25	426835	9E395109	Hs.129327	ESTa	8.8 8.7
35	433426	H69125	Hs.133525	ESTS ESTs	8.5
	437960 441081	AI669586 AI584019	Hs.222194 Hs.169006	ESTs, Moderately similar to plakophilin 2b [H	8.3
	440048		Hs.158469	ESTs, Weekly similar to envelope protein [H.s	7.3
	447835	AW591623	Hs.164129	ESTs	7.2
40	440B70		Hs.160539	Homo septens cDNA FLJ13793 fis, clone THYRO10	7.1
	412925		Hs.179243	ESTs	7.0
	408562		Hs.31141	Roundabout homolog 2 transmembrane receptor (robo2)	7.0
	429272		Hs.110667	ESTS	6.9 6.3
45	453197		Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM ESTs; Weakly similar to Geg-Pol polyprotein	5.2
73	437938 420610		Hs.99348	distal-less homeo box 5	6,2
	448672		Hs.225106	ESTs	6.1
	452461		Hs.108106	transcription factor	6.1
	413335		Hs.48442	ESTs	6.1
50	449611		Hs.197075	ESTs .	6.0
	449260		Hs.29879	ESTa	6.0
	412140		Hs.73625	RAB6 Interacting, kinesin-like (rabkinesin6)	6.0
	443715		Hs.9700	cyclin E1	6.0 5.9
55	432113 424834		Hs.152385 Hs.153408	ESTs Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.7
35	410658		Hs.192035	ESTs	5.7
	426465			gb:ty16/07.x1 NCI_CGAP_Ut3 Home sepiens cDNA	5.7
	446704		Hs.1970B3	ESTs	6.5
	419503		Hs.137422	ESTs	5.5
60	444342			similar to lysosome-essociated membrane glyco	5.4
	436076		Hs.120954	ESTS	5.4 5.3
	406687		Hs.272620	pregnancy specific bela-1-glycoprotein 9	5.3
	445258 440901		Hs.147613 Hs.128612	ESTs ESTs	5.3
65	434638		Hs.241334	ESTS	5.3
	429334		Hs.186180	Homo septens cDNA: FLJ23038 fils, clone LNG020	5.2
	418853	BE537037	Hs.273294	hypothetical protein FLJ20069	5.2
	459563			gb::IL-BT152-080399-004 BT162 Homo sapiens cDN	5.2
70	436787		Hs.192756	ESTs	5.2
70	40030		Hs.1657 .	Estrogen receptor 1	5.1
	42877		Hs.193143	KIAA1069 protein ESTs	5.1 5.0
	444929 453923		Hs.161354 Hs.36708	es is budding uninhibited by benzimidazoles 1	5.0
	40560		1 0.00104	blaqued exou	5.0
75	41010		Hs.279727	ESTs;	5.0
	43328		Hs.175622	ESTs	4.8
	44327	D NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	4.8
	41024	7 AF1B1721	Hs.61345	RUZS	4.7
QΛ	42258		Hs.179725	ESTs	4.7
80	45277			gb:EST03366 Fetal brain, Stratagene (cat93620	4.7
	40727 42044		u ness	gb:qw34h07.x1 NCI_CGAP_Ut4 Homo saplens cDNA mammaclobin 2	4.7 4.8
	45110		7 Hs.97644	gb:wi60b11.x1 NCI_CGAP_Cg16 Homo saplens cDNA	4.6
	-T-0 () ()	~ mm1044		4	750

	400040	N14 002400	*I- 9004C	dimale assessment light intermediate network	4.6
	453616 424115	NM_003462 AA335497	Hs.33846 Hs.293965	dyneln, exonemal, light intermediate polypept ESTs	4.6
	414245	BE148072	Hs.75850	WAS projein family, member 1	4.6
_	423244	AL039379	Hs,209602	ESTs, Weakly similar to ubiquitous TPR modif,	4.5
5	441031	Al110684	Hs.7645	fibrinogen, B beta polypeptide	4.5
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLI23537 fis, clone LNG076	4.4 4.4
	458861 428758	AI630223 AA433988	Hs.98502	PHD finger DNA binding protein isoform 1 (int Homo septens cDNA FLJ14303 fis, clone PLACE20	43
	420149	AA255920	Hs.88095	ESTs	4.3
10	433479	AW511459	Hs.249972	ESTs	4.3
	449416	AI651016	Hs.246311	ESTs	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone HEP106	4.3
	450109	A1539295	Hs.17967 Hs.130425	ESTs ESTs	4.3 4.3
15	43 69 54 415511	AA740151 AI732617	Hs.182362	ESTs	4.3
10	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM40	4.3
	406411			predicted exon	4,2
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homofo	4.2
20	416456	H57052	Hs.176626	hypothetical protein EDAG-1	4.2 4.1
20	454692 452249	AW813350 BE394412	Hs.61252	9b:MR3-ST0192-100100-024-g07 ESTs	4.1
	436211	AK001681	Hs.80961	polymerase (DNA directed), garrura	4.1
	449765	N92293	Hs.206832	EST, Moderately similar to ALUB_HUMAN ALU SUB	4.1
25	434988	A1418055	Hs.161160	ESTB	4.1
25	423515	AA327017	Hs.162204	ESTs	4.0 4.0
	435407 440886	A1149774 AW511032	Hs.117178 Hs.190516	ESTs ESTs	4.0
	444783	AK001468	Hs.62180	ESTs	4.0
	452039	Al922988	Hs.172510	ESTs	4.0
30	407300	AA102616	Hs.120769	Homo septens cDNA FLJ20483 file, clone KAT0614	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	4.0 3.9
	449433 419335	AI672096 AW960146	Hs.9012 Hs.284137	ESTs Homo seplens cDNA FLJ12888 fis, clone NT2RP20	3.9
	422711	D60641	Hs.21739	Homo sapiens mRNA; cONA DKFZp58611518	3.9
35	453096	AW294631	Hs.11325	ESTs	3.9
	441962	AW972542	Ha.289008	Homo saplens cONA: FLJ21814 fis, done HEP010	3.9
	445034	AW293376	Hs.160323	ESTs	3.8
	418677 422219	S83308 AW978073	Hs.87224	SRY (sex determining region Y)-box 5 gb:EST390182 MAGE resequences	3.8 3.6
40	440304	BE159984	Hs.125395	ESTS	3.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cONA DKFZp434P228	3.8
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK	3.8
	400250		11- 004B	predicted exon	3.8
45	428227 420092	AA321649 AA814043	Hs.2248 Hs.88045	INTERFERON-GAMMA INDUCED PROTEIN ESTs	3.8 3.8
43	415138		Hs.78045	tissue factor pathway inhibitor 2 TFP12	3.8
	437212		Hs.210775	ESTs	3.8
	409867			gb:UI-HF-BR0p-eir-g-12-0-UI.r1 NIH_MGC_52	3.7
50	421477		Hs.104650	hypothetical protein FLJ10292	3.7
50	427119 458154		Hs.114574	ESTs gb:QV4-ST0234-181199-035-g01 ST0234	3.7 3.7
	434539		Hs.214410	gp:Qv4-5102:34-181189-055-gu1 510234 (3.7
	424717		Hs.152213	wingless-type MMTV integration alto family	3.7
EE	412078		Hs.73149	paired box gene 8 (PAX-8)	3.7
55	447342		Hs.19322	ESTs; Weskly similar to !!!! ALU SUBFAMILY J	3.7 3.7
	413472 446619		Hs.75379 Hs.313	solute carrier family 1 (glist high affinity secreted phosphoprotein 1 (osteopontin)	3.7
	453891		Hs.36353	Homo sepiens mRNA full length Insert cDNA do	3.7
	449613			gb:oz39b09.s1 Soares_NhHMPu_S1 Homo seplens c	3.6
60	441285		Hs.167	microtubule essociated protein 2	3.6
	409731		Hs.56145	Orymosin, beta, Identified in neuroblastoma c	3.8 3.5
	417847 441484		Hs.288312 Hs.58972	Homo sapiens cDNA: FLJ22316 fis, clone HRC052 ESTs	3.6
	415802		Hs.6006	ESTs	3.6 1
65	448112	AW245919	Hs.301018	ESTs	3.6
	428330		Hs.2256	matrix metalloprotelnase 7 (metrilysin)	3.6
	402806		11-202000	predicted exon	3.6 3.6
	407905 424917		Hs.252905 Hs.96901	ESTs Homo spriens cONA: FLJ23049 fis, clone LNG025	3.6
70	436982		Hs.5378	spondin 1, (f-spondin) extracellular matrix p	3.6
-	451842		Hs.267087	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.6
	455666			gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapl	3.6
	431731		Hs.211374	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	3.6
75	443694 410358		Hs.112759 Hs.13337	ESTs, Weakly simitar to AF126780 1 retinal sh ESTs, Weakly simitar to unnamed protein produ	3.6 3.5
	406031			predicted exon	3.5
	40974	5 AA077391		gb:7B14E12 Chromosoma 7 Fetal Brain cDNA Libr	3.5
	43048		Hs.203269	ESTS, Moderately similar to ALUB_HUMAN ALU SU	3.5
80	43764		Hs.291911 Hs.155986	ESTS ESTS; Highly similar to SPERM SURFACE PROTEIN	3.5 3.4
90	41521° 44345		Hs.133529	ESTS; FIGURY SINURUE OF SPERM SORPACE PROTEIN	3.4
	45743			FLVCR protein	3.4
	45126		Hs.172967	ESTs	3.4

	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.4
	427778	AA412323	Hs.105323	ESTs	3.3
		A1632091	Hs.116877	ESTS	3.3 3.3
5	407366 417411	AF026942 AW500008	Hs.6966	gb:Homo sapiens cig33 mRNA, partiel sequence. Human DNA sequence from clone RP1-187J11 on c	3.3
,		A1834273	Hs.9711	Homo sapiens cDNA FLJ13018 fls, clone NT2RP30	3.2
	432415	T16971	Hs.289014	ESTs .	3.2
		AA322245	Hs.290165	ESTs	3.2
10		A)674093	Hs.293961	ESTS	3.2 3.2
10		AA687378 AA045848	Hs.194624 Hs.11817	ESTs nudix (nucleoside diphosphata linked molety X	3.2
		AA889120	Hs.110637	Homeo box A10	3.2
		AA761526	Hs.163853	ESTs	3.2
4.5		AA320068	Hs.93701	Homo szpiens mRNA; cDNA DKFZp434E232 (from cl	3.1
15		AW138437	Hs.24790	KIAA1573 protein	3.1 3.1
		AI656166 AW088642	Hs.7331 Hs.97984	ESTs ESTs; Weakly similar to WASP-family protein [3.1
		AA689490	Hs.289109	dimethylarginine dimethylaminohydrolase 1	3.1
0	416623		Hs.38761	Homo sepiens cDNA: FLJ21564 fls, clone COL064	3.1
20	405174			predicted exon	3.1
	403776			predicted exon	31
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily, m	3.1 3.1
	431255 442353	AA497043 BE379594	Hs.115685 Hs.49136	ESTS ESTs	3.1
25	456662		Hs.1494	msh (Drosophila) homeo box homolog 1 (former)	3.1
	416530	U62801	Hs.79361	kalitareln 6 (neurosin, zyme)	3.1
		BE260893		gb:601150677F1 NIH_MGC_19 Homo seplans cDNA c	3.1
	406400			kallikrain 8 (neuropsin/ovasin)	3.0
30	439949	AW979197	Hs.292073	ESTs gb:RC3-ST0186-240400-111-d07 ST0186 Homo sapi '	3.0 3.0
30	430704 401517	AW813091		gracia-a tu 166-240400-111-001 a 10166 nonto sapi	3.0
	417830	AW504786	Hs.132808	epithellal cell transforming sequence 2 cncog	3.0
	435267		Hs.110114	ESTs ,	3.0
0.5	426384	A1472078		ESTs	3.0
35	422797		Hs.120908	KIAA1238 protein	3.0
	428832 449722		Hs.23960	gb:ni22612.st NCL_CGAP_HSC1 Homo sapiens cONA cyclin B1	3.0 3.0
	418478	U38945	Hs.1174	cyclin-dependent kinsse inhibitor 2A	3.0
	422689		162.712.7	gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	3.0
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	TABLE	18B			
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50 55 60 65 70	CAT ma Accessing Pkey 409745 409867 42219 42268 426458 426458 426458 426458 43670 431922 437936 43651 44951 45656 45815 45886 45886 45815 45886	mber: Gene on: Genb CAT nun 115237_ 1186530 213547_ 219896_ 266211_ 267664_ 286144_ 322217_ 331543_ 44573_2 34573_2 34573_2 31543_ 34573_2 31543_ 34573_2 31543_ 34573_2 31543_ 34573_2 31543_ 34573_2 31543_ 34573_2 31543_ 34573_2 31543_ 34573_2 31543_ 34573_2	cluster number ank accession in their Accession in AA077391 1 AW50216 1 AW50216 1 AW50216 1 AW50216 1 AW50216 1 AW50856 1 AW75082 1 AW50851 1 AA95939 1 AA95939 1 AA95939 1 AA95939 1 AM50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851 1 AW50851	AI347818 AI361453 AI083754 AW207491 AW960912 AA921874 AA28 I AW502587 AW502345 3 AW978072 AA807550 AA305567 5 AA315006 AW954733 AA377209 AA855807 AA379527 AA379948 AA379262 AW963933 1 AW205655 AA481440 2 AA503009 AA502998 AA502989 AA502805 T92188 N70208 R97040 N38809 AI308119 AW567677 N35320 AI251473 H59; 4 AI660251 AW874068 AL134043 AW235363 AA663345 AW008282 AV 8 AI872193 AI763273 AW173586 AW16029 AI653892 AI762688 AA61 8 AI872193 AI763273 AW173586 AW16029 AI653802 AW512843 AW512843 A 4 AI65925 AW205862 AI683388 II688509 AW276905 AI633006 AA97 184729 H60652 T92487 AI022068 AA780419 AA551005 W80701 AW61 1867840 AA300207 AW969581 T63226 F04005 5 AA634879 AI926361 8 AI916584 R61781 T77332 F07756 F08149 F07647 W223287 AW4177770 AI859360 I AW880941 AW880937 T07855 AI917711 30 AA078319 R85057 AW803024 H65811 AA078293 30 AW86082 AW813476 AW813383 3 BE065788 BE065889 BE065832 78 AA588222 AA879046 AA879195 3 AI630470	B97 AW971573 R97278 W01059 AW987671 AA90859B 102 R34725 AA884922 BE328517 Al219788 AA884444 N92578 F13493 A88954 AA283144 A890387 Al950344 A1741346 A1689062 AA282915 38777 AA488802 A1356394 AW103813 A1539642 AA642789 AA856975 A044209 AW856538 AA180009 AA337499 AW961101 AA251669 2584 AA908741 AW072828 AW9613996 AA292773 AA969759 N75628
50 55 60 65 70 75	CAT ma Accession of the control of t	mber: Gerie Genb CAT nun 115237_1156530 213547_2 219596_2 266211_3 286144_3 322217_3 31543_4 4573_2 31543_4 4573_2 31543_4 575391_4 794817_5 859083 1 930983 1 12891_6 134954_4 91768_1 798085_1 798085_1 798085_2 112891_6 134954_4 57656_1 798085_2 112891_6 134954_4 57656_1 798085_2 112891_6 134954_4 57656_1 798085_2 115895_2 11	cluster number eark accession in the Accession in AA077391 1 AW950861 1 AW950861 1 AW950861 1 AW97082 1 AW97082 2 A950087 AA251874 AW910289 AW50561 AA251874 AW910289 1 AA02899 1 AA0289 1 AA02899 1 AA02899 1 AA02899 1 AA02899 1 AA02899 1 AA02899 1	AJ347818 AJ361453 AJ088754 AW207491 AW960912 AA921874 AA25 1 AW502587 AW502345 3 AW978072 AA807550 AA305567 5 AA315006 AW954733 AA377209 AA85507 AA379527 AA379948 AA379262 AW963933 9 AA438432 AA481375 AA481363 1 AW20555 AA481375 AA481353 1 AW20555 AA48440 2 AA503009 AA502998 AA502999 AA502805 T92188 N70208 R97040 N38809 AJ308119 AW567677 N35320 AJ251473 H595 4 AJ650251 AW874068 AL134043 AW235363 AA663345 AW008282 AV 8 AJ872193 AJ763273 AW173586 AW160329 AJ653832 AJ762888 AA91 4 AJ819225 AW205862 AJ683338 AJ858509 AW276905 AJ633006 AA97 84729 H60052 T92487 AJ022058 AA780419 AA551005 W80701 AW61 8AJ87249 AA300207 AW959581 T63228 F04005 5 AAB34879 AJ926361 8 AJ917717 AJ858360 1 AW680941 AW680937 T07855 AJ917711 50 AW316082 AW813476 AW813383 3 BE055788 BE055839 BE055832 79 AA382282 AA879046 AA879195 9 AI630470 spondling to an Eos probesel he 7 digit numbers in this column are Genbank Identifier (Gi) numbers.	B97 AW971573 R97278 W01059 AW987671 AA90859B 102 R34725 AA884922 BE328517 Al219788 AA884444 N92578 F13493 A88954 AA283144 A890387 Al950344 A1741346 A1689062 AA282915 38777 AA488802 A1356394 AW103813 A1539642 AA642789 AA856975 A044209 AW856538 AA180009 AA337499 AW961101 AA251669 2584 AA908741 AW072828 AW9613996 AA292773 AA969759 N75628
50 55 60 65 70 75	CAT ma Accessing Pkey 409745 409867 42219 426884 426488 426488 426488 426488 42648 431924 431924 431924 4361 44903 45110 45277 45139 45468 45868 45818 45886 45818 45886	mber: Gerie Genb CAT nun 115237_1156530 213547_2 219596_2 266211_3 286144_3 322217_3 31543_4 4573_2 31543_4 4573_2 31543_4 575391_4 794817_5 859083 1 930983 1 12891_6 134954_4 91768_1 798085_1 798085_1 798085_2 112891_6 134954_4 57656_1 798085_2 112891_6 134954_4 57656_1 798085_2 112891_6 134954_4 57656_1 798085_2 115895_2 11	cluster number eark accession in the Accession in AA077391 1 AW950861 1 AW950861 1 AW950861 1 AW97082 1 AW97082 2 A950087 AA251874 AW910289 AW50561 AA251874 AW910289 1 AA02899 1 AA0289 1 AA02899 1 AA02899 1 AA02899 1 AA02899 1 AA02899 1 AA02899 1	AI347618 Al361453 Al088754 AW207491 AW960912 AA921874 AA28 1 AW502587 AW602345 3 AW978072 AA807550 AA306567 5 AA316006 AW954733 AA377209 AA865807 AA379527 AA379948 AA379262 AW963933 1 AA438432 AA461375 AA481363 1 AW206855 AA84440 2 AA603009 AA502998 AA502989 AA502805 T92188 N70208 R97040 N38809 AI308119 AW567677 N35320 AI251473 H593 4 AI650251 AW874068 A1134043 AW255363 AA663345 AW008282 A4 8 AI872293 AI763273 AW173585 AW160329 AI653832 AI762688 AA98 8 AI872193 AI763273 AW173585 AW160329 AI653832 AI762688 AA98 18 AI872925 AW302682 AI883338 AI88509 AW276905 AI633006 AA97 18 AI84840 AA300207 AW859561 T63226 F04005 5 AA634879 AI926361 8 AI916584 R61781 T77332 F07756 F08149 F07647 18 W23287 18 AW880941 AW880937 107855 AI91771 3 AA078319 R85657 AW803024 H65811 AA078293 3 BC055788 BE0655839 BC056832 79 AA888282 AW813476 AW813383 3 BC055788 BE0655839 BC056832 79 AA888282 AW819466 AA879195 9 AI630470	897 AW971573 R97278 W01059 AW967671 AA90859B 102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 IA88954 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 IB6777 AA488822 AI356394 AW10313 AI259842 AA642789 AA856975 IA044209 AW656538 AA180009 AA337499 AW961101 AA251669 2584 AA398741 AW072828 AW513996 AA293273 AA969759 N75628 I3456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056

Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons. Strand: Nt_position:

5	Pkey	Ref	Strand	Nt_position
J	401517	7677912	Plus	29278-29770
	402606	9909429	Minus	81747-82094
	403776	7770611	Minus	1414-1513.1624-1766
10	403899 405174 405609	7381715 7108030 5757553	Minus Minus Minus	9144-9350 102814-103063 42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702- 52918,55469-55601,57111-57307,58169-58296,60215-80332,61482-61727
15	406030	8312328	Minus	96123-96547 -
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	406411	9256407	Plus	7400-7527

Table 19A: 225 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, UTERINE Cancer Versus Normal Adult Tissues 20

Table 19A lists about 225 genes up-regulated in uterine cencer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

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Pkey: Unique Eos probesel klentifiar number
Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
PSDomein: Protein Structural Domain
R1: Ratio of tumor vs. normal tissue

	Pkey	ExAcon	UnigenelD	Ungene Title	PSDomain	R1
	452838	U65011	Hs.30743	Preferentially expressed artigen in melanoma	TM	27.3
35	438993	AAB28995	Hs.52620	integrin; beta 8	SS,TM,integrin B	16.7
33	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromo	SS,hemopexin	12.3
	44660B	N75217	Hs.257846	ESTS	TM	8.9
	433426	H69125	Hs.133525	ESTS	TM	8.7
			Hs.150539	Homo saplens cDNA FLJ13793 fls, clo	TM.PAX	7.1
40	440870	AI687284		Roundabout homolog 2 transmembrane	SS,TM,lp,fn3	7.0
40	408562	AI436323	Hs.31141		TM.homeobox	6.2
		A)6831B3	Hs.99348	distal-less homeo box 5	TM, kinesin	6.0
	412140	AA219691	Hs.73625	RABS Interacting, kinesin-like (rab		6.0
	443715	Al583187	Hs.9700	cyclin E1	TM,cyclin	5.9
AE	432113	AA935065	Hs.1523B5	ESTs	M	
45	419503	AA243642	Hs.137422	ESTs	TM	5.5
	444342	NM_01439B	Hs.10887	similar to typosome associated memb	TM,Lamp	5.4
	436076	AI 193277	Ha.120954	EST8	M	5.4
	405687	M31128	Hs.272620	pregnancy specific beta-1-glycoprot	TM hemopexin	5,3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.2
50	459593	AI907673		gb:IL-BT152-080399-004 BT152 Homo s	TM	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	TM,harmone_rec,zf-C4	5.1
	405809			predicted exon	TM,Myosin_tall,myosin_head	5.0
	453922	AF053306	Hs.36708	bucking uninhibited by benzimičazol	TM	5.0
	410102	AW24850B	Hs.279727	ESTs;	SS,TM,	5.0
55	433283	BE041135	Hs.176622	ESTs	TM	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gen	TM '	4.8
	410247	AF181721	Hs.61345	RU2S	TM	4.7
	422589	AA312735	Hs.179725	ESTs	TM	4.7
		Al364186		ab:gw34h07.x1 NCL_CGAP_Ut4 Homo sap	TM	4.7
60		NM_002407	Hs.97644	mammaglobin 2	TMUteroglobin	4.6
	453616		Hs.33846	dynein, exonemal, light intermediat	TM,Ribosomal_S27e	4.6
	424115		Hs.293965	ESTs	TM	4.6
	414245		Hs.75850	WAS protein family, member 1	TMWH2	4.6
		A1630223		PHD finger DNA binding protein Isof	TM,PHD	4.4
65		AI651016	Hs.246311	ESTs	SS,TM,	4.3
00	420149		Hs.88095	ESTs	TM	4.3
	433479		Hs.249972		TM	4.3
	457551		Hs.268928		TM	4.3
	406411		1 10.200329	predicted exon	TM,ywe,FG-GAP	4.2
70	416458		Hs.176826		TM	42
, ,	454692		115.17 002.0	db:MR3-ST0192-100100-024-007 ST0192	TM	41
	436211		Hs.80961	polymensse (DNA directed), gamma	TM ·	4.1
	434988		Hs.161160		TM ,	4.1
	444783		Hs.62180	ESTS	TMPH	4.0
75	440886		Hs.190516		TMLFG-GAP	4.0
13					TM,Glypo_transt_29,TEA	4.0
	425176		Hs.301430		TM	3.8
	445034		Hs.160323			3.8 -
	418677		Hs.87224	SRY (sex determining region Y)-box	TM,HMG_box	3.B
80	400250		11- 0045	predicted exon	TM,Hist_deacetyl	
φV	428227		Hs.2248	interferon-garma Induced protein	TM/ILB	3.8
	415138		Hs.78045	Ussue factor pathway Inhibitor 2 T	TM,Kunitz_BPTI,G-gamma	38
	458154		11- 40/2	gb:QV4-ST0234-181199-035-g01 ST0234	TM, WW	3.7
	421477	AJ904743	Hs.104650	hypothetical protein FLI10292	'TM	3.7

	413472	BE242870	Hs.75379	solute cerrier femily 1 (glial high	TMSDF	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to UII ALU SU	TM	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopon	TM,Osteopontin	3.7
_	453891	AB037761	Hs.36353	Homo sapiens mRNA full length Inser	TM	3.7
5	441285	NM_602374	Hs.167	microtubule-associated protein 2 thymosin, beta, identified in neuro	TM, tubulin-binding TM, Thymosin	3.6 3.6
	409731 4414B4	AA125985 AA9354B1	Hs.56145 Hs.58972	ESTs	TM,fn3,lg,Y_phosphalase	3.6
	428330	L22524	Hs.2256	matrix metalloproteinese 7 (matrity	SS,Peptidase_M10	3.6
4.0	407905	AW103855	Hs.252905	ESTs	SS,TM,Ephán	3.6
10	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellula	SS,TM,	3.6
	402606 443695	AW204099	Na 449750	predicted exon ESTs, Weakly similar to AF125780 1	TM TM	3.6 3.6
	443695	AA811452	Hs.112759 Hs.291911	ESTs	TM	3.5 -
	415211	R64730.comp	Hs.155986	ESTs: Highly similar to SPERM SURFA	TM,IQ,Rila	3.4
15	443450	N66045	Hs.133529	ESTs	TM	3.4
	45743B	NM_014053	Hs.270594	FLYCR protein	TM TH BhoGEE BH	3.4 3.3
	435031 417411	A1632091 AW500008	Hs.116877 Hs.6966	ESTs Human DNA sequence from clone RP1-1	TM,RhoGEF,PH TM	3.3
	435174	AA687378	Hs.194624	ESTs	TM,SPRY	3.2
20	444743	AA045848	Hs.11817	nudix (nucleoside diphosphata linke	TM,mut7	3.2
	433420	A1674093	Hs.293961	ESTs	TM	3.2
	419917 417728	AA320068 AW138437	Hs.93701 Hs.24790	Horno saplens mRNA; cDNA DKFZp434E23 KIAA1573 protein	TM TM	3.1 3.1
	403776	W44 (2040)	118.24730	predicted exon	SS,TM,ILB	3.1
25	426274	D38122	Hs.2007	tumor necrosis factor (ligand) supe	TM,TNF	3.1
	416623	N74925	Hs.38761	Homo sapiena cDNA: FLJ21564 fis, cl	TM, Ets	3.1
	405174	A 4 6070 42	Un 44CCOC	predicted exon ESTs	TM TM	3.1 3.1
	431265 456662	AA497043 NM_002448	Hs.115685 Hs.1494	rish (Drosophila) homeo box homolog	TM,hameobox	3.1
30	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	TM, trypsin, pro_isomerase	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapt	TM	3.1
	406400			kalikrein 8 (neuropakriovasin) predicted exon	TM,trypsin TM,HMG14_17	3.0 3.0
	401517 417B30	AW504786	Hs,132808	eplitiellel cell transforming sequen	TM	3.0
35	435287	N23797	Hs.110114	ESTS	TM	3.0
	449722	BE280074	Hs.23960	cyclin Bi	TM,cyclin	3.0 3.0
	418478 422689	U38945 AW856665	Hs.1174	cyclin-dependent kinase inhibitor 2 gb:RC3-CT0297-290100-013-603 CT0297	TM,ank TM,SNF2_N	3.0
	441794	AW197794	Hs.253338	ESTs	TM,ank	2.9
40	41665B	U03272	Hs.79432	fibrillin 2 (congenital contractura	TM,EGF,TB	2.9
	431130		Hs.2719 Hs.83484	epididymia-specific; whey-addic pr ESTs	SS,wap TM,HMG_box	2.9 2.9
	418113 402373		Hs.301865	dopachrome tautomarese (dopachrome	TM,TEA	2.9
4.0	431989	AW972870	Hs.291069	ESTs	SS .	2.9
45	400284		11: 40 84 88	Estrogen receptor 1	TM.homone_rec,zf-C4	2.9 2.9
	438578 423513		Hs.164168 Hs.129719	ESTs transglutaminase 5	TM,formy[_transf,AIRS,GARS TM _Transglutamin_N	28
	448966		Hs.287462	Homo saplens cDNA FLJ11875 ffs, clo	TM	2.8
50	431870	AW449902	Hs.105500	ESTs	TM,MHC_J,ig	28
50	409457		Hs.142179	gb:CM4-ST0276-101299-059-b09 ST0276 ESTs, Wealdy similar to ORF2 [M.mus	TM TM	2.8 2.8
	438777 451807		Hs.27099	DKFZP564J0863 protein	TM	2.8
	433326		Hs.159430	ESTs	M	28
	448221			gb:601440775T1 NIH_MGC_72 Homo sapi	TM	2.8
55	448141		Hs.197531	ESTS	TM,6ZIP TM,Sec7	2,8 2.8
	456311 405454		Hs.190016	ESTs predicted exon	TM	2.8
	459287			gb:DKFZp584G2378_r1 564 (synonym: h	TM	2.8
<i>c</i> 0	438939		Hs.31564	ESTs	TM	2.7
60	421312		Hs.291670 Hs.89433	ESTS	TM,G-paich TM,ABC_membrane,ABC_tran	2.7 2.7
	418883 424341		Hs.145479	ATP-binding cassette, sub-femily C Homo sapiens cDNA FLJ 10518 fis, clo	TM	27
	417950		Hs.190465		SS,sushi	2.7
65	445537		Hs.12844	EGF-like-domain; multiple 6	\$8,EGF	27
65	448089		Hs.173698		SS,TM, TM,Clat_edaptor_s	26 26
	44664: 45667:		Hs.282060 Hs.114293		TM	2.6
	45725	8 AA459443	Hs.231B16		SS	2.6
70	43896	5 AF085888	Hs.269307		TM,Spin-Ssty	2.5 2.5
70	43531 41735		Hs.189729 Hs.15049	ESTS ESTS	TM,MBD TM,CH	2.5 2.5
	41219		Hs.69165	ESTs	TM -	2.5
	41327	8 BE563085	Ha.833	interferon-stimulated protein, 15 k	TM,ublquitin	25
75	42150		Hs.105039		TM,Na_Pi_colrans TM,pkinase	2.5 2.5
15	41809 41000		Hs.106604	gbzm20h12.s1 Stratagene pancreas (TM,FG-GAP	2.5
	42036	2 U79734	Hs.97206	huntingfin interacting protein 1	TM,ENTR.I_LWEQ	2.5
	43197		Hs.200934		TM,bZIP	2.5 · 2.5
80	43820 44757		Hs.6111 Hs.13658	KIAA0307 gens product S ESTs	Tim,Hlh,Pas Tim	2.5 2.5
	41481	2 X72755	Hs.77367	monolisine induced by gamma interfero	SS,IL8	2.5
	42151		Hs.10535		TM,Glyco_transf_29 TM suchi	24 24
	41640	12 NM_000715	Hs.1012	complement component 4-binding prot	TM,sushi	2.4

	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HU	тм	24
		H55709	Hs.2250	leukemia inhibitory factor (choline	SS.LIF_OSM	2.4
		AW959741	Hs.40368	adaptor-related protein complex 1,	TM,Clat_adaptor_s	2.4
5		AA431765 AA708958	Hs.168732	gb:zw80c03.s1 Soares_testis_NHT Hom ESTs	TM,HECT TM	2.4 2.4
•		AA393351	Hs.132121	ESTs	TM	24
	426698	AA394104	Hs.97489	ESTs	ТМ	24
		AF098158	Hs.9329	Homo saplens mRNA for fls353, compl	TM	2.4
10		AAB33930	Hs.288036	tRNA Isopentenylpyrophosphate trans	TM,IPPT	2.4
10	434808 432441	AF155108 AW292425	Hs.256150 Hs.163484	ESTs, Highly similar to NY-REN-41 a EST	TM TM,Fork_head	23 23
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	TM	2.3
	402298	,	124510	predicted exon	TM,zf-C2H2,KRAB	23 .
1.5	435542		Hs.269533	ESTS	TM	2.3
15		A1743261	Hs,131860	ESTs	TM	2.3
	418203 429228	X54942 A1553633	Hs.83758	CDC28 protein kinase 2	TM,CKS	2.3
	418969	W33191	Hs.104985 Hs.28907	ESTs hypothetical protein FLJ20258	TM TM,SH3	2.3 2.3
	447570	A1868315	Hs.99669	ESTs	TM,PHD	23
20	405032			predicted exon	TM,FMO-like	2.3
	- 416566	NM_003914	Hs.79378	cyclin A1	TM,cyclin	2.3
	420900	AL045633 AA481269	Hs.44269 Hs.178381	ESTs	TM,FAD_binding_5	2.3
	417372		Hs.290814	ESTs	TM,ABC_membrane,p450 TM	2,3 2.3
25		AJ948808	Hs.191144	ESTs	TM	23
	410361	BE391804	Hs.62661	guanytate binding protein 1, interf	TM,GBP	2.3
	434131	AI858275	Hs.143659	ESTs	TM	2.3
	431846	BE019924	Hs.271580	Uroplakin 1B pasopharyngeal epithelium specific	TM,transmembrane4	2.3
30	425638 440006	NM_012397 AK000517	Hs.158450 Hs.6844	hypothetical protein FLJ20510	TM TM	23 23
	445870	AW410053	Hs.13408	synlaxin 18	TM	23
	430839	AW025427	Hs.233552	ESTs	TM,pkinase	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	SS,TM,	2.3
35	422095	AIB68872	Hs.288966	ceruloplasmin (ferroxidase)	SS,TM,Cu-oxidese	2.2
55	411558 408380	AA102670 AF123050	Hs.70725 Hs.44532	"Human GABA-A receptor pi subunit m diubiquitin	TM,neur_chan TM .7tm_3,ANF_receptor	2.2 2.2
	403721	74 123030	110.77000	predicted exon	ТМ	22
	440711	AA904389	Hs.143511	ESTs	TM,rcm	2.2
40	457285	A1038858	Hs.228780	ESTs, Highly similar to AF199597 1	TM_eftand	2.2
40		BE545072 Al953499	Hs.122579	ESTS	TM	22
	433462	AA523686	Hs.152617 Hs.222695	ESTs Homo sepiens cDNA: FLJ20986 fis, cl	TM TM	2.2 2.2
	420777	AA280223	Hs.130865	ESTs	ŤM	22
4.00	446659	Al335361	Hs.226376	ESTs	TM	2.2
45	410227	AB009284	Hs.61152	exastoses (multiple)-like 2	TM	2.2
	422282	AF019225	Hs.114309	shojibokofeju F	TM Conduction	22
	4317 01 426910	AW935490 AA470023	Hs.14658 Hs.190089	ESTs ESTs	TM,Occludin TM,MMR_HSR1	2.2 2.2
	405836	70711.0023	Hs.153595	predicted exon	SS,TM,EGF,kil_recept_a	2.2
50	401933			predicted exon .	TM.ton_trans	2.1
	436679	Al127483	Hs.120451	ESTs, Weakly similar to unnamed pro	TM	2.1
	451061 410664	AW291487	Hs.213659 Hs.65370	ESTs, Weakly similar to KIAA1357 pr lipase, endothellal	TM SS,TM,Ribosomal_122,lipasa	21 21
	449378		Hs.59892	ESTs	TM	21
55	433345		Hs.1529B2	EST cluster (not in UniGene)	TM	2,1
	425851	NM_001490	Hs.159642	glucosaminyi (N-acetyl) transferase	SS,TM,Branch	21
	431832	AW276868	Hs.192715	ESTs	TM,Ets,SAM_PNT	21
	448275 423049	BE514434 X59373	Hs.20830 Hs.188023	synaptic Ras GTPase activating prot ESTs	TM,kinesin ,abhydrofase_2 TM,homechox	2.1 2.1
60	427510		Hs.178312	small nuclear RNA activating comple	TM	2.1
	418076		Hs.6724	ESTs	TM	21
		AB000115	Hs.75470	hypothetical protein, expressed in	TM	21
	429183		Ha.197955	KIAA0704 protein ob:Homo sapiens full length insert	ŢM	21
65	439031 431060		Hs.249171	homeo box A11	TM. TM:homeobox	2.1 2.1
0.5	451494		Hs.247095	ESTs, Moderately similar to ALU7_HU	TM	2.1
	419978	NM_001454	Hs.93974	forkhead box J1	TM,Fork_head	2,1
	404535		Hs.121483	chtoride charael 1 , skeletal muscl	SS	21
70	445181 452367		Hs.147471	ESTs	TM TM Underland	21
70	443591		Hs.29279 Hs.179240	eyes absent (Drosophila) hornolog 2 ESTs	TM,Hydrolase TM	2.1 2,1
		AW591433	Hs.170675		TM,trypsin	21
	424310		Hs.50334	ESTS	TM	2.0
75	450193		Hs,224623		TM,pklnase	2.0
13	436009 453313		Hs.120925		SS,TM,Ephrin The	2.0
	419833		Hs.153746 Hs.220697		TM TM,WHEP-TRS	2.0 2.0
	437555	AA759263	Hs.14041	ESTs	TM,Nramp	20 ·
00	411828	AW161449	Hs.72290	wingless-type MMTV integration site	TM,wnt	2.0
80	440052		Hs.195648		TM.PAC	2.0
	410718 404767		Hs.191435	ESTs predicted exon	TM,SQS_PSY TM	2.0 2.0
	447462		Hs.158973		TM	2.0

5	410292 A 442748 A 458760 A 409799 E 401324 432140 A	ND16713 N498631 D11928 NK000404	Hs.202388 Hs.124194 Hs.135787 Hs.111334 Hs.76845 Hs.272688	ESTs ESTs ESTs ferritin, light polypeptide phosphoserine phosphatese-like predicted exon hypothetical protein FLL/20397	TM TM TM TM,HCO3_cotransp TM,Hydrofase TM,nycsin_head SS	20 2.0 2.0 2.0 2.0 2.0 2.0 2.0
10	447541 A 421379 \ TABLE 198	/15221	Hs.18800 Hs.103982	typothetical protein FLJ20281 small inducible cytokine subfamily	TM,z4CCHC SS,TM,IL8	2.0 2.0 ·
				_		
15	Pkey: CAT numbe Accession:	ar. Gene cluste	probeset idenli r number cession numbe			-
	Pkey	CAT sumbe	Accession			
20	409457 410008 422689 428679 438993	1132521_1 116812_1 219896_1 294049_1 467651_1	AA079552 B AW856665 A AA431765 A	\W392887 AW614700 AW392881 E142525 BE142527 \A315006 AW954733 A432015 A334879 AJ926361		
25	439031 448221 454392 454692 458154 458861	46798_1 755341 115882_1 1229118_1 491768_1 798085_1	AF075079 H BE622615 BE260893 A AW813350 /	48601 H48795 A078319 R85057 AWB03024 H85811 AA078293 AWB16082 AWB13476 AWB13383 AA88E282 AA879046 AA879195		
30	459287	977129_1	AL079369 D			
	TABLE 19	C				
35	Pkey: Ref;	Sequence s	curce. The 7 o	ding to an Eos probeset figit numbers in this column are Genbank Identitier Dunham I. et al., Nature (1999) 402:489-495.	(Gi) numbers. "Dunham I. et al." refers to the	o eaneupes AMC ent't belitine notice tidual
	Strand: Ni_position	Indicates Di	NA strand from	which exons were predicted. xns of predicted exons.		
40	Pkey	Ref	Strand	Nt_position		
	401324 401517	9863791 7677912	Plus Plus	234057-234174 29278-29770		
45	401933 402298	3810668	Minus	48725-49057,51864-51955,52424-52589		
73	402606	6598824 9909429	Plus Minus	36758-37953 81747-82094		
	403721 403776	7528046 7770511	Minus Minus	156647-157368 1414-1513,1624-1756		
50	404767 405032	7882827	Minus	23244-23759		
30	405032	7107731 7108030	Minus Minus	131945-132224 102814-103063		
	405454 405609	7656676 5757553	Plus Minus	133507-134053 42814-43010,43583-43783,44863-45033,46429	A6554 A7845 A8048 A0064 E0452 E469A	
55	70000	010100	14minus	51727,51823-51959,52702-52918,55469-55601		
33	405636	5123990	Plus	60332,61482-61727 56384-56587		
	405400 406411	9256298 9256407	Plus Plus	1553-1712,187B-2140,4262-4385,5922-6077		
60	400411	3230407	rus	7400-7627		
60						
	Table 20A	c 56 Up-Regula	ted Genes End	oding Extracellular/Cell Surface Proteins, Uterine	Cancer Versus Normat Adult Tissues	
65	molecules	. These were s	elected as for 1	ated in alerine cancer compared to normal adult fo Labla 18A, except that the railo was greater than or d by small molecules (e.g. planese, peptidase, ison	requal to 2.0, and the predicted protein conta	ined a structural domain that is indicative of
	Pkey:	Uninus Eco	s probeset Iden	niffer number		
70	Unigene ?	Exemplar / D: Unigene m litte: Unigene ge n: Protein Str	Accession num Imber ene litte	ber, Genbank accession number		
75	Pkey	ExAcon	OleneginU	Unigene Title	PSDomain	R1
	428187	AI687303	Hs.285529		7tm_1	24.2
	400289 447350	X07820 Al375572	Hs.2258 Hs.172634	Matrix Metalloproteinase 10 (Stromoly HER4 (o-erb-B4)	hemopaxin kinase	12.3 9.8
80	420610	A16B3183	Hs.99348	distal-less homeo box 5	homeobox	6.2
	405609 458861	NM_007358	Hs.31016	predicted exon PHD linger DNA binding protein	Myosin_tait, myosin_head PHD	5.0 4.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone	NA	4.3
			•	2	.57 ·	
			•		J	

		AK001581	Hs.80961	polymerase (DNA directed), gamma	NA.	4.1	
	444783	AK001468	Hs.62180	ESTs	PH	4.0	
	418677		Hs.87224	SRY (sex determining region Y)-box 5	HMG_box	3.8	
5		BE242870 AI079356	Hs.75379 Hs.21807	solute carrier family 1 gb:oz39b09.s1 Soares_NhHMPu_S1 Homo s	SDF zf-C2H2	3.7 3.6	
J	428330		Hs.2256	matrix metalloproteinase 7 (matrilysin)	Peptidese_M10	3.6	
		AW204099	Hs.112759	ESTs, Weakly similar to AF128780 1 re	NA	3.6	
		Al632091	Hs.116877	EST's	RhoGEF,PH	3.3	
		AW500008	Hs,6966	Human DNA sequence from clone RP1-187	NA .	3.3	
10		AA669490	Hs.289109	dimethylarginine dimethylarninohydrola	NA	3.1	
	416530		Hs.79361	kalikrein 6 (neurosin, zyme)	trypsin,pro_feomerase	3.1	
		AA343829	Hs.104570	kalfikrain B (neuropsin/ovasin)	trypsin	3.0	
		U38945	Hs_1174	cyclin-dependent kinase Inhibitor 2A	ank	3.0	
		AW197794	Hs.253338	ESTs	ank	29	
15		AL135225	Hs.301865	dopactrome tautomerase (dopactrome de	TEA	29	
	423513	AF035960	Hs.129719	transglutaminese 5	Transglutamin_N	2.8	
	44B141	AI471598	Hs.197631	ESTs	bZIP	2.8	
		NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	guanylate_cyc	2,7	
00		NM_004996	Hs.89433	ATP-binding cassette, sub-family C	ABC_membrane,ABC_tran	2.7	
20	448435		Hs.182278	calmodulin 2	NA	2.6	
	417351		Hs.15049	ESTs	CH	2.5	
		Al206173	Hs.211375	ESTs	SH3,efkand,C2,PH	25	
		AW972689	Hs,200934	E87s	bZIP	2.5	
O.E		AW812795	Hs.155381	ESTs, Moderately similar to I38022 hy	ank	24	
25		Y11339	Hs.105352	GaINAc alpha-2, 6-stalyltransferase I	Glyco_transf_29	2.4	
	403095			predicted exon	homeobox,PAX	2.4	
	406815		Hs.288036	IRNA isopentenylpyrophosphate transfe	IPPT	24	
	435615	Y15085	Hs.4975	polassium voltage-gated channel	lon_channel	23	
20	40229B			predicted exon	zf-C2H2,KRAB	2.3	
30	418203		Hs.83758	CDC28 proteia kinase 2	CKS	2,3	
	430563		Hs,178381		ABC_mambrane,p450	2.3	
	447570		Hs.99669	ESTs	PHD	2.3	
	439018		Hs.26638	membrane-sparving 4-domains, subfamil	NA	2.3	
25	415539		Hs.72472	BMPR-lb;	bone morphogenetic protein NA	22	
35		A186B872	Hs.288966	ceruloplasmin (ferroxidase)	Cu-oxidase	2.2	
	408380		Hs.44532	ginpjdrigu	ANF_receptor,sushi,7tm_1	2.2	
	440711		HB.149511	ESTS	um ,	2.2	
	457285		Hs.228780		eshand	2.2	
40	418506		Hs.85339	G protein-coupled receptor 39	NA.	2.2	
40	410684		Hs.65370	Epase, endothelia!	Ribosomal_L22,fipase,PLAT	2.1	
	425851		Hs.159642		Branch	2.1	
	448275		Hs.20830	synaptic Ras GTPase activating protein	kinasin,PHD,abhydrolase_2	2.1	
	429782		Hs.2206B9		rm,NTF2	2.1	
45	404535		Hs.121483		NA	2.1	
45	448105		Hs.170675		trypsin	21	
	446342		Hs.14846	Cationic amino acid transporter (ecto	NA .	2.0	
	458760		Hs.111334		HCO3_potransp,zf-C3HC4	2.0	
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	2.0	
50	401324			predicted exon	myosin_head	2.0	
30	TARKE	non	-				
	TABLE	ZUB					
	Die	Helevo Es	o nachaeat Idae	differ mumber			
	Pkey:		is probeset ider	inner number			
55	Accessi	mber: Gene clus					
23	MERCEN	Cai. Gelwerk i	ocession numi	JES		-	•
	Discus	CAT					
	Pkey	CAT ROTTI	oer Accession				
	443613	575391_1	A1079356 V	M22707			
60	458861						
VV	430001	120002_1	AIDJUZZJ A	0000410			
	TABLE	200					
	INDUE	200					
	Pkey:	finlana mi	mber angreene	nding to an Eos probeset			
65	Ref:			digit numbers in this column are Genbank identific	or ICR numbers Thunbarn I of all motors to	the multipoline softled "The DMA a	ogunana af
0.5	1 401.			Dunham I. et al., Nature (1999) 402:489-495.	or food unumerer profits at it of sir seres fo	THE PROGRESSION THE DAY S	ednerice n
	Strand:			n which exons were predicted.			
	Nt post			tions of predicted exons,			
	пфия	MON. HURSANS	noceonga hoe	unis of predictal axions,			
70	Pkey	Ref	Strand	All mariflem			
7.0	I MAY	INDI	OTHIN	Ni_position			
	401324	9863791	Plus	224057 224474			
	402298			234057-234174	•		
	403095		Plus	36758-37953 150005-150040-151584-151600			
75	405095		Plus	150025-150240,151584-151690 42814-42010 (3583-43783-44863-45023-4642	D ACEEA A7D4E A0040 A0004 CD4C3 C4004		
, 5	-103009	5757553	Minus	42814-43010,43583-43783,44863-45033,4642		•	
				51727,51823-51959,52702-52918,55469-5560 60332,61482-61727	11,21111-01301,20103-00290,00215-		
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077		•	
	700)400	3230230	f.Mg	1100-226 COCH-2624-4001 31 11 11 11 11 11 11 11 11 11 11 11 11		•	
80							
30							

Table 21A: 270 Up-Regulated Genes, Uterine Cancer Versus Normal Uterus

Table 21A lists about 270 genes up-regulated in uterine cancer compared to normal uterus. These were selected as for Table 18A, except that the ratio was greater than or equal to 5.0, and the denominator was the median value for six non-malignant uterine specimens.

Pkey: Unique Ecs probeset Identifier number

Exaccn: Examplar Accession number, Genbank accession number

Unique number

Unique Title: Unique gene title

Ratio of tumor vs. normal tissue

5

10

10		. 225 24 (0	MOT TO TOURING	usaus	
	Pkey	ExAcon	UnigenelD	Unigena Tifa	R1
	449034	AI824049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens	CF 7
4.5	435094	Al580129	Hs.277523	EST	55.7 45.2
15	438461	AW075486	Hs.286049	phosphoserine aminotransferase	19.5
	434779		Hs.50151	potassium inwardly-rectifying channel	15.6
	441633 429183		Hs.112242	ESTS	15.2
	436775		Hs.197955 Hs.291891	KIAA0704 protein	14.6
20	441031	Al110684	Hs.7645	ESTs fibrinogen, B beta polypeptide	14.3
	446921	AB012113	Hs.16530	CC chemokine SCYA18 (MIP-4) (PARC)	14.0
	413753	U17760	Hs.301103	Laminin, beta 3 (nicela (125kD), kalinin	13,0 12.9
	421515		Hs.105352	GatNAc alpha-2, 6-sistyltransferase I, I	12.2
25	414646		Hs.901	CD48 antigen (B-cell membrane protein)	12.0
23	453891	AB037761	Hs.36353	Homo sepiens mRNA full length insert cDN	11.7
	425196 444863	AL037915 AW384082	Hs.155097	carbonic anhydrese II	11.4
	449785		Hs.301323 Hs.288300	ESTS	11.3
	446839	BE091926	Hs.16244	Homo sapiens cDNA: FLJ23231 fis, clone C mitotic spindle colled-coil related prot	11.1
30	449801	AA477355	Hs.288300	Homo septens cDNA: FLJ23231 fis, clone C	10.9
	411773	NM_006799	Hs.72026	_protease, serine, 21 (testisin)	10.3 10.3
	414812	X72755	Hs.77367	monokine induced by gamma Interferon	f0.2
	410361	BE391804	Hs.62661	guanylale binding protein 1, interferon-	10.1
35	423645	AI215632	Hs.147487	ESTs	10.1
J.J	442438 415786	AA995998 AW419196	U- orzoni	gb:os26b03.s1 NCI_CGAP_Kld5 Homo saplens	10.0
	458017	AAB13426	Hs.257924 Hs.192034	ESTS	10.0
	435525	AI831297	Hs.123310	ESTs, Weakly similar to KIAA0705 protein ESTs	10.0
40	413335	AI613318	Hs.48442	ESTs	9.9 9.7
40	420297	Al628272	Hs.88323	ESTa	9.6
	452799	A1948829	Hs.213786	ESTs	9.6
	434311	BE543469	Hs.266263	Homo saplens cDNA FLJ14115 fls, clone MA	9.4
	408243 430713	Y00787	Hs.624	intedeukin 8	9.3
45	452092	AA351647 BE245374	Hs.2642 Hs.27842	eukaryotic translation elongation factor	9.3
	444342	NM_014398	Hs.10887	hypothetical protein FLJ11210 similar to lysosome-associated membrane	9.2
	443830	A1142095	Hs.143273	ESTs	9.2
	442547	AA306997	Hs.268352	ESTs, Wealthy similar to hypothetical pro	9.1 9.0
50	421633	AF121860	Hs.106260	sorting nexts 10	9.0
50	403381			0	8.9
	426635 440500	BE395109	Hs.129327	ESTs	8.8
	436291	AA972165 BE568452	Hs.15030B	ESTS	8.7
	431668	AW969610	Hs.6101 Hs.151179	ESTs; Highly elmitar to protein regulati ESTs	8.7
55	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subtamily A	8.7
	424988	AU077312	Hs.153985	solute carrier family 7 (cationic amino	8.7 8.6
	425495	AA35B454	Hs.78026	ESTs, Weakly similar to similar to enkyr	8.6
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9	8.5
60	436986	AF085888	Hs.269307	ESTs	8.4
OU.	422731 441081	AL138411 Al584019	Hs.169006	gb:DKFZp434A1229_r1 434 (synonym: hles3)	8.4
	415992	C05837	Hs.145807	ESTs, Moderately similar to plakophilin Homo sapiens cDNA FLJ13593 fis, clone PL	8.3
	431211	M88849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, co	8.2
15	409865	AW502208		gb:UI-HF-BR0p-aju-e-09-0-UI.r1 NIH_MGC_6	8.2 6.0
65	448159	Al627292	Hs.190877	ESTe	8.0
	401519	11010000		0	7.9
	441730	A1243276	Hs.149017	EST3	7.9
	432441 448275	AW292425 BE514434	Hs.163484	EST .	7.8
70	438424	Al912498	Hs.20830 Hs.25895	synaptic Res GTPase activating protein 1	7.B
• •	447342	AH99268	Hs.19322	ESTs, Weakly similar to PL-3 kinase (PLs	7.8
	408369	R38438	Hs.182575	Solute carrier family 15 (H+/peptide tra	7.7
	423081	AF262992	Hs.123159	sperm associated antigen 4	7.7 7.6
75	414484	BE314385		gb:601154649F1 NIH MGC 19 Homo sanlens c	7.6
75	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.6
	459142 411094	A1903396		gb:RC-BT029-120199-219 1 BT029 Homo semi	7.5
	436679	8E068142 Al127483	Un 120/Er	gb:CM4-BT0320-221199-047-g10 BT0320 Homo	7.5
	452607	A/160029	Hs.120451 Hs.6143B	ESTs, Weekly similar to unnamed protein ESTs	7.5
80	443171	BE281128	Hs.9030	TONDU	7.5
	459081	W07808		gb:zb03a12.r1 Soares_fetal_lung_NbHL19W	7.4 7.4
	431195	AA5030B3	Hs.79742	ESTs	7.4
	444459	A1680624	Hs.148676	ESTs	7.4

	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	7.0
	414918		Hs.72222	Hypothetical protein FL/13459	7.3
	429334	D63078	Hs.186180	Homo saplens cDNA: FLJ23038 fis, clone L	7.3 7.3
~	44B865	R35027		gb:yg60g02.r1 Soares intent brain 1NIB H	7.3
5	409219	AA393383	Hs.133331	ESTs	7.3
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	7.2
	403485			0	7.2
	408350	AW183350	Hs.250127	ESTs	7.2
10	445873	AA250970	Hs.251946	Homo sepiens cDNA: FLI23107 fis, clone L	7.1
IU	400995			0	7.1
	406086			0	7.1
	403378	1107050	12 100101	0	7.0
	426227 42203B	U67058 R39098	Hs.168102	Human proteinase activated receptor-2 mR	7.0
15	431842		Hs.192028	ESTs	7.0
15	429732	NM_005764 U20158	Hs.271473	epithellal protein up-regulated in carci	6.9
	427494	AI628365	Hs.2488 Hs.130412	lymphocyte cytosolic protein 2 (SH2 doma	6.9
	429272	W25140	Hs.110667	ESTs, Weakly similar to sre-2 [C.elegans	6.9
	427258	AA400091	Hs.39421	ESTs ESTs	6.9
20	449309	AW589823	Hs.224189	ESTs	6.9
-	400104	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1	0	6.9
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	6,9
	404767		14011012	O examplement confrontent 4-printed biolisks	8.8
~~	406690	M29540	Hs.220529	CEA (carcinosmbryonic antigen-related ce	6.8
25	439760	AL359053	Hs.57664	ESTs	6.8
	403127	A1904493	Hs.99890	polymerase (DNA directed), delta 1, cata	6.8 6.8
	418203	X54942	Hs.83758	COC28 protein kinase 2	6.8
	42585B	AA364923		gb:EST75602 Pineal gland II Homo saplens	6.8
20	421712	AK000140	Hs.107139	hypothetical protein	6.7
30	456903	D49441	Hs.155981	mesothelin	6.7
	414564	AA164803	Hs.71994	ESTs	6.7
	457942	AW865665	Hs.153034	ESTs .	6.7
	410442	X73424	Hs.63788	propionyl Coenzyma A carboxylase, bela p	6.7
35	424598	AB020639	Hs.151017	estrogen-related receptor gamma	6.7
JJ.	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	6.7
	429597	NML,003816	Hs.2442	a disinlegrin and metalloproteinase doma	6.6
	413472 410564	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.6
	428575	NM_006033	Hs.65370	lipase, endothellat	6.6
40	406400	M19684	Hs.184929	serine (or cystelne) protelnese inhibito	6.6
. •	426317	AA312350	Hs.169294	kalikrein 8 (neuropsiniovasin)	6.6
	441460	Al952478	Hs.226804	transcription factor 7 (T-call specific,	6.5
	412570	AA033517	Hs.74047	ESTs, Moderately similar to ALUC_HUMAN !	6.5
	424349	AF141289	Hs.145550	electron-transfer-flavoprotein, beta pol solute carrier family 7 (cationic amino	6.5
45 ⁻	448581	AL109781	Hs.21754	Homo saplens mRNA full length insert cDN	6.5
	445258	Al635931	Hs.147613	ESTs	6.4
	456032	AW957446	Hs.301711	ESTs	6.4 6.4
	404727			0	6.4
50	422B10	AA317400		gb:EST19374 Retina II Homo saptens cDNA	6.4
50	440044	AW665167	Hs.259563	EST	6.4
	416498	U33832	Hs.79351	potessium channel, subfamily K, member 1	6.4
	426600	NML003378	Hs.171014	VGF nerve growth factor inducible	6.4
	422170	Al791949	Hs.112432	ang-Mullerian hormone	6.4
55	449611 402539	AI970394	Hs.197075	EST8	6.4
55	456983	AVV502761	Hs.30909	KJAA0430 gene product	6.3
	407910	AI081687	Hs.170225	thymopoletin	6.3
	457887	AA650274 Al240007	Hs.41296	Euronectin leucine rich transmernbrane p	6.3
	431765	AF124249	Hs.148812 Hs.268541	ESTs	6.3
60	420344	BE463721	Hs.97101	novel SH2-containing protein 1	6.3
	443494	T99719	Hs.270404	Putative G protein-coupled receptor GPCR	6.2
	456844	Al264155	Hs.1529B1	Home sapiens cDNA: FLJ22389 fis, clone H COP-diacylghycerol synthese (phosphatide	6.2
	416623	N74925	Hs.38761	Homo saplene cDNA: FLJ21564 Es, clone C	6.2
	413982	BE503035	Hs.279193	ESTs	8.2
65	458091	AF150286		gb:AF150286 Human mRNA from cd34+ stem c	6.2 6.2
	402104			0	6.2
	428771	AB02B992	Hs.193143	KIAA1069 protein	6.1
	435313	A1769400	Ha.189729	ESTs	5.1
70	441666	Al188346	Hs.301776	ESTs	6.1
70	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.1
	427308	D26067	Hs.174905	KIAA0033 protein	6.1
	423069	W15613	Hs.1613	adenosine A2a receptor	6.1
	416655	AW958613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.1
75	417079	U6559Q	Hs.81134	Interleukin 1 receptor antagonist	6.1
, ,	449409 400855	Al650935	Hs.301694	ESTs	6.1
	454692	AW813350		O	6.1
	414869	AN157291	Hs.72163	gl::MR3-ST0192-100100-024-g07 ST0192 Homo	6.0
	439662	H97552	Hs.269060	ESTs ESTs	6.0
80	445181	AW338972	Hs.209000	ESTs	6.0
-	437129	AL049327	140, 8-11-11	gb3homo saplens mRNA; cDNA DKFZp564E016	6.0
	44012B	AA962623	Hs.189144	ESTs. Weekly similar to NPT2_HUMAN RENAL	6.0
	443715	Al583187	Hs,9700	Cyclin E1	6.0
			-	-	6.0

		AW403724	Hs.140	immunoglobulin heavy constant gamma 3	5.9
	405291			0	5.9
		AA935065	Hs.152365	ESTs	5.9
~		AA923489	Hs.130432	ESTs	5.9
5		BE503432	Hs.66170	HSKM-B protein	5.9
	453028	AB006532	Hs.31442	RecQ protein-like 4	5.8
	407137	T97307	Hs.199067	EST	5.8
	443462	AI064690	Hs.171176	EST ₈	5.8
10	454392	BE280893		gb:601150677F1 NiH_MGC_19 Homo saplens c	5.8
10	456311	AA225632	Hs.190016	ESTs	5.8
	446501	A1302616	Hs.150819	ESTs	5.B
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo septens	5.B
	409615	AW444861		gb:Ul-H-BI3-ajz-a-04-0-Ul.a1 NCI_CGAP_Su	5.8
1.5	459360	BE384526		gb:601277913F1 NIH_MGC_20 Homo saplens c	5.8
15	403824			0	5,8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	5.8
	412140	AA219591	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	5.7
	410658	AW105231	Hs.192035	aTS3	5.7
20	426465	AJ758948		gb:ty16f07.x1 NCI_CGAP_Ut3 Homo sepiens	5.7
20	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retin	5.7
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	. 5.7
	405392			0	5.7
	437100	A1761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	5.7
25	449796	AA004321	Hs.194397	ES7s	5.7
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.7
	428987	NM_004751	Hs.194710	glucosaminyl (N-acelyl) bransferase 3	5.7
	404220			0	5.6
	420973	AA743415	Hs.291368	ESTs	5.6
20	430491	AL109791	Hs,241659	Homo seplens mRNA full length Insert cDN	5.6
30	442549	A)751601	Hs.8375	TNF receptor-associated factor 4	5.6
	409867	AW502161		gb;UHHF-BR0p-ajr-g-12-0-Ul.r1 NiH_MGC_5	5.6
	451110	A)955040	He.301584	ESTs	5.6
	418216	AA662240	Hs.283099	AF15q14 protein	5.6
25	411897	AW875066		gb:RC6-PT0001-180100-021-F04 PT0001 Homo	5.G
35	456181	BE264645	He.262093	Homo sapiens cDNA: FLJ21918 fis, clone H	5.6
	406536			0	5.6
	432540	AJ821517	Hs.105866	ESTs .	5.6
	446315	NM_016293	Hs.14770	bridging integrator 2	5.6
40	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.6
40	451035	AU076785	Hs.430	plastin 1 (l isoform)	5.6
	406685	M18728		gib:Human nonspecific crossreacting antig	5,5
	454590	AW809762	Hs.222056	Homo sepiens cDNA FLI11572 fs, clone HE	5.5
	402430			0	5.5
15	446704	AI337228	Hs.197083	E8Ts	5.5
45	435282	AA677428	Hs.189731	ESTs	5.5
	426062	N57014	Hs.44013	ESTs	5.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	5.5
	458002	Al628729	Hs.191450	ESTs, Weakly similar to type II membrane	5.5
50	409513	AW444B16	Hs.171537	Homo sapiens cDNA: FLJ21596 fis, clone C	5.5
30	430259	BE550182	Ha.127826	RaiGEF-like protein 3, mouse homolog	5.5
	434609	R76593		gb:yl60c11.r1 Soares placenta Nb2HP Homo	5.5
	430250	NM_016929	Ha.2B3021	chloride intracellular channel 5	5.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	5.4
55	400379	NM_018432	Hs.283076	Homo saplens ovarian cancer related prot	5.4
JJ	436076	AI193277	Hs.120954	ESTa	5.4
	432119	T80289		gb:yd03h04.r1 Soares Infant brain 1NIB H	5.4
	417175	R44558	Hs.94002	ESTs	5.4
	445774	A1254165	Hs.145504	ESTS	5.4
60	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	5.4
UU	411426	BE141714	U- erares	gb:QVO-HT0101-061099-032-c04 HT0101 Homo	5.4
	445262 413617	AW205650	Hs.253503	ESTS SHOULD ALCO DUME SHOULD BE	5.4
	412517	BE271584	th omore	gb:601141065F1 NTH_MGC_9 Homo sepiens cD	5.4
	434756	AA827650	Hs.259307	ESTs	5.3
65	454417	Al244459	Hs.110826	trinucleofide repeat containing 9	5.3
UJ	439949 414995	AW979197 C18200	Hs.292073	ESTs	5.3
	428071		11- 440000	gb:C18200 Human placenta cDNA (TFujiwara	5.3
		AF212848	Hs.182339	transcription factor ESE-3B	5.3
	412323	AW937143	11. mond m	gb:PM1-DT0041-281299-001-701 DT0041 Homo	5.3
70	434283	AW235341	Hs.58715	mouse Itlamin pyrophosphokinase homolog	5.3
10	447798	AI425049	Hs.119629	ESTs, Moderately similar to ALU1_HUMAN A	5,3
	401723			0	5.3
	406278	Atensara	Un annorm	D ECTs Months similar to d IDD 39.4 Ed a	5.3
	452194	A\694413	He.298262	ESTs, Weakly similar to dJBBJ8.1 [H.sapi	5.3
75	415757	AA830854	Hs.187810	ESTs	5.3
13	430051	AA464611	Hs.52515	transducin (bela)-like 2	5.2
	435615	Y15085	Hs.4975	potassium voltage-gated channel, KQT-lik	5.2
	459583 449009	A1907673 BE044755	Un nated	gb:IL-BT152-080399-004 BT152 Homo sapien	5.2
	424001		Hs.224812	ESTS	5.2
80		W67883	Hs.137478	KIAA1051 protein	5.2
50	409479 437852	BE163800 BE001836	Hs.136912		5.2
	435928	H64345	Hs.256897 Hs.183981	ESTs, Weekly similar to dJ365012.1 (H.sa ESTs	5.2 6.2
	447397	BE247676	Hs.18442	E-1 enzyma	5.2 5.2
	-+1 401	DEETITION	1 NS. 11/14/4/2	Er i etteljuna	5.2

Month AMPSIGNES March		449183	AW445022	Hs.196985	Homo saplars cDNA: FLJ21135 fis, clone C	5.2
101153 PG-11926 Horro septems CNA F-L12809 Horro SNA F-L12809						
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430984 AV9898815 Hs. 14912 Hs. 149	-					
12194 AMS002022 H. 1516142 H. 15071					gb:EST381912 MAGE resequences, MAGK Homo	5.1
A25188						
171712 US1937 181937 1	10					
## 433779 AMB/T745 # 54910 # 51	10					
454112 Nh. (100685 H-301606 ETT				110.01767		
15 434884 Allos (40 https://doi.org/10.1001/j.com/		454112		Hs.301808		5.1
AB115 AJ73075 Ho.292652 ESTE, Weekly shriller to S69818 hypetens 5.1	15					
46719 17973 42462 AF015405 ht. 104824 ht. 104	13					
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404517 AISSA43				Hs.104624		
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16969 All 16443 Ha. 283404 Ha. 283404 Ha. 18134 Ha. 18				H3,100686		
M-9929 MSS8941 Hs. 15134 ESTE Modify uninhibited by benzimidizacies 1 5.0				Hs.2R3404		
453922 APD\$305 Hb.36708 budding uninhibited by bendinidizacies 1 5.0 classes 1 5.0 cla						
414539 BE379046 425349 AA492524	25	453922		Hs.36708		
### 42549 AM25234 Hs 79886 page 5-phosphale isomerrae A (ribose 5 5 5.0 g) ### 47870 AM35450 Hs A85844 ESTs 5.0 ### 47879 AM35664 Hs 128022 ESTs (Weakly similar to FIGH MCUSE FIG-1 5.0 ### 47879 AM35664 Hs 128022 ESTs (Weakly similar to FIGH MCUSE FIG-1 5.0 ### 47879 ESTS 1513 homogentisate 1,2-dioxygenese 5						
449966				11. 70000		
418/17 A334430				HS./9886		
438769 A4830684 Hs.13026 EST1	30			Hs 86984		
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PRoy. Unique Exe probasel identifier number		441859		Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1	6.0
PRogr. Unique Eos probasol identifier number		446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase	5.0
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Accession: Genbank accession numbers					bher number	
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408815 1143425_1 AWA4861 BE074996 BE074996 BE074992 408867 1156530_1 AW502236 AW502236 AW502245 408867 1156530_1 AW502261 AW502265 AW502345 411046 1178974_1 AW502255 R05927 ROE316 411094 1231822_1 BE065142 AW517074 411021 123682_1 BE065142 AW517074 411021 1245515_1 BE141714 AW54593 AW53722 AW53332 AW533509 AW533511 AW533767 AW5333399 50 411426 1245515_1 BE141714 AW54593 AW5875075 AW575051 AW575051 AW575074 412323 126877_1 AW537165 AW537150 AW537151 AW537152 AW537161 AW537163 AW537167 AW537163 AW537163 AW537161 AW537165 AW537161 AW537165 AW537165 AW537169 AW537161 AW537165 AW537161 AW537165	40	1200000		2000011 144(11)		
409865 115653.1 AW902161 AW902187 AW502345 410146 1178974.1 AW502565 R05927 R06916 411094 1231892.1 BEGISH 2 AW502345 411024 1231892.1 BEGISH 2 AW502377 AW633332 AW6333509 AW633511 AW633767 AW633339 50 411426 1245515.1 BE141714 AW64593 AW64505 AW675051 AW875051 AW875074 411231 1226870.1 AW937143 AW637150 AW937161 AW937161 AW937163 AW937169 AW9		Pkey	CAT numbe	Accession		
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4 1094						
410148 1178974_1 AWS92555 R09927 R0S916 411094 1231982_1 BED65142 AWB17074 411231 123636_1 AW833501 AW833506 AW833722 AW833339 AW833511 AW8335767 AW833339 50 411426 1245516_1 BE141714 AW845893 AW845893 411897 1254597_1 AW837151 AW837507 AW875075 AW877165 AW937165 AW937166 AW937165 AW937165 AW937167 AW937165 AW937165 AW937165 AW937166 AW937165 AW937166 AW937165 AW937165 AW937166 AW937165 AW937166 AW937165 AW937166 AW937166 AW937166 AW937166 AW937167 AW937166 AW93716 AW937166 AW93716 AW	45					
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412323 1288770_1 AW937143 AW937150 AW937141 AW937161 AW937160 AW937160 AW937173 AW937160 AW937139 AW937171 AW937145 AW937165 AW937167 AW937167 AW937167 AW937170 BE271684 AA112511 BE314385 BE31	50					24
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55 414484 14528301 BE314385						
414539 1460320_1 BE379046 BE395459 414995 1511736_1 C18200 D7881 T82025 416719 1611345 1 H79731 H79732 422731 220507_1 AL138411 AL138412 AA315860 422810 221630_1 AA377400 AA34584 425858 25755_1 Z43509 H09001 AA375202 AW954383 425858 25755_1 AA364923 AW963483 BE182774 C21461 428465 26768_1 A755894 AA379527 AA379948 AA379262 AW963933 430604 321423_1 AW958824 AA528493 AA483165 AW968842 430279 381800_1 AW971745 AA581359 AA581358 433279 381800_1 AW971745 AA581359 AA581358 433921 377350_1 AA618174 A114549 R38464 R36465 435679 41426_1 A000073 AA380183 AA380181 AW963533 70 437129 43343_1 AL049327 AA847105 439031 45788_1 A400073 AA380183 AA380181 AW963533 449084 52469_1 A498865 76535_1 R35027 R12034 BE407120 449034 794817_1 AI624049 AW117770 AI858360 459081 BE91218_1 AW863350 AW813082 AW813476 AW813383 BE011188 BE011188 BE011181 BE011324 BE011161 BE011169 458081 BE9426_1 W07808 AI822066	55				AA112511	
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454692 1229118_1 AW813350 AW816082 AW813476 AW813383 455004 1337197_1 BE011130 BE011170 BE011333 BE011181 BE011324 BE011161 BE011169 458091 472385_1 AF150286 AA835657 80 459081 BB9425_1 W07808 AI822066	13					
455804 1337197_1 BE011170 BE01133 BE011181 BE011181 BE011324 BE011161 BE011169 458091 472385_1 AF150286 AA835857 80 459081 BB9426_1 W07808 AI822066						
458091 472385_1 AF150/286 AA835857 80 459081 889426_1 W07808 AI822066						BE011161 BE011169
	00	45809	472385_1	AF150286	AA835857	,
408142 3188/0-1 WARRY WA	80					
		40814	2 918906_1	AUSCOCURA	WISN2301 WISN2300	

TABLE 21C

5	Pkey: Ref:		Sequence so sequence of i	er corresponding to an Eos probeset urca. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I, et al." refers to the publication entitled "The DNA human chromosome 22." Dunham I, et al., Nature (1999) 402:489-496.
J	Strand: Nt_position:			A strand from which exons were predicted. leotide positions of predicted exons.
	Pkey	Ref	Strand	Nt_position
10	400855	1931571	Minus	17801-1822B
	400995	8099094	Plus	141186-141601
	401519	6649315	Plus	157315-157950
	401723	7656694	Plus	147273-147503
	402104	8119072	Plus	122409-122600
15	402430	9796372	Minus	62382-62552
	403378	9438244	Minus	44264-44443
	403381	9438267	Minus	26009-26178
	403383	9438267	Minus	119837-121197
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
20	403824	979846B	Plus	473-887
	404220	6706820	Plus	46107-46439
	404727	8081050	Plus	115534-115747
	404767	7882827	Minus	23244-23759
~ -	406291	3845420	Ptus	19999-20473,20672-21036,21147-21295,21378-21667
25	405392	6624069	Minus	116167-116289,118879-119030
	4060B6	7107817	Plus	9418-9573
	405270	7534217	Plus	13136-13591
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
20	406536	7711478	Plus	25655-25782
30				

TABLE 22A: 430 SIGNIFICANTLY DOWN-REGULATED GENES, UTERINE CANCER VERSUS NORMAL UTERUS

Table 22A Rists about 430 genes significantly down-regulated in utaine cancer compared to normal uterus. These were selected as for Table 21A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 14 (i.e., 14-fold down-regulated in tumor vs. normal uterus).

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Pkey: Unique Eos probeset Identifier number
Exacon: Exemplar Accession number, Genbank accession number
Unigene Title: Unigene gene title
R1: Ratio of tumor vs. normal tissue

40

	Pkey	ЕхАсся	UnigeneID	Unigens Title	RI
45					
	414063	H26904	Ha.75736	apolipoprotein D	93.0
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A, member 14	75.7
	407815	AW373860	Hs.301716	E8Ts	68.7
£Ω	452547	AA335295	Hs.74120	adipose specific 2	61.1
50	415165	AW887604	Hs.78065	complement component 7	55.1
	453655	AW960427	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	54.0
	429350	AJ754634	Hs.131987	ESTs	52.6
	407228	M25079	Hs.156376	hemoglobin, beta	52.0
~~	425869	AA524547	Hs.150318	FXYD domain-containing ion transport regulato	51.6
55	416585	X54162	Hs,79386	ielomodin 1 (smooth muscle)	51.4
	408614	AL13769B	Hs.46531	Homo seplens mRNA; cDNA DKFZp434C1915 (from c	49.7
	417542	J04129	Hs.82269	progestagen-associated endometrial protein (p	49.3
	412295	AW088826	Hs.22971	ESTs	48.0
	421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	47.0
60	452093	AA447453	Hs.27860	Homo saplens mRNA; cDNA DKFZp586M0723 (from c	46.7
	429707	W76631	Hs.211819	matrix metalloproteinase 238	45.7
	416950	AL049798	Hs.80552	dermatoponth	45.6
	408221	AA912183	Hs.47447	ESTs	44.6
	406791	A1220584	Hs.272572	hemoglobin, alpha 2	43.0
65	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	42.6
	407938	AA905097	Hs.85050	phospholamban	41.1
	410577	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	41.0
	412524	AA417B13	Hs.11177	ESTa	39.4
	452426	A1904B23	Hs.31297	Homo sapiens cDNA: FLJ23001 fis, clone LNG002	38.6
70	414290	AI568801	Hs.71721	ESTs	3B.2
	439627	BE621702	Hs.29076	Homo saciens cDNA: FLJ21841 fis. clone HEP018	38.0
	400258		Hs.79064	deaxyhypusine synthase	37.0
	414807	Al738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	36.1
	410023	AB017169	Hs.57929	slit (Drosophita) homolog 3	35.4
75	407663	NM 016429	Hs.37482	COPZ2 for nunciathrin coat protein zeta-COP	34.3
	410285	Al739159	Hs.61898	DKFZP586N2124 protein	33.8
	418986	Al123555	Hs.81796	ESTs	33.1
	409060	AI815867	Hs.50130	necdin (mouse) homolog	33.1
	436569	BE439539	Hs.279837	glutathione S-transfarase M2 (muscle)	32.8
80	420574	NM 000055	Hs.1327	butyrylcholinesterase	32.6
	417987	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, member	32.4
	450610	BE207588	Hs.25511	transforming growth factor beta 1 induced tra	31.7
	438150	AAD37534	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	31.6
					~

	400460	III. BARROTT	11. 400000	naT.	
	430468	NM_004673	Hs.130699	ESTs	31.5
	453060	AW294092	Hs.21594	ESTs 24 months	31.3
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular	30.8
5	422126	AW973784	Hs.112028	Misshapen/NIK-related kinase	30.5
3	406082	\$47833	Hs.82927	adenostne monophosphate deamhase 2 (isoform	30.3
	421639	NM_012082	Hs.297921	Homo sapians mRNA full length insert cDNA clo	30.3
	402520	4110-0-0	11 00014		29.9
	418043	AW377752	Hs.83341	H.saplens mRNA for tyrosine kinase receptor	29.7
10	443906	AA348031	Hs.7913	ESTs	29.7
10	450958	AL137669	Hs.25700	Homo saplens inRNA; cDNA DKFZp434M0435 (from c	29.4
	418828	AF020774	Hs.88844	Homo saplens hair and skin epidermal-type 12-	29.4
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob dise	29.4
	429507	NM_003102	Hs.2420	superoxide dismulase 3, extracellular	29.2
1.5	400545				29.1
15	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	29.1
	429942	A1338993	Hs.134535	ESTs	28.9
	438303	AB028998	Hs.6147	KIAA1075 protein	28.7
	419971	AA400027	Hs.296234	ESTs, Highly similar to miltogen-activated pro	28.7
~~	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	28.7
20	452877	AI250789	Hs.32478	ESTs	28.6
	412442	A1983730	Hs.26530	serum deprivation response (phosphatidylserin	28.6
	424378	W28020	Hs.184367	GTPase activating protein-like	28.6
	421823	N40850	Hs.28625	ESTs	27.9
	447786	BE620810	Hs.39619	hypothetical protein LOC57333	27.6
25	400023			AFFX control: 18S abosomal RNA	27.5
	453874	AW591783	Hs.36131	collageл, type XIV, alpha 1 (undulin)	27.2
	414134	X60188	Hs.861	mitogen-activated protein kinase 3	27.1
	428451	AW970451	Hs.98570	ESTs	26.9
	435520	AA297990	Hs.9315	HNOEL-Iso protein	26.6
30	437179	AA393508	Hs.171409	serologically defined colon cancer antigen 8	26.4
•	441481	AA935303	Hs.270553	ESTs	26.0
	450227	BE388192	Hs.78521	Homo segiens cDNA: FLJ21193 fis, clone COL001	25.6
	403731				25.5
	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	25.5
35	410038	R57171	Hs.57975	calsequestrin 2, cardiac muscle	25.5
	416854	H40164	Hs,60296	Purkinje celi protein 4	25.4
	418421	R58620	Hs.85050	phospholamban	25.4
	407000	U12139	1,0,0000	gb:Human alpha1(XI) collagen (COL11A1) gene,	25.3
	421803	NM_012205	Hs.108441	3-hydroxyanthranilate 3,4-dioxygenase	25.3
40	445613	BE550889	Hs.158491	ESTs	25.1
	432302	AA345857	Hs.274307	KIAA1442 protein	24,8
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-associate	24.8
	423720	AL044191	Hs.23388	Homo sepiens cDNA: FLJ21310 fis, clone COL021	24.7
	417302	BE245812	Hs.8941	ESTs	24.6
45	421913	AI934385	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	24.6
	440130	Al083899	Hs.157527	ESTS	24.5
	431967	AJ243653	Hs.283404	organic cation transporter	24.5
	424580	AA446539	Hs.35092	ESTs	24.4
	406907	Z25427	1 M.00052	gb:H.saplens protein-serine/threonine kinase	24.2
50	443745	AB039670	Hs.9728	ALEX1 protein	24.1
50	429101	AW452174	Hs.173780	ESTs	23.5
	410691	AW239226	Hs.65450	reticulon 4	23.A
	408853	AW291484	Hs.254967	ESTs	23,3
	407979	AA046306	Hs.62927	ESTs	23.1
55	448619	Al867182		ESTS	22.8
J.J	424585	AA464840	Hs.202255	ob:zx43h1f.r1 Soares_total_fetus_Nb2HF8_9w Ho	22.6 22.7
	407891		Lin 4449E		
	407196	AA488620 D11747	Hs.41135 Hs.177415	Endomucin 2 Finkel-Biskis-Reilly murine sercome virus (FB	22.6 22.5
60	426990 450493	AL044315	Hs.173094	Homo sapiens mRNA; cDNA DKFZp564H142 (from cl	22.5 22.1
50	420120	M93718 AL049610	Hs.166373 Hs.95243	nitric codds synthase 3 (endothelial cell)	22.1 22.0
	423690	AA329848		transcription etongetion factor A (Sti)-like	22.0 22.0
			Hs.23804	ESTs	
	402865 417387		Hs.21509	ESTa	21.9 21.9
65					
05	456898 459722		Hs.155597	D component of complement (adipsin)	21.9
			11- DD4 400	Home saplens cDNA: FLJ23449 fis, clone HSI058	21.8
	422927		Hs.301423	calcium binding protein 1 (calbrain)	21.8
	402195		11- 422007	TOT-	21.7
70	418213		Hs.127327	ESTs	21.6
70	440274		Hs.7122	scraple responsive protein 1	21.6
	455818		11-00007	gb:zn86d04.y5 Strategene lung carcinoma 93721	21.4
	420861		Hs.88827	Homo saplens mRNA for FLI00033 protein, parti	21.4
	405228				21.3
75		AF131218	Hs.7765	chromosome 16 open reading frame 5	21.3
75	432553		Hs.211095		21.3
	417098		His.173859		21.2
	453642		Hs.34074	dipeplidylpeplidase VI	21.2
	405313		b) men	more 411 12 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	21.1
QΛ	410243		Hs.289008		21.1
80	413186		Hs.75231	solute carrier family 16 (monocerboxylic acid	21.1
	425954		Hs.164476		21,0
	421770				21.0
	435265	AA779958	Hs.185932	ESTS	20.8

	430036	AL050284	Hs.227782	DKFZP586M1019 protein	20.7
	430233	AW367902	Hs.236443	Homo saplens mRNA; cDNA DKFZp564N1063 (from c	20.7
	436130	AA341497	Hs.31408	ESTs	20.7
_	434843	R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary proli	20.7
5	429303	AW137635	Hs.44238	ESTs	20.6
	442422	Al344415	Hs.156082	ESTs	20.5
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific prot	20.5
	435869	AF255910	Hs.54650	ESTs, Wealdy similar to (defline not available	20.5
	447384	Al377221	Hs.40528	ESTs	
10	440610	AI733098	Hs.130800	ESTs	20.5
- •	445805	AL137516			20.5
	433657		Hs.13323	hypothetical protein FLJ22059	20.4
		AI244368	Hs.8124	PH domain containing protein in retina 1	20.4
	436467	AW450278	Hs.91681	ESTs .	20.3
15	440191	AI990417	Hs.116107	Horno sapiens genomic DNA, chromosome 21q, sec	20.2
13	417511	AL049176	Hs.82223	chardin-like	20.2
	406976	M60299		gb:Human alpha-1 collagen type II gene, exons	20.1
	443547	AW271273	Hs.23767	ESTs	20.1
	41799B	AW967420		gb:E8T379495 MAGE resequences, MAGJ Homo sapi	20.1
~~	419313	AA843387	Hs.87279	ESTs	20.1
20	408322	AW181985	Hs.249986	ESTs	20.0
	448422	BE263813		gb:601194177F1 NIH_MGC_7 Homo sapiens cDNA cl	20.0
	403121			Second to the Curoo's troug substituting	19.9
	424198	AB029010	Hs.143026	KIAA1087 protein	
	45906D	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein D (AU	19.9
25	457829	A1742291	Hs.210843		19.9
45	445029			ESTs, Weakly similar to dJ1039K5.2 [H.sapiens	19,9
		AF196481	Hs.12256	midline 2	19.9
	424362	AL137646	Hs.146001	Homo sapians mRNA; cDNA DKFZp586F0824 (from c	19.8
	417067	AJ001417	Hs.B1086	solute carrier family 22 (extraneuronal monos	19.7
20	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYDROXYP	19.6
30	435891	AW249394	Hs.5002	copper chaperons for supercydde dismutase	19.6
	447551	8E066634	Hs,929	myosin, heavy polypeptida 7, cardiac muscle,	19.6
	400837				19.5
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (car	19.4
	430310	U60115	Hs,239069	four and a half LIM domains 1	
35	402741		*10(20000	NO GIO CITO CINTOGINA I	19.4
	401703				19.4
	409229	H60333	Hs.251928	aualaa	19.3
	453856	AA804789		nuclear pore complex interacting protein	19.3
			Hs.19447	Homo seplens mRNA for FLI00106 protein, parti	19,3
40	430342	NM_005938	Hs.239663	mysloid/lymphoid or mixed-lineage leukernia (t	19.3
TU	404033	a bassaus			19.2
	411939	Al365585	Hs.146246	ESTs	19.2
	431227	X63755	Hs.2743	keratin, cuticle, utrahigh sulphur 1	19.1
	452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced	19.1
4.00	439698	AW779654	Hs.55876	ESTs	18.9
45	416253	BE250659	Hs.15463	ESTs	18.9
	418556	T02850		gb:FB12A9 Fetal brain, Stratagena Homo saplen	18.9
	408877	AA479033	Hs.130315	ESTs	18.9
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24kD	
	417054	AF017060	Hs.174151	aldelyde oxidese 1	18.9
50	404654		1 20 12 7 14 1	anolyse sausse 1	18.8
	420174	AI824144	Hs,23912	ESTs	18.8
	400625	·	I NILUU IL	COIS	18.8
	406150				18.7
	457835	DESCOSO	11- 400275	FOT- Wild - Auto- A Management and A	18.7
55		BE256338	Hs.192375	ESTs, Highly similar to dJ127B20.3 (H.sapiens	18.6
در	420105	AW015571	Hs.32244	ESTs	18.6
	404619	BE514535	Hs.77171	minichromosome malntenance delicient (S. cere	18.5
	423282	AL137583	Hs.126378	putative ABC transporter	18.5
	424097	M139B1	Hs.1734	inhibh, alpha	18.5
60	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from c	18.5
60	427605	NM_000997	Hs.179779	ribosomeit protein 1.37	18,4
	406535				1B.4
	418947	W52990	Hs.22880	ESTs	18.4
	414323	NM_014759	Hs,239500	KIAA0273 gene product	1B.3
~~	457111	AA482027	Hs.142569	ESTs	18.3
65	418373	AW750770	Hs.84344	CGI-135 protein	
	424461	D83542	Hs.148090	cadherin 15, M-cadherin (myotubule)	18.3
	451565	NM_000897	Hs.456	leukotriene C4 synthase	18.2
	407751	BE276096	Hs.38205	from HeLa cyclin-dependent kinese 2 interacti	18.2
	432031	AF039196	Hs.284126	hairless (mouse) iromolog	18.2
70	404608	H58589	Hs.3515B	Long emigro a NA CT 144.000 43. PLANTA	18.1
	451962	AW078832		Homo saplans cDNA FLJ11027 fis, clone PLACE10	18.1
	424100		Hs.226806	ESTs	18.1
		A1793080	Hs.123525	ESTs, Weakly similar to NGAL RAT NEUTROPHIL G	18.1
	451509	A1969529	Hs.171637	Homo saplens cDNA: FLJ21937 fis, clone HEP044	18.1
75	453512	ALD40160	Hs.209542	ESTs, Weakly similar to B cell linker protein	18.0
13	429924	W39693	Hs.22613B	Homo sapiens mRNA; cDNA DKFZp566H2446 (from c	17.9
	423780	AA352013		gb:EST59935 Infant brain Homo sepiens cDNA 5	17.9
	427030	AA397600	Hs.97531	ESTs	17.9
	439872	T81058		gb:yd26c08.r1 Soares fetal liver spleen 1NFLS	17.9
0.0	407836	T79340	Hs.22576	Homo sapiens cDNA: FLJ21042 fis. clone CAF112	17.9
80	451427	A1091441	Hs.28401	burnor necrosis factor (Vigand) superfamily, m	17.9
	424462	AU076666	HS.1481131	SECUTO COUSUUBIU DOMPIN	
			Hs.148101 Hs.26530	serum constituent projeta serum deprivation response (obserbetidulende	17.9
	424462 451533 422319	NM_004657 AW403342	Hs.148101 Hs.26530 Hs.115232	serum deprivation response (phosphatidylserin spiking factor 3a, subunit 2, 65kD	17.9 17.8 17.8

	400489				17.8
	454421	BE409759	Hs.59563	Homo saplens mRNA for FLJ00007 protein, parti	17.8
	449282	A1.048056	Hs.23437	Homo sapiens cDNA FLJ13555 fls, clone PLACE10	17.7
5	420495 429790	AJ338247 AK001352	Hs.98314 Hs.221737	Homo sapiens mRNA; cDNA OKFZp586L0120 (from c hypothetical protein FLJ10490	17.7
-	422796	AW897265	140.22.11.01	gb:CMO-NN0057-150400-335-a04 NN0057 Homo sapi	17.7 17.7
	427980	AA418305		gb:xv96g05.s1 Soares_NhHMPu_S1 Homo saptens c	17.6
	409543 440206	AW410200 AJ762232	Hs.46794	gb:fh05b12x1 NIH_MGC_17 Homo sapters cDNA cl ESTs	17.6
10	455904	BE156173	113,40104	gb:QV0-HT0367-201299-079-a02 HT0367 Homo sapt	17.6 17.5
	427707	NM_005578	Hs.180398	LIM domain-containing preferred translocation	17.5
	437140	AA312799	Hs.283689	activator of CREM in lestis	17.5
	417637 419171	AA204969 NM_002846	Hs.234863 Hs.89655	Homo sepiens cDNA FLJ12082 fis, clone HEMBB10 protein tyrosine phosphatase, receptor type,	17.5
15	417808	AF177909	Hs.12828	tweety (Drosophila) homolog 1	17.4 17.4
	426232	Z70024	Hs.168157	nuclear transcription factor Y, gamma	17.4
	440747 415307	AW297225 F05232	Hs.137840 Hs.27495	ESTs, Moderetely similar to SIX1_HUMAN HOMEOB prostate cancer associated protein 7	17.4
20	407049	X72632	11521.400	(NONE)	17.3 17.3
20	454054	Al336329	Hs.301519	Homo sepiena cDNA FL112536 fis, clone NT2RM40	17.3
	4110B5 443104	AF022991 AA088470	Hs.68398 Hs.83135	period (Drosophila) homolog 1	17.3
	424106	AA412442	Hs.98132	p53-responsive gene 6 E8Ts	17.2 17.2
25	446716	AA436575	Hs.16602	ESTs	17.1
25	448677 434919	A1560769 A1821740	Hs.227051	ESTS	17.0
	401171	AA360954	Hs.116531 Hs.27268	ESTs Homo saplens mRNA; cDNA DKFZp564N196 (from c)	17.0 17.0
	456804	A1421645	Hs.139851	caveolin 2	17.0
30	453621 413419	AW749983 BE093686	Hs.48938	gb:QV3-BT0537-280100-070-e04 BT0537 Homo sepi	16.9
50	426515	BE394222	Hs.231444	Homo sapiens cDNA: FLJ21802 fis, clone HEP007 ESTs	16.9 16.9
	428937	T82221	Hs.56729	lymphocyte-specific protein 1	16.9
	424562 444655	AI420859 AF088886	Hs.150557	basic transcription element binding protein 1	16.9
35	447424	A)681105	Hs.11590 Hs.181641	cathepsin F ESTs	16.9 16.8
	425439	D38024	Hs.157425	double homeobox, 2	16.8
	446707	AI591214	Hs.156336	ESTs	16.8
	405324 434340	Al193043	Hs.128685	ESTs	16.8
40	422942	AF054839	Hs.122540	tetraspan 2	16.8 16.8
	421820	AW662990	Hs.108675	heme-binding protein	16.8
	420037 428818	BE299598 Al131291	Hs.135569 Hs.98666	ESTs, Weakly similar to NEUROD [H.sepiens] ESTs	16.7
*=	426485	NM_006207	Ha.170040	platelet-derived growth factor receptor-like	16.7 16.7
45	404947	Alteronoma			16.6
	412677 401551	AW029608	Hs.17384	E8Ts	16.6
	408053	AW139474	Hs_246862	ESTs	16.6 16.6
50	425016	AA376049	Hs.154162	ADP-ribosylation factor-like 2	16.6
50	418179 418994	X51630 AA296520	Hs.1145 Hs.89546	Wilms tumor 1 Selectin E (endothelial adhesion molecute 1)	16.6
	457514	AA775208	Hs.136423	ESTs	16.5 16.5
	426275	BE151551		gb:RC0-HT0297-201199-031-f12 HT0297 Homo sapi	16.5
55	457924 430712	AL390142 AW044647	Hs.268697 Hs.196284	Homo saplens cDNA FLJ13861 fis, clone THYRO10 E8Ts	16.5
	455144	AVV875942	110.100207	gb:CM1-PT0013-131299-067-b10 PT0013 Homo sepi	16.5 16.4
	407524	X64985		glo:Haaplens mRNA HTPCRX11 for olfactory rece	16.4
	428712 429954	AW173177 AI918130	Hs.197755 Hs.21374	ESTs ESTs	16,4
60	446208	BE258323	Hs.225795	ESTs, Highly similar to OTX1_HUMAN HOMEOBOX P	16.4 16.4
	442792	A3352340	Hs.131194	ESTs	16.3
	420485 426767	AF218588 AA384398	Hs.288835 Hs.192491	cell death-inducing DFFA-like effector b ESTs	16.3
c=	436950	L05779	Hs.113	epoxide hydrotase 2, cytoplasmic	16.3 16.3
65 .	415195	AK000150	Hs.78185	MAX-like bHLHZIP protein	16.3
	442197 433457	AW837912 AA830194	Hs.199417	gb:CV3-1.T0048-260400-068-c021.T0048 Homo sapt Homo septens mRNA for FL100027 protein, par0	16.3
	402316	70.000104	110,100711	ramo separa minter for Fill 20021 projetti, paru	16.2 16.2
70	409736	AA078628	NI- 004444	gb:7P07H07 Chromosome 7 Placental cDNA Librar	16.2
70	407964 433677	AW130334 AI791912	Hs.281111 Hs.190885	ESTs Moderately similar to ALU1_HUMAN ALU SU	16.2
	425507	A1684745	Hs.165983	hypothetical C2H2 zinc finger protein FLJ2250	16.2 16.2
	413724	AA131466	Hs.23767	Homo saplens cDNA FLJ12666 fix, clone NT2RM40	16.2
75	408922 413055	R87388 AV655701	Hs.75183	gb:ym88g04.r1 Soares adult brain N2b4HB55Y Ho	16.1
	435977	AL138079	Hs.5012	cytochrome P450, subfamily tiE (ethanol-induc brain-specific membrane-anchored protein	16.1 16.1
	44220B	AW296984	Hs.255595	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	16.1
	402426 412399	N53B16	Hs.14394	hypothetical protain FLJ20157	16.0
80	413200	AA127395	Hs.222414	ESTs	16.0 16.0
	404597	AADDOOA			15.9
	453143 455984	AA382234 BE177442	Hs.170121	protein tyrosine phosphatase, receptor type, gb:RC1-HT0595-200400-012-f01 HT0595 Homo sapi	15.9
				des outon cecolly interingentational	15.9
				A	

	416193	T25400		gb:PTH(069 HTCDL1 Homo sapieus cDNA 5/3' sim	15.9
	407065	Y10141		gb:H.sepiens DAT1 gene, partial, VNTR.	15.9
	441785	AW138139	Hs.244598	ESTs	15.9
_	413784	BE165819		gb:CM0-HT0486-220300-301-d12 HT0486 Homo sapi	15.9
5	429092	A1190864	Hs.178226	ESTs, Weakly similar to ALU1_HUMAN ALU SU8FAM	15.8
-	408499	AW205323	Hs.253475	ESTs	15.8
	453754	AW972580	Hs.172753	ESTs	
					15.8
	450826	U43030	Hs.25537	cardiotrophin 1	15.8
10	428486	AW583497	Hs.184604	pancreatic polypeptide	15.7
10	405895				15.7
	409108	AA339443	Hs.48793	ESTs	15.7
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	15.6
	422948	AW810824	Hs.21351	ESTs	15.6
	447852	AW504781	7101-1001	gb:UI-HF-BN0-alp-c-04-0-UI.r1 NiH_MGC_50 Homo	15.6
15	419084	AA496539	Hs.179902	transporter-like protein	15.6
	456771	AW016739	Hs.232201		
	438564			ESTs	15.6
		AA381553	Hs.198253	major histocompatibility complex, class II, D	15.6
	448705	H05072	Hs.124984	ESTs, Moderately similar to unnamed protein p	15.6
20	454460	X66945	Hs.748	fibroblast growth factor receptor 1 (fms-refe	15.5
20	458893	BE161733	Hs.97203	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.5
	426759	Al590401	Hs.21213	ESTs	15.5
	453769	R35261	Hs.24947	ESTs	15.4
	434179	A1743448	Hs.116177	ESTs	15.4
	404111	7 12 12 112		2010	15.4
25	402056				15.4
	458602	Alacados	He 276400	ССТ е	
		A1262208	Hs.276489	ESTs	15.3
	427530	AA405093	Hs.126519	ESTs	15.3
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	15.3
20	400632				15,3
30	443918	AA305475	Hs.22660	Homo sepiens cDNA FLJ11658 fis, clone HEMBA10	15.3
	432037	AW450592	Hs.300459	ESTs	15.3
	412921	BE009345	Hs.128942	ESTB	15.3
	421905	A1660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein (H, eap)	15.3
	441704	A1458766	Hs.201988	ESTs	15.3
35	414272	A1651603	Hs.46968	ESTs	
55	448224				15.3
		R48700	Hs.20733	EH-domain containing 2	15.2
	404611	H58589	Hs.35156	Homo sapians cDNA FLJ11027 fis, clone PLACE10	15.2
	448381	D61580	Hs.21036	Homo saplens mRNA; cDNA DKFZp434A1010 (from c	15.2
40	454719	BE006547	•	gb:RC2-BN0130-040400-011-b03 BN0130 Homo sapl	15.2
40	446973	H95724	Hs.42B3	ESTs	15.2
	457760	AA668123	Hs.134170	ESTs	15.2
	440144	AW082297	Hs.88523	ESTs	15.2
	407387	AB000695		gb:Homo saplens mRNA for cadherin FiB1, parti	15.2
	427850	AA416756	Ha.161051	ESTs, Moderately similar to ALUG_HUMAN ALU SU	15.2
45	404244	14410/00	1141101001	ED 14' INCOCREDIT SIGNED TO UTOOD TOUGHT VICE OF	
75	402959				15.1
		14107010	1) Approp	1 1 7 12 12 4	15.1
	435487	W07343	Hs.182538	phospholipid scrambiase 4	15.1
	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo saplens cDNA c	15.0
50	455916	BE156710		gb:QV0-HT0368-310300-181-d01 HT0368 Homo sapl	15.0
50	448943	A\$608810	Hs.193288	ESTs	15.0
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	15.0
	454082	AF283508	Hs.63168	cell death regulator even	14.9
	453308	AW959731	Hs.32538	ESTs	14.9
	458823	AW207574	Hs.179501	ESTs	14.9
55	452532	AI905811			
			Hs.110757	DNA segment ou chromosome 21 (unique) 2056 ex	14.9
	418464	R87580	11-000-0-	gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	14.9
	409473	AL197716	Hs.296567	Homo sapiena mRNA; cDNA DXFZp434D2030 (from c	14.8
	449779	AA004258	Hs.25218	ESTs, Weakly similar to ALUB_HUMAN ULL ALU C	14.8
60	457546	AA568484	Hs.153632	ESTs	14.8
60	403368				14.8
	432163	AK000440	Hs.272799	hypothetical protein FLJ20433	14.8
	421531	AA713505	Hs.291769	ESTs	14.B
	428283	AI439096	Hs.25832	Homo seplens mRNA; cDNA DKFZp564P116 (from c1	14.8
	443528	AK001778	Hs.9547	hypothetical protein FLJ10916	14.8
65 .	402399			-91	14.8
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	14.8
	450300	AL041440	Hs.58210	ESTs	
	403552	- 1124-1444	I IDANIZ IV	2510	14.8
	405052	1/04890		ability of the control of the contro	14.7
70				gb:Human olfactory receptor (OR17-210) gene,	14.7
70	436365	AW44454B	Hs.163118	ESTs .	14.7
	402550	*****			14.7
	441782	AW140126	Hs.132357	EST&	14.7
	415672	N53097	Hs.193579	EST8	14.7
	430582	Al215509	Hs.143964	ESTs	14.7
75	425770	NM_014363	Hs.159492	spastic ataxta of Charlevolx-Sequenay (sacsin	14.7
_	4326B3	AW995441	Hs.10475	ESTs	14.7
	441871	Al306150	Hs.153450	ESTs, Weakly similar to 1909123A Na glucose c	
	447481	AF052151	He.18688		14.6
	405114	A W2131	110.10000	Mouse Mammary Turmor Virus Receptor homolog	14.6
80					14.6
00	401082				14.6
	454316			gb:QV0-HT0101-061099-032-b12 HT0101 Homo sapi	14.6
	421572	AA531607	Hs.125143	ESTs, Weakly similar to POL2 MOUSE RETROVIRUS	14.6
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	14.6

	441503	AW172263	Hs.185202	ESTs	
	416199		16.100202		14.6
	420360		Hs.97203	gbryq12a08.r1 Soares fetal liver spicen 1NFLS	14.6
	425126		Hs.172944	small inducible cylokine subfamily A (Cys-Cys	14.6
5	417421		Hs.82120	chorlonic gonadotropin, bela polypaplida	14.5
	405100	71270201	118.02120	nuclear receptor subfamily 4, group A, member	14.5
	454012	M76424	Hs.37014	andronia polyudova 188	14.5
	402457	IIII O-TE-Y	11001014	carbonic anhydrase VII	14.5
		AWB10814		-LIMP MAKER STARS SALES CONSERVED	14.5
10	429821		Hs.225433	gb:MR2-ST0129-201099-004-e01 ST0129 Homo sepi Homo sepiens mRNA; cDNA DKFZp434G153 (from c)	14.5
	431073		Hs_249186	cone-rad homeobox	14.5
		AB024536	Hs.102171		14.5
	401223	***************************************	713.102.111	fmmunoglobulin superfamily containing leucine	14.5
		A)087335	Hs.123473	ESTs	14.4
15		RD8160	Hs.268857	ESTs, Weekly similar to ALU1_HUMAN ALU SUBFAM	14.4
	437217	AW779241	Hs.155316	ESTs	
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G protein	14.4
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	14,4 14,4
20	413237	Al468574	Hs.171965	ESTs	14.4
20	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,	14.4
	426488	X03350	Hs.4	alcohol dehydrogenase 2 (class I), beta polyp	14.4
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	14.4
	405479				
25	418432		Hs.85112	insulia-like growth factor 1 (somatomedia C) Human DNA sequence from clone 437G10 on chrom gb:CMO-NN0058-150400-337-b08 NN0058 Homo sept FSTs	14.3
25	426316		Hs.301852	Human DNA sequence from clone 437G10 on chrom	14.3
	412171			gb:CMO-NN0058-150400-937-b08 NN0058 Homo sapi	14,3
	447241	BE382838	Hs.19322	ESTs	14.3
	402100				14.2
30	430200	AW139268	Hs.134807	Homo saptens cDNA FLJ12057 ffs, clone HEMBB10	14.2
50		Al500332	Hs.102367	ESTs, Weakly similar to hTcf-4 [H.saptens]	14.2
	402275 402358				14.2
		AAB38771	D-404407	500	14.2
			Hs.124407	ESTs	14.2
35	455314	AI149879 Y 17114	Hs.175024	Homo sapiens cDNA: FLJ23447 fis, clone HSI033	14.2
23	400014	AAB35058	Hs.73393	eyes absent (Drosophile) homolog 4	14.2
	400828	AW501112	Hs.21111	ESTs	14.2
	4140020	NM_006732	Hs.34487	hypothetical protein FLJ23412	14.2
	4426B2	Al014545	Hs.75678 Hs.231027	FBJ murine esteesarcoma viral encegane homolo	14.2
40		AF029674	Hs.173422	EST KIAA1606 prototo	14.1
		R97457	Hs.63984	KIAA1605 protein	14.0
	401007	1101 101	18300004	cadherin 13, H-cadherin (heart)	14.1
		AF149297	Hs.8087	NAG-5 protein	14.1
		D19687	Hs.245146	ESTS	14.1
45		AA570454	Hs.186467	ESTs, Moderately similar to ALU1_HUMAN ALU SU	14.1
	425352	NM_000939	Hs.1897	prooplemelanocortin (adrenocorticotropin) bet	14.1
	433887	AW204232	Hs.279522	ESTs	14.1
	434927	H46612	Hs.293815	ESTs, Weakly similar to PLM_HUMAN PROSPHOLEMM	14.1
50	404282			Talah Marah angga manga manga takan at 12021 MCTEWIM	14.1
50	422581	NM_016339	Hs.118562	Link guanina nucleotida exchange factor il	14.1 14.0
	424B23	NM_006226	Hs.153322	phospholipase C, epsilon	14.0
	408107	AA806754	Hs.62835	ESTS	14.0
	401577				14.0
55	433883	AI925688	Hs.222312	ESTs, Weakly similar to 824264 proline-rich p	14.0
23	408104	AW972927	Hs.293968	ESTa	14.0
	404642				14.0
	400575				14.0
	406059	4.0002700		144-4	14.0
60	448386 407287	AB037750	Hs.21061	KIAA1329 protein	14.0
OO	407207	Al678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	14.0
	TABLE 2	3 D			
	TABLE 2	LD			
	Pkey:	historia Esa -		Faa. 4-1	
65		ber: Gena cluster	robeset identi	aer numaer	
-	Accession		session nampa		
		A COMBINAC	COSTOIL URIUMS	18	
	Pkey	CAT number	Acception		
		CALL HOLLING	ACCOPPINI		
70	408922	109017_1	R87388 D843	328 AAD58916	
	409543	1138723 1	AW410200 A	W409705 AW411433 BE296786 BE270309	
	409736	115189_1	AA078628 R	09051 AA078197 AA077334 AW748808 AW748807	
	412171	1280759 1	AWB97452 7	20302 D55805 D52877 D60432	
76	413784	1369150 1	BE185819 RE	E165853 W01386	
75	414213	1426375_1		262061 BE302686 T83915	
	416193	1577102_1	T25400 H268	134 H44554 R73193	
	416199	1577561_1			
	417998	171375 <u>1</u>	AW967420 A	A210915 AA236991 AA210916	
90	418464	17590382	RB7580		
80	418556	17678681	T02850		
	422796	221500_1	AW897265 A	W897274 AL119504 AW897275 AW897270 AW897312 AW89	7318 AW897317 AA317940 AW081921
	422700	221055 4	TOURS TOWN	3124 VC190(20 YAA401812 YAA8885\\	
	423780	231952_1	AA352013 AA	E0E389WA 9769EEAA 87806EA	
				V 0	

```
AA464840 AA343628
BE151551 AA373783 BE162852 BE008826 BE008827 BE008781 BE008699
           424585
                        241151_1
           426275
                        263712_1
           427960
                        285225_1
                                      AA41B305 Al264351
                                      T81058 AL357200 T70270
           439872
                        47823_1
  5
           442197
                        535550_1
                                     AW837912 AW837934 AA984476 AW997490
           447852
                                      AW504781 BE620394
                        73973 1
                                      BE263813 BE253504 Al500202 BE251145
           448422
                        762770_1
           453621
                        974526_1
                                     AW749983 AL045823
           454316
                        1109350_1
                                     AW366144 AW366154 AW366142 AW366151 AW366140 AW366155 BE141715 BE141718 BE141698
10
                                     AW810814 AW810737 AW810854 AW810773 AW810735 AW810786 AW810660 AW810834 AW810874 AW810723 AW810881 AW810791 AW810844 AW810659 AW810676
           454613
                        1226904_1
           454719
                        1230646_1
                                      9E006547 AW815578 AW815311 AWB56304
           455144
                        1254914_1
                                     AW875942 AW858234 AW875938 AW875941 AW858235 AW875958
           455818
                                     Al733747 AA129802
BE156173 BE156305 BE156198
                        137219 1
15
           455904
                        1382290_1
           455916
                        1382748_1
                                     BE156710 BE156726 BE156712
           455984
                        1397288_1
                                     BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433
           TABLE 22C
20
           Pkay:
                        Unique number corresponding to an Eos probeset
                        Sequence source. The 7 digit numbers in this column are Genbank Identifier (Gi) numbers. "Ounharn I, et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I, et al., Nature (1999) 402:489-495.
           Ref:
                        Indicates DNA strand from which exons were predicted.
           Strand:
25
           N'_position:
                        indicates nucleotide positions of predicted exons.
           Pkey
                                     Strand
                        Ref
                                                   Nt_position
           400489
                        8954013
                                     Plus
                                                   131475-131652
30
                        9800107
7228177
           400545
                                      Minus
                                                   124618-124881
           400625
                                                   117266-117441
72875-73447,75874-76425
                                     Minus
           400632
                        3818355
                                     Plus
           400637
                        8894326
                                                   68901-69507
                                     Plus
           400675
                        8118750
                                     Plus
                                                   11223-11816
35
           401007
                                                   140821-141050
22937-23494,27677-27966
                        8117933
                                     Minus
           401082
                        3242744
                                     Plus
           401223
                        8099068
                                      Plus
                                                   148940-150214
           401551
                        8096896
                                      Minus
                                                   189824-190728
           401577
                        9280797
                                     Minus
                                                   139377-139674,141195-141281,142217-142340
40
           401703
                                                   135-1229
                        4826475
                                     Plus
           402056
                        8084234
                                                   207002-207288
                                     Plus
           402100
                        8117697
                                     Plus
                                                   133649-133792
                                                   147901-148884
31065-31233,33680-33771,34345-34411,38890-39125,39779-39943
10751-10919,18817-19052,22131-22328
           402195
                        7689778
                                     Minus
           402275
                        2935596
                                     Minus
45
           402316
                        7527774
                                      Minus
           402358
                        8886976
                                     Minus
                                                   131788-132729
           402399
                        1905915
                                     Minus
                                                   24502-24666,24986-25102
           402426
                        9796361
                                                   73590-73824
16513-16577,16838-16926
                                     Minus
           402457
                        9796782
                                      Minus
50
           402520
                        7596899
                                      Minus
                                                   171761-171996
           402550
                        7652009
                                     Minus
                                                   80413-80673
                                                   18603-18760,19719-19890
3197-3429,3722-3914,5795-5987,6802-6961,8553-8815,9292-9660
           402741
                        9212200
                                     Minus
           402865
                        9716300
                                      Plus
           402959
                        9368493
9180223
                                     Plus
                                                   36729-37084
55
           403121
                                     Plus
                                                   4059-4258
                                                   70286-70429,75165-7525B
           403368
                        4388738
                                      Plus
           403552
                        6862638
                                      Minus
                                                   117504-117662
           403731
                        7643752
                                      Minus
                                                   144000-144618
           404033
                        8122195
                                     Plus
Plus
                                                   7976-8156
161506-161781
60
           404111
                        9408736
           404244
                        5672609
                                                   98173-98517
                                     Minus
           404282
                        2276311
9958262
                                                   61503-62205
                                     Minute
                                                   114369-114599
           404642
                        9796810
                                                   102999-103145
                                     Plus
65
           404654
                        9797010
                                      Plus
                                                   6275-6527
           404947
                        7382205
                                      Plus
                                                   29740-30105,30176-30412
           405100
                        8076846
                                     Phis
                                                   144114-144234
                        8096938
           405114
                                                   97013-97560
                                     Minus
           405228
                        7248990
                                     Plus
                                                   92234-95905
70
           405313
                        3638954
                                                   68924-69093
                        3342751
6453391
           405324
                                     Minus
                                                   5475-5677
           405479
                                     Plus
                                                   1668-1844
           405895
                        7677903
                                                   66990-67484
                                     Minus
           406059
                        9103984
                                      Minus
                                                   13856-14004
75
           406150
                        9986026
                                     Minus
                                                   59331-59701
           406535
                        7711477
                                     Plus
                                                   83135-83362
```

Table 23A lists about 626 genes upregulated in uterine cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each protein obtained from this analysis

⁸⁰ TABLE 23A: 626 genes upragulated in uterino cancer relative to normal body tissues

was expressed as average Intensity (AI), a normalized visiue reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Unique Eos probeset identifier number

5

Pkey: ExAcon: Exemplar accession number, GenBank accession number UnlGenelD: UniGene number Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280). Pred.Prot.Domains: 10 UniGene Title: 95th percentile of uterine cancer Als divided by the 50th percentile of normal tissue Als, where the 10th percentile of all normal tissue Als was subtracted from both the numerator and denominator 15 Pkøy; ExAcon; UnigenelD; Unigene Title; Pred.Prot.Domains; R1 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysln.; Peolidase, M10; 35.11 420440; NM_002407; Hs.97644; memmaglobin 2; Uteroglobin; 22.80
439335; AA74;597; Hs.62492; NM_052863;Homo saplens secretoglobin, fa; none;; 21.66
425723; NM_014420; Hs.159311; dickkopf (Xenopus lasvis) homolog 4; none;; 21.11
421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 20.20
437936; AI950087; Hs.369628; gb:wq05c02.x1 NCL_CGAP_Kid12 Homo saplen; none,none; 19.83 20 437938; Al950087; Hs.369628; gb:wq05c02x1 NCL_CGAP_ktd12 Horno sapten; none, none; 19.83
406587; M31126; Hs.352054; matrix metalloprobinase 11 (stromelysin; hemopexin, Peptidase_M10;; 17.68
446619; AU078643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; ; 17.69
446619; AU078643; Hs.313; secreted phosphoprotein 1, 120kD (mucin 9; Glyco_hydro_18;TM=M;SS=M; 17.48
431130; NM_006103; Hs.2719; HE4; epididymb-specific, whey-acidic pr; wap;TM=M;SS=Y; 16.59
400301; X03636; Hs.1657; estrogen receptor 1; F-box,hormone_rec,zf-C4,Oest_recep,adh_zinc,ketoacyl-synt,pp-binding,Acyl_transf,Thioesterase,ketoacyl-synt_C,AAA,E7,RFX_DNA_binding;TM=Mi;SS=N; 16.11
419356; Al656166; Hs.7331; hypothetical protein FL122316; Asparaginase_2,none; 15.90
433222; AW514472; Hs.238416; dickkopf (Xenopus laevis) homolog 4; none,PHO4; 15.39
417931; W95642; Hs.82961; trefoll factor 3 (Intestinal); trefoll; 15.39
400284; ;; NM_000125*:Homol saptens estrogen receptor, homone_rec,zf-C4,Oest_recep;TM=M;SS=M; 15.23
456662; NM_002448; Hs.1494; msh (Drosophila) homeo box homolog 1 (fo; homeobox,none; 15.04
438817; Al023799; Hs.163242; ESTs; none,none; 13.72 25 30 436817; Al023799; Hs.163242; ESTs; none,none; 13.72 438817; Al083799; Rs.163242; ESTs; none,none; 13.72
453857; Al080235; Hs.35861; Ras-Induced senescence 1 (RIS1); none;TM=Y;SS=M; 13.87
424687; Al080235; Hs.35861; Ras-Induced senescence 1 (RIS1); none;TM=Y;SS=M; 13.87
424687; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (S; HMG_box;TM=M;SS=N; 13.44
410001; A8041035; Hs.57771; talliferein 11; trypsin;TM=M;SS=M; 13.41
421445; AA913059; Hs.104433; Homo saplens, clone IMAGE:4054868, mRNA; lon_trans,K_letre,asp; 13.27
445048; Z45051; Hs.2590; similar to S68401 (cettle) glucose Indus; Lamp;TM=M;SS=M; 12.76
436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 12.59
450693; AW408461; Hs.203965; ESTs; Semalg,none; 12.52 35 40 446048, Z45051; Ha. 22520; similar to \$58401 (cattle) glucose Indus; Lamp;TN=Hy,5S=M; 12.76
450783, AW450461; Ha. 20040; claudin 3; PMP2, Claudin;TMP4*;SS=M; 12.59
450783, AW450461; Ha. 200505; ESIE; Semalg, none; 12.52
415457; AW05170; Ha. 20059; Horn supiens babes specific A2 borndog; MORN, augar_b;TM=Y;SS=M; 12.46
413719; BE439580; Ha. 75498; small industribe cytokine subdarnity A (O₇; ILR; 12.23
431623; AMD77025; Ha. 265627; interferon, alpha-Industribe protein (cit, none;TM=M;SS=Y; 12.06
407786; AM687638; Ha. 38972; Intraspan 1; transmembrane4;TM=Y;SS=M; 11.91
444381; BE339735; Ha. 28973; interface protein protein protein (cit, none;TM=M;SS=Y; 12.06
407786; AA687638; Ha. 38972; Intraspan 1; transmembrane4;TM=Y;SS=M; 11.91
444381; BE33935; Ha. 28973; hypothesial growth promoting factor; TPI, MK;TM=M;SS=Y; 12.06
44606; N75217; Ha. 776622; ESTE; Armadilla, seg. HEAT_PSB;TM=M;SS=M; 11.85
44606; N75217; Ha. 776622; ESTE; Armadilla, seg. HEAT_PSB;TM=M;SS=M; 11.91
444381; AM39093; Nat. 168951; ESTE; none.lg.pixinase.lkR;LRRCIT; 14.9
45123; N46299; Ha. 26126; claudin 10; PMP2.C (audin, Peptidase, MIX, Letra;TM=Y;SS=M; 11.45
45396; AA847843; Ha. 52711; High mobility group (nonhistone chromost; HMG_box,none; 11.42
441313; AA721376; Ha. 37766; lotale receptor 1 (abtl); Foldate, not.MY;TM=1,45
45239; VU71207; His.2978; syes absent (Drosophila) horndog 2; Hybrialese; 11.01
462397; U71207; His.2978; syes absent (Drosophila) horndog 2; Hybrialese; 11.01
462397; U71207; His.29944; issue factor patrwey inhibitor; X kunitz, BPTI, note; 10.91
41536; C18356; Ha. 259944; issue factor patrwey inhibitor; X kunitz, BPTI, note; 10.91
41536; C18356; Ha. 259944; issue factor patrwey inhibitor; X kunitz, BPTI, note; 10.91
41536; C18356; Ha. 259944; issue factor patrwey inhibitor; X kunitz, BPTI, note; 10.91
41536; C18356; Ha. 259944; issue factor patrwey inhibitor; X kunitz, BPTI, note; 10.91
41536; C18356; Ha. 259944; issue factor patrwey inhibitor; X kunitz, BPTI, note; 10.91
41536; C18356; Ha. 259945; issue factor patrwey inhib 45 50 55 60 65 70 75 80 456062; Al866286; Hs.71962; ESTs, Wealdy similar to B36298 proliner; none,none; 9.50

```
418113; Al272141; Hs.83484; SRY (sex determining region Y)-box 4; HMG_box,homeobox;TM=M;SS=N; 9.38 412791; Al131192; Hs.143199; ESTs, Weakly similar to 372481 probable ; pkinasee,PBD,none; 9.36 432435; BE218886; Hs.282070; ESTs; none,none; 9.35
                                                                416630; U62801; Hs.79361; katikrain 6 (neurosin, zyme); trypsin;TM=M;6S=M; 9.32
                                                             416530; U62801; Hs.79361; kallwein 6 (neurosin, zyme); typsin;TM=M;SS=M; 9.32
439018; AW300387; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23
445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF-MAM; 9.19
410407; X66339; Hs.63287; carbonic anhydrase IX; carb_anhydrase;TM=M;SS=M; 9.19
417165; R80137; Hs.302738; Horno saplans cDNA: FI,J21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 9.17
43365; BE047032; Hs.257789; ESTs; none,none; 9.14
431674; AA088901; Hs.301642; G-protein coupled receptor; none,GCV_H; 9.05
418004; U37619; Hs.87539; aldehyde dehydrogenese 3 family, member : aldeth;TM=M;SS=M; 9.00
413276; BE563085; Hs.87539; intexferon-stimulated protein, 15 kDs; ubiquitin; 8.93
436954; AA740155; Hs. 130425; ESTs; none, nore; 8.91
           5
10
                                                                   436954; AA740151; Hs. 130425; ESTs; none,none; 8.91
                                                             436954; AA740151; Hs. 130425; ESTs; none,none; 8.91
420344; BE43372; Hs. 97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 8.89
425397; Ju4088; Hs. 156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB_DNA_topoisoV,HATPase_c;; 8.85
407792; Al077715; Hs. 3384; putative secreted ligand homologous to f; none;TM=M;SS=M; 8.80
451027; AW519204; Hs. 40808; Homo sepiens, Similar to RIKEN cDNA 2810; none,none; 8.79
42509; AK001379; Hs. 121028; hypothetical protein FLJ10549; lQ;TM=M;SS=N; 8.70
43385; M34455; Hs. 840; indolearnine-pyrrole 2,3 dioxygenase; IDC;TM=M;SS=N; 8.70
444784; D12485; Hs. 11951; ectoruckedide pyrophosphataset/phosphodi; Sometomedin_B,Endonuclease,Phosphodlest;TM=Y;SS=M; 8.69
421502; AF111856; Hs. 105039; solute carrier family 34 (sodium phospha; Ribosomel_L20,Na_Pi_cotrans;TM=Y;SS=N; 8.67
437935; AW939591; Hs.5940; much 13, epithetial transmembrane; EGF,SEA;TM=Y;SS=M; 8.56
408692; AL040127; Hs. 34074; dipeptidylapsidase Vt; DPPN_M, term.Peptidase_S9,none; 8.55
414812; X72755; Hs. 77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 8.53
428187; Al687303; Hs.285528; G protein-coupled receptor 49, 7fm_1,none; 8.49
448672; Al955511; Hs.374290; ESTs; ing_chan,ANF_receptor,SBP_bac_3;TM=Y;SS=M; 8.40
425776; U25126; Hs. 159499; parathyroid hormone receptor 2; 7m_2,HRM;TM=Y;SS=M; 8.40
15
20
                                                      409592, ALOHOTZ, Na. 34074. dipeptidylapidisas VI, DPPN J, Jemn Peptidess, Silpnone, 8.55
448182, YAZSES, 18-73679, montifice Induced by garminal Interferon, IEA/TM-McSS-Pt, 9.33
428187, Al857302, Na. 285529, G profish -coupled mecapicr 45, 71m., 1, none, 8.49
448727, Al857302, Na. 285529, G profish -coupled mecapicr 45, 71m., 1, none, 8.49
448727, Al857302, Na. 285529, G profish -coupled mecapicr 45, 71m., 1, none, 8.49
445727, U25120, Na. 159498, parathyroid hormone receptor 27, 7m., 2, IFRKTIM-Y, SS-M, 8.40
445737, U25120, Na. 159498, parathyroid hormone receptor 27, 7m., 2, IFRKTIM-Y, SS-M, 8.40
445737, U25120, Na. 159498, parathyroid hormone receptor 27, 7m., 2, IFRKTIM-Y, SS-M, 8.40
445727, ALST 18-14, 1132, phosphalman metalyric and the receptor of 
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                                                                        418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.87
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418203; X54942; Hs. 83758; CDC28 protein kinase 2; CKS;; 6.85
410467; AF102546; Hs. 63931; dechshund (Drosophila) homolog; Ski_Sno;TM=M;SS=M; 6.86
425247; NM, 005940; Hs. 155324; maritx metalloproteinase 11 (stromelyalin; hemopesin,Peptidase_M10;; 6.85
435046; A8018345; Hs. 27557; KJAA0802 protein; none;TM=M;SS=N; 6.79
452046; A8018345; Hs. 27557; KJAA0802 protein; none;TM=M;SS=N; 6.79
47771; AA804638; Hs. 62547; retinoic sold receptor responder (lazaro; none,none; 6.79
472223; X94453; Hs. 114366; pyrroline-5-carboxyldate synthetases (glut; aldedh,aakinase;TM=M;SS=N; 6.77
431470; AA832417; Hs. 139650; ESTs; none; ip, kinase, LRR,LRRCT; 6.76
418738; AW388533; Hs. 6862; solute carrier family 7; (celionic amino; none,none; 6.74
418738; AW388533; Hs. 6862; solute carrier family 7; (celionic amino; none,none; 6.74
418738; AW388533; Hs. 6862; solute carrier family 7; (celionic amino; none,none; 6.74
418738; AW388533; Hs. 327548; phosphoinostikle-3-kinase, regulatory su; SH2,none; 6.74
417886; AA214584; ; ESTs; SPRY,7tm, 3-AMF_receptor,none; 6.72
417386; AA214584; ; ESTs; SPRY,7tm, 3-AMF_receptor,none; 6.72
4173960; Al559586; Hs. 369312; ESTs; none,none; 6.58
429953; AA306610; Hs. 346183; lumor necrosis factor receptor superfamil; 60s_ribosomal_Ribosomal_L10,TNFR_c6,DEAD;; 6.66
44006; BES95085; Hs. 334762; type ib transmembrane protein Fn14; idl_recept_a_PKD,MHC_l;TM=M;SS=Y; 6.65
413040; AA193338; Hs. 12321; sodium calclum exchanger; Na_Ca_Ex;TM=Y;SS=M; 6.62
444905; BES95085; Hs. 334762; type ib transmembrane protein for the protei
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                                                                                                              431259; BE550182; Hs.375142; RaiGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 6.62
434263; N34895; Hs.79187; ESTs; Ig,none; 6.49
418322; AA284166; Hs.84113; cyclin-dependent kinase Inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 6.48
419942; U25138; Hs.93841; potassium large conductance calcium-edi; CakB;TM=Y;SS=M; 6.47
421064; AI245432; Hs.101382; turnor necrosis factor, alpha-induced pro; nons;TM=M;SS=N; 6.47
422064; AI245432; Hs.278582; claudin 7; PMP22_Claudin;TM=Y;SS=M; 6.45
431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 6.44
428332; AA578229; Hs.324239; ESTs, Moderately similar to ZN91_HUMAN Z; Osteopontin,nome; 6.39
438775; AA731111; Hs.372225; ESTs; none,none; 6.39
4284343; AW995360; Hs. 4748; adentified cycling orderedtide; 7tm 2 NBM append 374
  30
                                                                                                331655-AW296136; Nb. 257656; vau 3 enceganic CH DAC, FF Shirt PH, RooSEF, SH2, SH3, DC (17M-MASS-N), 6.44
28322-AM27622N; ha. 201323; ESTE, Molecularly aminion to ZNRO J-HJMAN 2; Ostropoulin, nome 6.39
438776; AA731111; hs. 27228; ESTE, nons nome 6.39
424034; AW39530; hb. 6478; eBSTE, work nome 6.39
424034; AW39530; hb. 6478; eBSTE, work nome 6.39
424034; AW39530; hb. 6178; eMy4hydrocabon researching polypophics; Pm. 24184; em. 48534; ed. 37
43909; AA22995; ; jbr.07169.81 NCI_GORP, Ov2 Horn septime; EGF, meliblio, Integrin, B. PSU, nome, 6.27
43909; AA22995; ; jbr.07769.81 NCI_GORP, Ov2 Horn septime; EGF, meliblio, Integrin, B. PSU, nome, 6.27
43909; AA22995; ; jbr.07769.81 NCI_GORP, Ov2 Horn septime; EGF, meliblio, Integrin, B. PSU, nome, 6.27
429556; AW133999; Hb. 314807; ESTE; nome(TM-MSS-N); 6.26
43939; AA721675; hb. 22727; absted 5 diphe-reductable 2-88; HSVR g; Steroid_dtr, TM-Y; SS-N; 6.25
43939; AP229177; hb. 21354; keurian chri repeat and death domain corn; nome, nome; 6.24
43936; AW3939; Hb. 314807; ESTE; nome(TM-MSS-N); 6.26
43936; AW3939; Hb. 314807; ESTE; nome(TM-MSS-N); 6.27
43956; AW3939; Hb. 314807; ESTE; nome(TM-MSS-N); 6.27
43956; AW3939; Hb. 314807; ESTE; nome of the corn of the c
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453102; NM_007197; Hs.31664; frizzled (Orosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.87 426761; Al015709; Hs.172089; POR\MIN Pro-oncosis receptor Inducing me; none;TM=Y;SS=M; 5.85
                                                         425367; BE271188; Hs. 155975; protein tyrosine phosphatase, receptor in one;TM=M;5S=M; B. 425367; BE271188; Hs. 155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 5.B5 426108; AA522037; Hs. 166468; programmed cell death 5; DUF122;TM=M;SS=N; 5.84 450502; T08065; Hs. 118262; ESTs; lon_trans.jon_trans; 5.84 442662; AI006163; Hs. 201378; Homo saplens cDNA FLJ40427 fis; none;TM=M;SS=N; 5.83 424917; AI636208; Hs. 95901; hypothetical protein FLJ23049; none;TM=M;SS=N; 5.83
            5
                                                          42567; Alc3d2uc; ns.96901; hypothetical protein FLI23043; none; tw=MtSS=N; 5.65
448569; BE382657; Hs. 21486; signet trensducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 5.82
422616; BE300330; Hs. 118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 5.82
445133; AW157646; Hs.198689; ESTs; efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FIID,bZIP,Tropomyosin,Myo-LZ,M,kth_C,CH,AIP3;TM=M;SS=N; 5.79
426215; AW963419; Hs.155223; stanniocalcin 2; Stanniocalcin; 5.78
10
                                                         426215; AW963419; Hs. 155223; stanniocalcin; 2; Stanniocalcin; 5.78
414482; SS7498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 5.75
414809; Al434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=M; 5.74
452583; Al089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 5.72
432201; Al538613; Hs.298241; Transmembrane protease, serine 3; IdI_recept_a, trypsin;TM=Y;SS=M; 5.72
432345; R11141; Hs.199695; hypothetical protein; K_letra,SAM; 5.72
449456; Al805076; Hs.208261; EST's; Fizzted,Fz,none; 5.72
418526; BEO19020; Hs.85838; solute carrier fam3y 16 [monocarboxyllc; none;TM=Y;SS=M; 5.71
418848; Al805051; Hs.193465; ESTs; PDZ,pkinses,none; 5.70
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                                                              426227; U67058; Hs.154299; Human proteinese activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 5.69
                                                          41199; AA305342; Hs.69171; protein kinase C-like 2; pklnase.pklnase.c., IR1; TM=1,55=N; 5.69
411263; BE297802; Hs.69360; kinasin-like 6 (mitotic centromere-assoc; kinasin; TM=M;SS=N; 5.69
445136; Al348014; Hs.143949; ESTs, Wealdy similar to Achaete-Scute ho; ion_trans,ion_trans; 5.69
409223; AA312572; Hs.362852; phospholnositide-3-kinase, regulatory su; SH2,SH3,RhoGAP,none; 5.67
                                                    411253; BE297901; B. 59390; Intersi-like 6 (milotic centromer-easor; kinseln; TM-M;SS-M; 5.59
449323; A.4312672; Hs. 59395; Discopholocitido-3-kinase, regulatory str; SH2,SH3,Rh0GAP,none; 5.67
49016; NM, 004736; Hs. 270756; zendroting and polyhogin retrovirus ret; STS-XEXSTIM-Y;SS-M; 5.68
429638; A1916662; Hs. 271577; kinectin 1 kinesin receptor; biZiP,Tropomyosin,specifini,18P_BPL_CETP,856,M;TM=Y;SS=M; 5.65
429638; A1916662; Hs. 241907; eukaryofin translation initiation factor; none; 5.64
429638; M67414; Hs. 161303; tachydrin receptor; 27 7m. 1;TM=Y;SS=M; 5.64
429639; M67414; Hs. 161303; tachydrin receptor; 27 7m. 1;TM=Y;SS=M; 5.64
429639; M67414; Hs. 161303; tachydrin receptor; 27 7m. 1;TM=Y;SS=M; 5.64
429267; Av4976029; Hs. 1007246; ESTs; none-none; 5.64
41304; A.4447849; Hs. 288680; refinois acid induced 3; 7m. 3, none; 5.63
441304; A.4447849; Hs. 288680; refinois acid induced 3; 7m. 3, none; 5.63
44717; BE465754; Hs. 17776; neutroplin 2; CUB,MAMFS FB, Uppe_CTM=M;SS=M; 5.61
440122; AV492569; Ps. 13070; Order of protein FL2150; 20G-Fell_Oxy;TM=M;SS=M; 5.61
440124; AV492596; Ps. 13070; Order of protein FL2150; 20G-Fell_Oxy;TM=M;SS=M; 5.61
440124; AV492596; Ps. 13070; Order of protein FL2150; Ps. 40070; M670; 
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                                                              450402; BEZ18027; Hs.89995; ESTs; SH3,none; S.42
428484; AF104032; Hs.184601; solute carrier family 7 (catlonic amino; az_permeases.pyrtdoxal_dec.promodomain,PHD,MBD,AT_hook,DDT,PI3_PM_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 5.42
430596; AAS11276; Hs.59509; ESTs; pkinase,PPZC,none; S.42
412350; Al659306; Hs.73826; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;TM=M;SS=N; 5.42
414783; AK001466; Hs.62160; anilifa (Drasophita 6craps homolog), act; PH,none; 5.41
448795; Al097463; Hs.21095; KIAA1130 protein; none,Zip; 5.41
410082; AA081594; Hs.158311; Musashi (Drasophita) homolog 1; rmr;TM=M;SS=N; 5.40
411817; BE302900; Hs.72241; mitogen-activated protein Kinase kinase; pkinase;TM=M;SS=M; 5.40
414813; AA151342; Hs.12677; CGI-147 protein; UPF0099;TM=M;SS=M; 5.39
451863; AL120634; Hs.331803; ATPase, Ca transporting, plasma membrane; opn60_TCP1,E1-E2_ATPase,Cation_ATPase_N,Hydrolase;; 5.38
442875; BE623003; Hs.23625; Homo esplans done TCCCTA00142 mRNA sequ; K_letra,DUF51,none; 5.38
439963; AN1247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH_lb,Lipase_GDSL;TM=M;SS=N; 5.36
441031; AA110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 5.33
408369; R38438; Hs.11874; SLC15A2 Solute carrier family 15 (H-/pep; PTR2,TM=Y;SS=N; 5.33
4135391; AA704588; Hs.58934; E876; PIPSK,none; 5.33
411779; AA292211; Hs.72050; non-metastable cells 5, protein expresses; NDK;; 5.33
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                                                                  435391; AA704508; Hs.58934; ESTS; PIPSK, none; 5.33
411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK;; 5.33
422170; AI791949; Hs.112432; anti-Mullerian hormone; TGF-bela;; 5.32
447350; AI375572; Hs.172634; v-erb-a arian erythroblastic leukemia vi; pidnase; Recep_t_domain, Furin-like, YLP, none; 5.32
447360; AW001741; Hs.24243; hypothetical protein FLJ10706; pidnase; TM=M;SS=N; 5.31
426427; M86699; Hs.169840; TTK protein kinase; pidnase;; 5.30
430407; H233561; Hs.30974; ESTs; pkinase, PBD, none; 5.29
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416847; L43821; Hs.80261; enhancer of filamentalion 1 (cos-like do; SH3;TM=M;SS=N; 5.27
425308; M97639; Hs.150585; receptor tyrosine kinase-like orphan rec; (j.kthrigle, pkinase, Fz;TM=Y;SS=M; 5.27
424596; AB020639; Hs.150107; estrogen-related receptor gamma; hormone_psc_xF-C4;TM=M;SS=N; 5.27
426913; AF151020; Hs.181444; hypothetical protein; none;TM=Y;SS=M; 5.28
447384; A3377221; Hs.49528; ESTis: SH3,Sorb,none; 5.26
447384; A3377221; Hs.49528; ESTis: SH3,Sorb,none; 5.26
44384; A337721; Hs.49528; ESTis: SH3,Sorb,none; 5.26
44384; A337721; Hs.49529; Captriot 11, type 2_UB-scatherin (osleody sr. SH2,SH3,RhoGAP;TM=M;SS=N; 5.26
428679; NM_005756; Hs.164942; G protein-coupled receptor 64; 7tm_2,CFPS;TM=Y;SS=M; 6.25
414359; MS2194; Hs.73929; calchier 11, type 2_UB-scatherin (osleody cardherin, Catherin, Catheri
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                                                                                                                    | 498444 | AA720997 | Is. 128295 | ESTE, none, CAP. GLY. HCO3. cotransp. Glyco. Jurdin. 62 PH; 5.11
| 419833 | AA273131 | Is. 220697 | Horn apalians byrophonal-WiRN aymbetas; WHEP_TRS_REWA-synt_tb,none; 5.10
| 45397; A1990741 | In. 22090; ESTEs No. Ca. Extrone; 5.07
| 45397; A1990741 | In. 22090; ESTES No. Ca. Extrone; 5.07
| 45397; A199084 | In. 21365; A1990 | In. 21360 | I
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                                                                                          425195, AP 120 (03; TEX 197 500, SINDOLINERO (NOSCONDER) NOTIONAL, CONSCIENT, WITE, GE, death, Lipoprotein, E, TILTM=Y; SS=M; 4.60
409220; BE243323; Hs.51233; tumor necrosis factor receptor superfemt; TNFR_c6, death, Lipoprotein_E, TILTM=Y; SS=M; 4.60
421921; H83365; Hs.35593; translocase of inner mitochondital membr; zf-Tim10_DDP, ethand, CH, spectrin, serpin; TM=M; SS=N; 4.60
42903; Y09397; Hs.227817; BC12-related protein A1; Bc1-2; TM=M; SS=N; 4.69
400290; H18836; Hs.31608; hypothetical protein FLJ20041; none, Cys_Lond; 4.59
430379; AF134149; Hs.240395; potaselum channel, subfamily K, member 6; lon_brans; TM=Y; SS=M; 4.59
430379; AF134149; Hs.240395; potaselum channel, subfamily K, member 6; lon_brans; TM=Y; SS=M; 4.59
427373; AB007972; Hs.130760; myosin phosphalase, target subunit 2; ank; TM=M; SS=N; 4.58
437212; AV765021; Hs.210775; ESTs; UDPGT, none; 4.58
430396; D49742; Hs.241303; hypluronan-binding protein 2; ank,death; ZU5,EGF,kringle,trypsln,Nebulin,LiM;; 4.57
452069; AB002949; Hs. 183994; KlA41026 protein; Metallophos; TM=M; SS=N; 4.56
416041; AA345547; Hs.53263; hypothetical protein FL113287; WD40;; 4.55
434511; R28992; Hs. 18106; ESTs; pkinase,Glyco_hydro_39; 4.55
418758; AW959311; Hs.172012; hypothetical protein DKFZp4341037; pkinase,RIO1; TM=M; SS=N; 4.55
418758; AA923729; Hs.26322; cell cycle related kinase; pkinase; TM=M; SS=N; 4.54
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### 17450 BEZ70756; Hz. 82126; 514 encordulal braphobates (p)expending: LRRLIRRIY_LRRCT, Tub*/SS=M, 4.54
### 14126; BEZ70750; Hz. 10114; growth suppressor 1; 27G-Felf, OnyTub-MS-94-M, 4.53
### 14126; BEZ70750; Hz. 10114; growth suppressor 1; 27G-Felf, OnyTub-MS-94-M, 4.53
### 14126; BEZ70750; Hz. 10114; growth suppressor 1; 27G-Felf, OnyTub-MS-94-M, 4.53
### 14126; BEZ70750; Hz. 10114; growth suppressor 1; 27G-Felf, OnyTub-MS-94-M, 4.53
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444664; N26362; Hs. 11615; map kinase phosphalase-like protein MK-S; OSPc;TM=M;SS=N; 4.33 429655; U48959; Hs. 211582; myosin, light polypeptide kinase; pkinase, fn3,ig,none; 4.32 409121; AA902256; Hs. 78979; Golgi apparatus protein 1; cys_rich_FGFR,none; 4.32 430280; AA361268; Hs. 237868; Interleukin 7 receptor; fn3,none; 4.32
                                    409121; AA90122bb; HS. //B3/P; Golgi apparatus protein 1; cys_rich_FGFR,none; 4.32
430280; AA361256; Hs. 237868; Interleukin 7 receptor; fn3,none; 4.32
423798; AFO47033; Hs. 132904; solute carrier family 4, sodium bloarbon; HCO3_cotransp;TM=Y;SS=M; 4.29
425554; AB033022; Hs. 158654; KIAA1196 protein; zf-CzH2;TM=M;SS=N; 4.29
425554; AB033022; Hs. 158654; KIAA1196 protein; zf-CzH2;TM=M;SS=N; 4.29
427127; AW902282; Hs. 227659; pruvate dehydrogenase phosphalase; PP2C,none; 4.29
427191; NM_014521; Hs. 17667; SH3-domain binding protein 4; SH3;TM=M;SS=N; 4.29
447191; NM_07240; Hs. 44229; dual specificity phosphalase 12; DSPc;TM=M;SS=N; 4.29
440331; NM_07240; Hs. 44229; dual specificity phosphalase 12; DSPc;TM=M;SS=N; 4.29
441130; A1160734; Hs. 237604; Homo saplens PNAS-129 mRNA, complete ods; BTB,Kelch,K_latra_DSPc;TM=M;SS=N; 4.28
430057; AW450303; Hs. 2534; bone morphogenetic protein receptor, typ; Activin peop,pkinase;TM=Y;SS=M; 4.28
430250; NM_016929; Hs. 283021; chloride intracellular channel 5; none;TM=M;SS=N; 4.28
430250; NM_016929; Hs. 283021; chloride intracellular channel 5; none;TM=M;SS=N; 4.28
43089; L25851; Hs. 851; integrin, alpha E (antilgen CD103, human; vwa_Integrin_AFG-GAP;TM=M;SS=N; 4.27
443960; A1093677; Hs. 2837; EST5; for lenderaley similar vwa_Integrin_AFG-GAP;TM=M;SS=N; 4.27
41204; A1125607; Hs. 24937; EST5; for lenderaley similar to Is4373*4 gene; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.26
452486; N74921; Hs. 184389; EST5; none;TM=M;SS=N; 4.26
452486; N74921; Hs. 184389; EST5; none;TM=M;SS=N; 4.26
452486; N74921; Hs. 182890; EST5; none;TM=M;SS=N; 4.26
452486; N74921; Hs. 182890; EST5; none;TM=M;SS=N; 4.26
452487; AA022637; Hs. 1812272; EST5; effenderaley similar to Is4373*4 gene; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.26
452486; N74921; Hs. 128980; EST5; none;TM=M;SS=N; 4.26
452486; N450945; Hs. 1812272; EST5; effenderaley similar to Is4374*4 gene; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.26
452486; A1589645; Hs. 128980; EST5; none;TM=M;SS=N; 4.26
452486; A1589645; Hs. 128980; EST5; none;
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                                        TABLE 23B
                                                                                          Unique Eos probeset identifier number
  75
                                          CAT number: Gene cluster number
                                          Accession
                                                                                       Genbank accession numbers
                                                                                        CAT Number Accession
MH1944_5 BI030997 AA921874 AW188822 BI027862 Al347618 Al361453 Al088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
BI027864 BI009100 BI006275 BI0036270 BI031000 BI029864 BI005277 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518
BI027818 BG015789 BI033807 AA341445
                                        Pkey
409745
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                                                                                         1031334_1 AA210987 D57294 AA214584 AA207006 D56572 2580163_1 Al926361 AA834879 AA828995
                                          438993
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418869

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447164 402047

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452943 416661 427099

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431808

411750 418612

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423020

AF026941 AK001921 BE263782

BE247449 AA634543 AB032953 AW236021

AJ001696 NM_000857 AW368397 AJ753709

M30703

BE562298 AB037788 BE379623

AI097560

AA383092

Hs.17518 Hs.169675 Hs.77695

Hs.77695 Hs.31082 Hs.79440 Hs.173560 Hs.78531 Hs.241407

Hs.77890

Hs.150042 Hs.152484

Hs.270833

Hs.71827

Hs.224961 Hs.27693 Hs.61210

Hs.1608

12789_14 AA229762 AA230035

	416907	1112245_1	W60909 W610	51 M78905 BG959483							
5	TABLE 23C										
	Pkay: Ref:	Sequence so	que number corresponding to an Eos probeset uence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA legged of burgers decreased 13". Dunham I. et al." refers to the publication entitled "The DNA								
10	Strand: Nt_position:	Indicates DN	quence of human chromosome 22.° Dunham L. et al., Nature (1999) 402:489-495. Ricales DNA strand from which exons were predicted. Ricales nucleolide positions of predicted exons,								
	Pkey	Ref	Strand t	Lposilion							
15	405400 403362 404210 404287 405484 400517	9256298 8571772 5006246 2326514 5922025 9796686	5298 Plus 1553-1712,1878-2140,4252-4385,5922-6077 1772 Plus 64093-64290 5246 Plus 169926-170121 5514 Plus 53134-53281 2025 Plus 199214-199579,199672-199920,200262-20049								
20				•							
	TABLE 24A:	571 GENES U	P-REGULATED	IN HEAD AND NECK TUMORS COMPARED WIT	H NORMAL RODY TISSUES						
25	Table 24A lis Hu03 Gened	als about 571 g	enes up-regulat	ed in head and nack humans compared with normal	body dissues. These genes were selected from 59680 probesets on the Eos/Aflymetrix is was expressed as everage intensity (AI), a normalized value reflecting the relative						
30	Pkøy; ExAccn: UnigenelD: Unigene Title R1:	Exemplar Acc Unigene num Onigene gene	ber e tille	ir number Genbank accession number and neck cancer samples vs. the 80th percentile of	the Al for normal body tissues						
35	Pkey	ExAcon	UnigeneID	Unigene Title	R1						
	421155	H87879	Hs.102267	lysyl oxidese	166.00						
	452401 434377	NM_007115 AW137148	Hs.29352 Hs.306593	tumor necrosis factor, alpha-induced pro Homo seplens cDNA FLJ 11382 fis, clone HE	156.00						
40	438274	Al918906	Hs.55080	ESTs	80.00 28.00						
40	401486	1 14 F4 F00	II. ee toos		121.00						
	446999 423887	AA151520 AL080207	Hs.334822 Hs.134585	hypothetical protein MGC4485	126.00						
	419569	A1971651	Hs.91143	DKFZP434G232 protein jagged 1 (Alagille syndrome)	13.00						
45	428505	AL035481	Hs.2281	chromogranin B (secretogranin 1)	98.00 1.00						
45	420502	AF060877	Hs.99236	regulator of G-protein signalling 20	35.00						
	445019 452281	A1205540	Hs.281295	ESTs	93.00						
	449722	T93500 BE280074	Hs.28792 Hs.23960	Homo sapiens cDNA FLI11041 fis, clone PL cyclin B1	270.62						
	423575	C18863	Hs.163443	Homo sepiens cDNA FLI11576 fls, clone HE	9.81						
50	424086	Al351010	Hs.102267	lysyl oxidase	373.00 200.00						
	447078	AW885727	Hs.301570	ESTE	184.00						
	429597 409506	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	177.00						
	426471	NM_006153 M22440	Hs.54589 Hs.170009	NCK adaptor protein 1	170.00						
<i>5</i> 5	41326B	AL039079	Hs.75256	transforming growth factor, eipha regulator of G-protein signaling 1	158.00						
	419948	AB041035	Ha.93847	NADPH oxidese 4	155.00 140.00						
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	139,00						
	442875	BE623003	Hs.23625	Homo sepiens clone TOCCTA00142 mRNA sequ	111_00						
60	452795 420931	AW392555 AF044197	Hs.18878	hypothetical protein FLJ21620	109.00						
	416283	NM_005429	Hs.100431 Hs.79141	smail inducible cytokine B subfamily (Cy vascular endothellal growth factor C	106.00						
	450221	AA328102	Hs.24641	cyloskeleton associated protein 2	95.00						
	449101	AA205847	Hs.23016	G protein-coupled receptor	92.00 92.00						
65	442611	BE077155	Hs.177537	hypothetical protein DKFZp76181514	86.00						
65	438533	A1440256	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	85.68						
	414132 447164	Al801235 AF026941	Hs.48480	ESTs	85.00						
	77/ IUG	ACU2034 I	Hs.17518	Home seriens clas mRNA model common	00.00						

ESTs
Homo sapiens clg5 mRNA, partial sequence
hypothetical protein MGC2550
KIAA0008 gene product
hypothetical protein FLJ10S25
IGF-II mRNA-binding protein 3
odd Oz/ten-m homolog 2 (Drosophila, mous
Homo sapiens, Similar to RIKEN cDNA 5730
serine (or custolea) proteins a lobbite.

serine (or cystelne) proteinase Inhibito guanylate cyclase 1, soluble, beta 3 Homo saplens cDNA FLJ14438 fis, clone HE

riomo sapiens cuva FLJ14448 fis, cione III ESTs, Weakly similar to 138022 hypotheti amphiregulin (schwannome-derived growth KIAA0112 protein; homolog of yeast ribos cleavage and polyadenyletion specific fe peptidylprotyl isomanase (cyclophilin)-! ESTs, Weakly similar to 138022 hypotheti replication protein A3 (14kD)

85.00 83.00

80.00 74.00 74.00

71.00 70.19 66.25 66.00

64.00

63.00

60.00 58.00

57.00

57.00

54.00 54.00

	40				
	422426	W79117	Hs.58559	ESTs	49.00
	406747	AI925153	Hs.217493	annexin A2	46.00
	445828	F05802	Hs.81907	ESTs	46.00
5	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	44.00
J	452909	NM_015368	Hs.30985	pannexin 1	43.95
	432226	AW182766	Hs.273558	phosphale cylidylyltransferase 1, cholin	43.00
	458027	L49054	Hs.85195	rsycloid leukemia factor 1	43.00
	443354	AW970672	Hs.9247	protein klnase, AMP-activated, alpha 1 c	43.00
10	416049	AI970536	Hs. 16603	hypothetical protein FLJ13163	42,00
10	431494	AA991355	Hs,298312	hypothetical protein DKFZp434A1315	40.00
	433859	AW896758	Hs.273789	ESTs	38.00
	426753	T89832	Hs. 170278	ESTs	37.00
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	36.00
15	402034				35.00
13	424073	U03493	Hs.138959	gap Junction protein, alpha 7, 45kD (con	34.09
	45B424	A10B4049	Hs.205761	EST _{\$}	34.00
	435159	AA668679	Hs.116649	ESTs	33.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	32.00
20	444361	W76027	Hs.23920	hypothetical protein FLI11105	31,00
20	439128	A1949371	Hs.153089	ESTs	29.20
	420795	AA323037	Hs.128645	sorting nexin 16	26.00
	422505	AL120862	Hs.124165	EST ₈	25.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	24.00
26	410561	BE540255	Hs.6994	Homo saplens cDNA: FLJ22044 fis, clone H	22.10
25	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	19.00
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	19.00
	414869	AA157291	Hs.21479	ubinuclein 1	17.37
	453049	BE537217	Hs.30343	ESTs	16.00
20	417801	AA417383	Hs.82582	Integrin, bela-like 1 (with EGF-like rep	14.00
30	435243	AW292686	Hs.261373	hypothetical protein dJ434014.3	13.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10,60
	407746	AK001962	Hs.36114	hypothetical protein FLJ11100	10.00
	416498	U33632	Hs.79351	polassium channel, subfamily K, member 1	9.60
0.5	414231	A1468004	Hs.278956	hypothetical protein FLI12929	9.00
35	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	· 8.09
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	8.07
	439999	AA115B11	Hs.6838	ras homolog gene family, member E	8.07
	417791	AW965339	Hs.111471	ESTs	8.04
40	436486	AA742221	Hs.120633	ESTs	7.23
40	432731	R31178	Hs.287820	fibronactin 1	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	5.1B
	435039	AW043921	Hs.130526	ESTs	5.00
	419743	AW40B762	Hs.5957	Homo sapiens cione 24416 mRNA sequence	4.25
AC	457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	4,24
45	450684	AA872805	Hs.25333	interleuten 1 receptor, type II	3.74
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member 810	3.19
	458531	AA36771B	Hs.1590B3	EST8	3.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.53
EΛ	411388	X72925	Hs.69752	desmocolin t	1.00
50	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, ciona NT	1.00
	429370	C19097	Hs.59709	glutamate-cysteine ligase, modifier subu	1.00
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	1.00
	449467	AW205006	Hs.197042	ESTS	1.00
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1,00
55	453637	NM_002589	Hs.34073	BH-protocadherin (brain-heart)	1.00
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	517.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstilia)	616.00
	428366	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	226.00
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily 8 (Cy	278.00
60	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	56.11
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmki metaph	264.00
	424717	H03754	Hs.152213	wingless-type MMTV integration site famil	124,00
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.00
65	420159	A1572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	1.00
65	415511	AI732617	Hs.182362	ESTs	1.00
	406467				141.00
	422330	D30783	Hs.115263	epireguin	98,00
	452461	N78223	Hs.108106	transcription factor	159.00
70	415542	R13474	Hs.290263	ESTs, Wealdy similar to 138022 hypotheti	1.00
70	413324	V00571	Hs.75294	corticotropin releasing harmone	1.00
	431571	AVV500486	Hs.180610	splicing factor proline/glutamine rich (7.60
	443211	A1128388	Hs.143655	ESTs	99.00
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00
75	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	3.00
75	439926	AVV014875	Hs.137007	ESTs	2.79
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp58600724 (f	94.00
	421103	A1625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	1.22
	448062	AW295923	Hs.255472	KIAA1843 protein	1.00
90	432222	A1204995		gb:sn03c03.x1 Strategene schizo brain S1	1.27
80	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00
	421187	NM_014721	Hs.102471	KIAA0680 gens product	5.00
	408908	BE296227	Hs.250822	sedne/threonine kinase 15	89.00
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	1.00
				279	
				, 10	

	A Acress		11		
	449773 -	R76294	Hs.302383	ESTs	1.00
	443054	A)745185	Hs.8939	yes-associated protein 65 kDa	90.00
	432097	X51730	Hs.2905	progesterane receptor	1.00
_	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	0.38
5	430184	AB013802	Hs.234790	contactin 5	1.00
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.23
	415025	AW207091	Hs.72307	ESTs	1.00
	416575	W02414	Hs.38383	ESTs	
	443171	BE281128	Hs.9030		1.00
10	424834			TONDU	0.92
10		AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	20.30
	400844				0.60
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.96
	412420	AL03566B	Hs.73853	bona morphogenetic protein 2	1.38
10	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2,60
15	400751			· · ·	1.34
	436361	AA825614	Hs.149065	ESTs	0.92
	455612	BE042896	Hs.274848	ESTs	0.81
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupi	1.55
	404148		,	purincigio receptar i 24, O-protein toupi	
20	431089	BE041395	Hs.283676	CCTe Mookly similar to Wales and another	0.77
	446619	AU076643	Hs.313	ESTs, Weakly similar to unknown protein	1.00
	416658			secreted phosphoprotein 1 (osteopontin,	6.47
		U03272	Hs.79432	fibrilin 2 (congenital contractural ara	3.92
	442994	AJ026718	Hs.16954	ESTs	0.40
25	415327	H22769		gb:ym54c02r1 Soares infant brain 1NIB H	0.47
25	418624	AI734080	Hs.104211	ESTs	1.90
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	0.54
	401747			Homo sapiens keralin 17 (KRT17),	7,22
	442432	BE093589	Hs.38178	hypothetical protein FLI23468	5.10
	418259	AA215404	Hs.137289	ESTs	1.28
30	432374	W68815	Hs.301885	Homo saplens cDNA FLJ11346 ffs, clone PL	8.13
	403381	*******		Trothe deplote destrict that form is being it	
	420923	AF097021	Hs.273321	differentially assessment in houselensing	21.00
	418216	AA662240	Hs.283099	differentially expressed in hematopoles	0.00
				AF15q14 protein	11,29
35	444649	AW207523	Hs.197628	ESTs	0.10
J.J	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP entagon	4.64
	402230			•	1.64
	412530	AA766268	Hs.266273	hypothetical protein FL313346	2.97
	447334	AA515032	Hs.91109	ESTs	0.62
40	432829	W60377	Hs.57772	ESTs	0.86
40	418686	Z36830	Hs.8726B	annexin A8	8.44
	421508	NM_004833	Hs. 105115	absent în melanoma 2	2.68
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	2.22
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	
	425721	AC002115	Hs.159309	uroplakin 1A	78.00
45	420370	Y13645			0.86 ,
	417720	AA205625	Hs,97234	uropłakin 2	0.87
			Hs.208087	ESTs	5.83
	437852	BE001836	Hs.256897	ESTs, Weakly similar to d.1365012.1 [H.sa	1.07
	431753	X76029	Hs.2841	neuromedin U	7.00
50	402075				286.00
30	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	363.00
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.B1
	405064				1.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	2.00
	441233	AA972965	Hs.135568	ESTs	1,00
55	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.23
	414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.23 0.65
	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	
	405494	THEODES		Severan processor (At-900 D.IA050 HOLIO	1.00
	407189	AA598927		character of Character (18) was been added as	1.00
60	403085	141030321		gb:ze37e03.s1 Gessler Wilms tumor Horno s	1.00
-	408633	AW963372	Un ACCT?		1.00
			Hs.46677	PRO2000 protein	2.46
	435257	AA677026	Hs.191217	ESTs	1.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in lauc	1.00
65	445182	AW189787	Hs.147474	ESTs -	0.50
UJ	417275	X63578	Hs.295449	parvalbumin	1.00
	418406	X73501	Hs.84905	cytokeratin 20	1.00
	421110	AJ250717	Hs.1355	cathepsin E	1.00
	406081			·	2.13
	449448	D60730	Hs.57471	ESTs	123.00
70	45166B	Z43948	Hs.326444	cartilage acidic protein 1	0.37
	408243	Y00787	Hs.624	Interieukin 8	3.35
	436246	AW450963	Hs.119991	ESTs	
	440304	BE159984	Hs.125395	ESTs	51.00
	402778	DC.00304	1197157027	wig.	1.00
75	406117				1.00
, ,					1.00
	406360		44 44		71.00
	435347	AW014873	Hs.116963	ESTs	1.00
	445550	A1242754	Hs.137306	ESTs	1.00
90	451359	H85334	Hs.336623	ESTs	1.00
80	419559	Y07828	Hs.91096	ring finger protein.	1.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	58.00
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00
	402901			-At hatert stot FL	0.85
					0.00

	44.4040	AI210207	11- 20000	hundhafiad and - El 142460	0.07
	41 4 918 41 7 715	AI219207 AW969587	Hs.72222 Hs.86366	hypothetical protein FLJ13459 ESTs	0.87 5.12
	442577	AA292998	Hs.163900	ESTs	2.19
_	418667	D31771	Hs.89404	msh (Dresophila) homeo box homolog 2	1.54
5	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.11
	412610	X90908	Hs.74126	falty acid binding protein 6, ileat (gas	1.27
	414683	S78296	Hs.76888	hypothetical protein MGC12702	0.67
	431322 403903	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.03 0.87
10	405033				0.13
	422282	AF019225	Hs.114309	apolipoprotein L	2.13
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ 14950	2.59
15	430168	AW968343	Hs.24255	DKFZP43411735 protein	1.69
15	459702	AI204995	No desire	ron-	1,00
	446082 400843	Al274139	Hs.156452	ESTs	0.60 0.76
	417409	BE272506	Hs.82109	syndecan 1	1.78
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	1.20
20	437181	Al306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.50
	404875				0.80
	436293	A1601188	Hs.120910	ESTs	1.40
	422809 425883	AK001379	Hs.121028	hypothetical protein FLJ10549	3.03
25	404977	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f Insulin-like growth factor 2 (somatomedi	0.94 0.99
25	431347	AI133461	Hs.251664	insulin-like growth factor 2 (sometomedi	1.10
	413804	T64682	(101201001	gb:yc48b02.r1 Stratagene liver (937224)	0.85
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.20
20	420876	AA918425	Hs.177744	ESTs	0.85 \
30	422119	Al277829	Hs.111862	KIAA0590 gene product	0.71
	400846	43440.040.00	11 404000	sortlin-related receptor, L(DLR class)	0.75
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	4.01
	430152 402777	A8001325	Hs.234642	aquaporin 3	1.74 0.70
35	417151	AA194055	Hs.293858	ESTs	0.99
	411248	AA551538	Hs.334605	Homo saplens cDNA FLJ14408 fis, clone HE	1.48
	405034	AL035754	Hs.2474	tolHike receptor 1	1.00
	406671	AA129547	,Hs.285754	met proto-oncogene (hepatocyte growth fa	18.68
40	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.94
40	453134	AA032211	Hs.118493	ESTs	0.70
	440006 418068	AK000517 AW971155	Hs.6844 Hs.293902	hypothetical protein FLJ20510	2.19 0.25
	424364	AW383226	Hs.201189	ESTs, Weakly similar to ISHUSS protein d ESTs, Weakly similar to G01763 atrophin-	2.74
	439780	AL10968B	110,401100	gb:Homo sepiens mRNA full length insert	3.07
45	438315	R56795	Hs.82419	ESTs	0.65
	418937	T7/1508	Hs.13861	ESTs, Weakly similar to T42383 probable	1.18
	444163	AJ125098		gbrqc54g07.x1 Soares_placenta_8to9weeks_	0.85
	444444	AJ149332	Hs.14855	ESTs	0.59
50	407581	R48402	Hs.173508	P3ECSL	0.82
50	433078 417003	AW015188 AL038170	Hs.121575 Hs.80756	Homo sepiens cDNA FLJ12231 fis, clone MA betaine-homocysteine methyltransferase	0.92 0.62
	446024	AB040946	Hs.284227	NIAA1513 protein	0.92
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.42
	419741	NM_007019	Hs,93002	ubiquitin carrier protein E2-C	1.68
55	453883	A1638516	Hs.22630	cofactor required for Sp1 transcriptions	1.57
	426847	\$78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.08
	446009 457292	A1989885 A1921270	Hs.231926 Hs.334882	ESTs hypothetical protein FLJ14251	1.00 0.98
	415949	H10562	Hs.21691	ESTs	0.61
60	420281	Al623693	Hs.191533	ESTs	7.01
	446673	NM_016361	Hs.15871	LPAP for lysophosphalidic acid phosphala	0.72
	4509B3	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2,21
	414792	BE314949	Hs.87128	hypothetical protein FL123309	0.99
65	437553	AI829935	Hs.130497	ESTs, Weakly similar to MATS_HUMAN CHLOR	0.54
05	421218 426900	NM_000499 AW163564	Hs.72912 Hs.142375	cytochrome P450, subfamily I (aromatic c ESTs	0.06 0.48
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	0.83
	402305		12200010	1/3 00/10042	0.89
-	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.04
70	445911	Al985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
	436508	AA628980	Hs.192371	down syndrome critical region protein DS	0.65
	423916	AW993496	Hs.17235	Homo seplens clone TCCCIA00176 mRNA sequ	0.63
	405932 401760				1.76
75	452240	AI591147	Hs.61232	ESTs	2.61 453.00
, ,	421064	A1245432	Hs.1013B2	tumor necrosis factor, alpha-induced pro	1,04
	421373	AA808229	Hs.167771	ESTs	17.00
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.16
80	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.6B
δU	422406	AF025441	Hs.116206	Opa-Interacting protein 5	3.19
	413278	BE563085	Hs.833	Interferon-stimulated protein, 15 kDa	1.73
	453389 454789	BE273648 BE156314	Hs.32963	cacherin 6, type 2, K-cadherin (fetal kl gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.00 1.00
	-V-11 U-3	DE 1000 14		Spinish and and a tongon a stand to the formation	1,00

	434487	AF143B67	Hs.337588	ESTs, Moderately similar to S65657 alpha	0.06
	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	2.45
	418067	Al127958	Hs.83393	cystafin E/M	1.41
	441801	AW242799	Hs.86366	ESTs	140.00
5	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	
	410153	BE311926	Hs.15830		2.45
	400409	AF153341	Hs.283954	hypothetical protein FLJ12691 Homo sapiens winged hellwforkhead trans	58.00
	452316	AA298484			1.17
			Hs.61265	ESTs, Moderately similar to G786_HUMAN P	0.86
10	427587	BE348244	Hs.202628	ESTs, Weakly similar to 178885 serine/th	0.91
10	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	1.00
	453204	R10799	Hs.191990	ESTs	1.13
	437240	AA747537		gbmx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	1.00
	405531				0.92
4-	440249	AI246590	Hs.337275	ESTs	1.32
15	426783	Z19084	Hs.172210	MUF1 protein	1.17
	434192	AW387314	Hs.34371	ESTs	
	407881	AW072003	Hs.40968		1.00
	402001	7117072000	115,40500	heparan sulfale (glucosamine) 3-O-sulfot	87.14
		AT440040	11- 004000	Darbana II	37.00
20	433967	AF113018	Hs.284302	PRO1621 protein	1.00
20	451592	AJ805416	Hs.213897	ESTs	18.00
	422170	A1791949	Hs.112432	anti-Mullerian hormone	0.67
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cONA DKFZp564N1662 (f	1.00
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.99
~-	441940	AW298115	Hs.12B152	ESTs	0.68
25	425048	H05468	Hs.164502	ESTS	0.33
	444008	BE544855	Hs.220756	ESTs, Weakly shrilar to SFR4_HUMAN SPLIC	1.01
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DXFZp434B0426 (f	
	423853	AB011537	Hs.133466		1.06
	407846	AA426202		sili (Drosophia) homolog 1	0.45
30			Hs.40403	Cbp/p300-Interacting transactivator, wit	0.62
50	410348	AW182663	Hs.95469	ESTs	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	0.04
	414907	X90725	Hs.77597	polo (Orosophie)-like kinase	1,04
	441795	N58115	Hs.21137	AD024 protein	10.00
25	418583	AA604379	Hs.86211	hypothetical protein	1.22
35	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	106.67
	413385	M34455	Hs.B40	Indoleamine-pyrrole 2,3 dioxygenase	2.30
	441495	AW294603	Hs.127039	ESTs	0.44
	417933	X0230B	Hs.82962	thymidylata synthetase	2.48
	412661	N32860	Hs.24611	ESTs, Weakly similar to 154374 gane NF2	
40	411880	AW872477	I NALE TOTAL	gbhm30f03.x1 NCI_CGAP_Thy4 Homo saptens	1.00
•••	417771	AA604698	Hs.82547		1.00
	430034	X60155		relinoic acid receptor responder (lazaro	1.44
			Hs.227767	zinc finger protein 41	1,00
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.87
45	454417	A1244459	Hs.110826	trinucleotide repeat containing 9	0.54
43	429257	AW163799	Hs.198365	2,3-bîsphosphoglycerete mutase	2.27
	417599	AA204688	Hs_136201	ESTs	1.01
	438366	AA805760	Hs.303567	ESTs	1.00
	438746	A1885815	Hs.184727	ESTs	1.47
~~	409691	T89983	Hs.246042	Homo saplens, clone MGC:5437, mRNA, comp	1.00
50	40B827	AW275730	Hs.254B25	ESTs	1.00
	414735	BE468016	Hs.281904	ESTs	1.00
	42227B	AF072873	Hs.114218	frizzled (Drosophile) homolog 6	
	412719	AW016610	Hs.129911	ESTs	5.21
	417034	NM_006183	Hs.80962	neurolensin	494.00
55	430486	BE062109			1.00
	407788	BE514982	Hs.241551 Hs.38991	chloride channel, calcium activated, fam	23,36
				S100 calcium-binding protein A2	6.98
	413753	U17760	1%.75517	laminin, beta 3 (nicein (125kD), kalinin	7.50
	424012	AW358377	Hs.137569	burner protein 63 kDa with strong homolog	9.77
60	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	445.00
w	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	13.93
	423673	BE003054	Hs.1695	metrix metalloproteinase 12 (macrophage	12.77
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	45.00
	418663	AK001100	Hs.41690	desmocollin 3	10.89
~-	409632	W74001	Hs.55279	serine (or cystelne) proteinase inhibito	6.29
65	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palete lung and nas	0.88
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	
	421948	LA2583	Hs.234309	keratin 6A	38.31
	431846	BED19924	Hs.271580		36.81
				proplakin 1B	1.37
70	424098 452084	AF077374	Hs.139322	smell proline-rich protein 3	8.85
10	453964	A1961486	Hs.12744	ESTs	0.40
	446856	A)B14373	Hs.164175	EST ₈	1.16
	443648	AI085377	Hs.143610	E8Ts	2.15
	408522	AJ541214	Hs.46320	Small proline-rich protein SPRK [human,	4.39
70	431384	BE158000		gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.18
75	42215B	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.22
	435505	AF200492	Hs.21123B	interleukin-1 homolog 1	164.00
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comitin)	
	431958	X63629	Hs.2877	cadherin 3, lype 1, P-cadherin (placenta	9.85
. .	441020	W79283	Hs.35962	ESTs	5.59
80	423217	NM_000094			5.76
	448733	NM_005629	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.97
			Hs.187958	solute carrier family 6 (neurofransmitte	1.09
	444371	8E540274	Hs.239	forkhead box M1	2.44
	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psortas	8.39

	429259	A A 4204ED	t1- apan44	CCT- (C-th-1-1) A CCCTADY AR	
	425259 426440	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.53
	437044	BE382756 AL035864	Hs.169902	solute corrier family 2 (facilitated glu	1.67
	423562		Hs.69517 Hs.130881	cDNA for differentially expressed CO16 g	2.30
5	428484	AK001035 AF104032		B-cell CLL/lymphoma 11A (zinc finger pro	1.04
-	401781	AT 104032	Hs.184601	solute carrier family 7 (cationic amino	3.11
	401780				11.07
	429211	AF052693	Hs.198249	con function position hate E (named 2	9.54
	417389	BE260964	Hs.82045	gap junction protein, beta 5 (connexin 3	1.62
10	423634	AW959308	Hs.1690	midkine (neurite growth-promoting factor	1.12
~ -	417515	L24203	Hs.82237	heparin-binding growth factor binding pr	947.00
	441362	BE614410	Hs.23044	alaxia-telangiectasia group D-associated RAD51 (S. cerevisiae) homolog (E coll Re	2.79
	440704	M69241	Hs.182	insulin-like growth factor binding prote	3.16
	425322	U63630	Hs.155637	protein kinase, DNA-ectivated, catalytic	1.08 5.20
15	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	2.53
	449003	X76342	Hs.389	elcohol dehydrogenase 7 (class IV), mu o	72.00
	431009	BE149762	Hs.48956	gap junction protein, bela 6 (connexin 3	19.96
	409103	AF251237	Hs.112208	XAGE-1 protein	0.47
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	0.66
20	428471	X57348	Hs.184510	siratifin	3.39
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.61
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	231
	451541	BE279383	Hs.26557	plakophilin 3	1.82
25	418203	X54942	Ha.83758	CDC28 protein kinase 2	5.60
25	447343	AA256641	Hs.236894	E8Ts, Highly similar to S02392 alpha-2-m	278
	437016	AU076916	Hs.5398	guanine monphosphate synthetase	2.01
	429512	AF062649	Hs.252587	pitaliary tumor-transforming 1	2.18
	449230	BE613348	He.211579	melanoma cell adhesion molecule	2.58
30	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.63
30	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.25
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	11.88
	430677	Z26317	Hs.94560	desmoglein 2	1.38
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.09
35	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1,09
55	422963 418462	M79141 BE0D1596	Hs.13234	ESTs	2.28
	450832	AW970602	Hs.85266	integrin, beta 4	1.40
	410274	AA381807	Hs.105421 Hs.61762	ESTs	13.31
	408353	BE439638	Hs.44298	hypoxie-inducible protein 2	1.25
40	458933	A1638429	Hs.24763	mitochondrial ribosomal protein S17 RAN binding protein 1	1.89
	439394	AA149250	Hs.58105	ESTs	1.54
	41647B	U38945	Hs.1174	cyclin-dependent kinese inhibitor 2A (me	3.B9
	453533	AA357001	Hs.34045	hypothetical protein FL120764	1.77 1.52
4 44	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.11
45	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	210
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	0.61
	439606	W79123	Hs.58561	G protein-coupled receptor 87	303.00
50	453884	AA355925	Hs.36232	KIAA0186 gene product	10.55
50	452934	AA581322	Hs.4213	hypotheticai protein MGC16207	1.38
	451743	AW074266	Hs.23071	ESTs	2.90
	413129	AF292100	Hs.104613	RP42 homolog	2.38
	406974	M57293	ti. Antonia	gb:Human parathyroid hormone-related pep	1.00
55	413281 444781	AA881271	Hs.222024	transcription factor BMAL2	5,92
55	416B19	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	218
	451320	U77735 AW118072	Hs.80205 Hs.89981	plm-2 encogene	1.01
	418543	NM_005329	Hs.85962	diacylglycerol kinase, zete (104kD)	0.67
	454034	NM_000691	Hs.575	hyduronan synthase 3	1.19
60	425397	104088	Hs.156346	aldehyde dehydrogenase 3 family, member lopolsomerase (DNA) II alpha (170kD)	2.55 3.06
_	413004	T35901	Hs.75117	interleukin enhancer binding fector 2, 4	3.06 1.64
	407634	AW016569	Hs.136414	UDP-GlcNActbetaGal beta-1,3-N-acetylcluc	7.04
	415817	1.88967	Hs.78867	protein tyrosine phosphatase, receptor-t	203.00
~~	435013	H91923	Hs.110024	NADH:ubkulnone oxidoreductase MLRO subu	1.33
65	430337	M36707	Hs.239600	calmodulin-like 3	1,32
	4191.21	AA374372	Hs.89628	parathyroid hormone-like hormone	B1.00
	448993	A1471630	Hs.8127	KIAA0144 gene product	1.03
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	28.00
70	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.24
70	425245	Al751768	Hs.155314	XIAADO95 gane product	1.40
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.55
	420462	AF050147	Hs.97932	chondromodulin I precursor	1,00
	418678	NM_001327	Hs.167379	cancertestis antigen	0.82
75	428182 427335	BE386042 AA448542	Hs.293317	ESTs, Wealdy similar to GGC1_HUMAN G ANT	1.00
, 3	409420	Z15008	Hs.251677	Gantigen 7B	0.91
	438956	W00847	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	6.53
	421917	AB028943	Hs.135056 Hs.109445	Human DNA sequence from clone RP5-850E9	1.35
	404440	110000370	1 103741	KIAA1020 protein	0.94
80	409582	R27430	Hs.271565	ESTs	38.57 3.19
	415569	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.45
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.61
	408122	AJ432652	Hs.42824	hypothetical protein FLJ10718	1.95

	408380	AF123050	Hs.44532	diubiqulu	7.23
	437412	BE069288	Hs.34744	Homo saplens mRNA; cDNA DKFZp547C136 (fr	1.35
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	0.81
5	446102	AW168067	Hs.252956	ESTs	1.03
J	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	137.00
	422487 423761	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.91
	436291	NM_006194	Hs.132576	paired box gens 9	35.00
	423725	BE568452 AJ403108	Hs,5101	prolein regulator of cytokinesis 1	5.35
10	440659		Hs.132127	hypothetical protein LOC57822	207.00
10	434360	AF134160 AW015415	Hs.7327 Hs.127780	claudin 1 ESTs	3.06
	437915	Al637993	Hs.202312		3.89
	438898	AIB19863	Hs.106243	Homo septens clone N11 NTera2Dt teratoca ESTs	1.28
	441553	AA281219	Hs.121296	ESTs	1.73
15	418379	AA218940	Hs. 137516	fidgetin-like 1	1.47
	436396	AI683487	Hs. 152213	wingless-type MMTV integration site fami	40.42
	429413	NM_014058	Hs.201877	DESC1 protein	14,25
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	5.17
	41538D	F07953	Hs.16085	pulative G-protein coupled receptor	1.95
20	423849	AL157425	Hs.133315	Homo septens mRNA; cDNA DKFZp761J1324 (f	0.18
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.00
	429538	BE182592	Hs.11261	small proline-rich protein 2A	2.09
	447269	AW247017	Hs.36978	melanoma antigen, family A, 3	6.1 4 1.00
	428004	AA449563	Hs.151393	glutamate-cysteine Tgase, catalytic sub	44.00
25	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	149.00
	416209	AA236776	Hs.79078	MAD2 (milotic snest deficient, yeast, h	127.00
	408572	AAD55611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	20.00
	404996		. 10.22222	EO 14, modulata) alinkal (O NEO 1_) loles 447.	147.00
	438915	AA280174	Hs.285681	Willams-Beuren syndrome chromosome regi	1.00
30	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	54.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	139.00
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR	22.00
	438702	AI879064	Hs,54618	ESTs	1.00
	444378	R41339	Hs.12569	ESTs	1.00
35	433485	A1493076	Hs.201967	aldo-keto reductase family 1, member C2	41.00
	407839	AA045144	Hs.161566	ESTs	7.50
	439223	AW238299	Hs.250618	UL16 binding protein 2	3,39
	409041	AB033025	Hs.50081	KIAA1199 protein	245.00
	429228	Al553633	Hs.337139	ESTs	10.89
40	409757	NM_001898	Hs.123114	cystatin SN	3.19
	4110B9	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	0.78
	436511	AA721252	Hs.291502	ESTs	0.23
	449207	AL044222	Hs.23255	sucleoporin 165kD	1.68
	453331	A1240665	Hs.8895	ESTs	5.21
45	409935	AW511413	Hs.278025	ESTs	0.75
	428969	AF120274	Hs.194689	artemin	1.17
	445443	AV653838	Hs.322971	ESTB	1.00
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spieen	11.42
	401785				2.76
50	412723	AA648459	Hs.335951	hypothetical protein AF301222	107.00
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fls, clone MA	2.17
	405770				2,42
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.24
FF	4207B3	A165983B	Hs.99923	tectin, galactoside-binding, soluble, 7	4.50
55	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.95
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.44
	437789	AI5B1344	Hs.127B12	ESTs, Weakly similar to T17330 hypotheti	1.00
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.33
60	453958	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.11
OU	427441	AA412605	Hs.178053	SPANX family, member C	5.00
	403478			•	0.78
	400842	4741044007	11- 40mmon	COT	0.15
	441525	AW241867	Hs.127728	ESTs	0.79
65	452866	Al924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	1.50
U.J	405646	A 6 0000 40		about 70h00 =4 Charles	1.06
	427260 431413	AA563848 AA504777	Lie 10E202	gisae70b06.s1 Stratagene schizo brain S1	0.79
	401994	101204111	Hs.105293	ESTs	1.00
	402420				3.25
70	404298				0.05
, 0	404927				0.64
	434105	AW952124	Hs.13094	presentins associated rhombold-like pro	68.00
	436961	AW375974	Hs.156704	Presentins associated monitorid-like pro ESTs	0.96
	429563	BE619413	Hs.2437	eukaryetic translation initiation factor	3.58
75	426067	AVV664691	Hs.97053	ESTs	0.92
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	0.97
	426897	AW976570	Hs.97387	ESTs	0.66 1.20
	443892	AJ889572	Hs.134791	ESTs	1,29 1,00
	413223	A1732182	Hs.191866	ESTs	0.79
80	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.51
	423934	UB9995	Hs.159234	forkhead box E1 (thyrold transcription f	2.59
	425159	NM_004341	Hs.154868	carberroyl-phosphate synthetase 2, aspart	1,39
	420758	AW297536	Hs.33053	ESTS	0.89

	423816	AL031985	Hs,133034	hypothetical protein	1.00				
	447534	AW953935	Hs.30837	ESTs	1.88				
	451919	W05086	Hs.114256	ESTs, Wealdy similar to 178885 serine/th	0.11				
	409228	R16911	Hs.22010	ESTs, Weakly similar to 2109260A B cell	0.92				
5	403715			• • • • • • • • • • • • • • • • • • • •	0.89				
		AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00				
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monocxyg	37.90				
	436839	AA767346	Hs.291614	ESTs	1.00				
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	59.00				
10	413573	A1733859	Hs.149089	ESTs .	78.00				
10	430686	NM_001942	Hs.2633	desmoglein 1	127.0B				
	438993	AA828995	115.2000	gb;od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	1.00				
	448243	AVV369771	Hs.52620	inlegrin, bela 8					
	444783		Hs.62180		133,00 -				
15	426427	AK001468		anillin (Drosophlia Scraps homolog), act TTK protein kinase	232.00				
IJ		M86699	Hs.169840	TIN protein setase	66.00				
	422956	BE545072	Hs.122579	hypothetical protein FLJ 10461	148.00				
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	40.75				
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.00				
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	106.00				
20	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	159.00				
	415989	Al267700	Hs.317584	ESTs	196.00				
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	32.44				
	453160	A1263307	Hs.239884	H2B histone family, member L	7.00				
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophlia) homolo	4.13				
25	41620B	AW291168	Hs,41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	45.0D				
	TABLE 248								
20									
30	Pkey:		robeset idenlifie	r number					
		: Gene cluster							
	Accessions:	Genbank acc	ession numbers						
25	Pkey	CAT number	Accessions						
35									
	411880	1263110_1		088101 T05990					
	412296	1288043_1	AW936233 AW						
	413804	1390710_1	T64662 BE168						
40	414221	142695_1 AW\$50979 AA136655 AA136656 AW\$19381 AA984358 AA492073 BE168945 AA609054 AW238038 BE011212 BE011359 BE011367							
40				111362 8E011215 BE011365 BE011363					
	415327	1534137_1 H22769 R35182 Z43545 F05783 N92089 H71928							
	427260	276598_1		100100 AA401424					
	431322	331543_1	AW970622 AA	503009 AA502998 AA502989 AA502805 T92188					
	431384	33264_1		157999 H75671 H70965 C18895 BE386512 BE385815 BE390298 Al341	995 BE074534 AA055592 AA132265 A1733757				
			AA134504 BE	145037 AA055887 BE070191 R66492 AW868018 AW868058 AW817057	AW862031 AW861688 AW862029 AW858805 AW858792				
45				VB58017 AW819164 AW853698 AI522161 AW854769 AW817408 BE152					
45			ATTODZUZO AT						
45	432222	343347_1		127539 AW969908 AW440776 AA52B756					
45	432222 437214	343347_1 434730_1	Al204995 AW	127539 AW969908 AW440776 AA52B756 092269 BE092497 BE092051 AA746882 Al336378					
			AJ204995 AWI BE092336 BE						
45 50	437214	434730_1 435139_1	AI204995 AW6 BE092336 BEI AA747537 BEI	092259 BE092497 BE092051 AA746882 Al336378					
	437214 437240	434730_1	AI204995 AW6 BE092336 BEI AA747537 BEI	092259 BE092497 BE092051 AA746882 Al336378 089068 BE089070 034879 Al926361	,				
	437214 437240 438993	434730_1 435139_1 467651_1	AI204995 AW6 BE092336 BE0 AA747537 BE0 AA828995 AA AL109688 R23	092259 BE092497 BE092051 AA746882 Al336378 089068 BE089070 034879 Al926361	,				
	437214 437240 438993 439780	434730_1 435139_1 467651_1 47673_1	AI204995 AW6 BE092336 BE0 AA747537 BE0 AA828995 AA AL109688 R23	092259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 334879 Al926361 1865 R25578 14746 Al148521					
50	437244 437240 438993 439780 444163 451844	434730_1 435139_1 467651_1 47673_1 593658_1	Al204995 AWI BE092336 BEI AA747537 BEI AAB28995 AAI AL109688 R22 AI126098 AI18 T61430 AI820	092259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 334879 Al926361 1865 R25578 14746 Al148521	,				
	437214 437240 438993 499780 444163	434730_1 435139_1 467651_1 47673_1 593658_1 886230_1	A1204995 AWA BE092336 BEI AA747537 BEI AA828995 AA A1,109688 R23 A1126098 A118 T61430 A1820 A1,137967 BEI	092259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 134679 Al926361 13565 R25578 14746 Al148521 546 Al821336	,				
50	437214 437240 438993 439780 444163 451844 453823 454789	434730_1 435139_1 467651_1 47673_1 593658_1 886230_1 982526_1 1234742_1	A1204995 AWI BE092336 BEI AA747537 BEI AAB28995 AA A1.105698 A118 T61430 AI820 AL.137967 BEI BE156314 BE	192259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 184679 Al926361 18655 R25578 14746 Al148521 546 Al821336 154160 BE064186 156316 AW820750	•				
50	437214 437240 438993 439780 444163 451844 453823	434730_1 435139_1 467651_1 47673_1 593658_1 886230_1 982526_1	A1204995 AWI BE092336 BEI AA747537 BEI AA228995 AA A1.109688 R23 A1126098 A120 T61430 A1820 A1.137967 BEI BE156314 BE AW450979 AA	092259 BE092497 BE092051 AA746682 Al336378 089068 BE089070 034679 Al926361 0665 R25578 04746 Al148521 546 Al821336 058316 AW820750 1136533 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090	•				
50	437214 437240 438993 439780 444163 451844 453823 454789	434730_1 435139_1 467651_1 47673_1 593658_1 886230_1 982526_1 1234742_1	A1204995 AWI BE092336 BEI AA747537 BEI AA228995 AA A1.109688 R23 A1126098 A120 T61430 A1820 A1.137967 BEI BE156314 BE AW450979 AA	192259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 184679 Al926361 18655 R25578 14746 Al148521 546 Al821336 154160 BE064186 156316 AW820750	•				
50 55	437214 437240 438993 439780 444163 451844 453823 454789	434730_1 435139_1 467651_1 47673_1 593658_1 886230_1 982526_1 1234742_1	A1204995 AWI BE092336 BEI AA747537 BEI AA228995 AA A1.109688 R23 A1126098 A120 T61430 A1820 A1.137967 BEI BE156314 BE AW450979 AA	092259 BE092497 BE092051 AA746682 Al336378 089068 BE089070 034679 Al926361 0665 R25578 04746 Al148521 546 Al821336 058316 AW820750 1136533 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090	•				
50	437214 437240 438993 439780 444163 451844 453823 454789	434730_1 435139_1 467651_1 47673_1 583658_1 888230_1 992526_1 1234742_1 142696_1	A1204995 AWI BE092336 BEI AA747537 BEI AA228995 AA A1.109688 R23 A1126098 A120 T61430 A1820 A1.137967 BEI BE156314 BE AW450979 AA	092259 BE092497 BE092051 AA746682 Al336378 089068 BE089070 034679 Al926361 0665 R25578 04746 Al148521 546 Al821336 058316 AW820750 1136533 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090	•				
50 55	437214 437240 43893 439780 444163 451844 453823 454789 456034	434730_1 435139_1 467651_1 47673_1 583658_1 888230_1 992526_1 1234742_1 142696_1	A1204995 AWI BE092336 BEI AA747537 BEI AA228995 AA A1.109688 R23 A1126098 A120 T61430 A1820 A1.137967 BEI BE156314 BE AW450979 AA	092259 BE092497 BE092051 AA746682 Al336378 089068 BE089070 034679 Al926361 0665 R25578 04746 Al148521 546 Al821336 058316 AW820750 1136533 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090	•				
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50 55 60	437214 437240 437240 43993 43993 439780 444163 451844 453823 454789 456034 TABLE 24C Pksy:	434730_1 435139_1 467651_1 47673_1 593658_1 886230_1 992526_1 1234742_1 142696_1	A204995 AWA BE092336 BEE AA747537 BEI AA828995 AA A109868 R22 T61430 AI820 A1137967 BEI BE16314 BE BE16314 BEI	192259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 1834679 Al926361 1865 R25578 14746 Al148521 546 Al921336 1564160 BE064188 156316 AW820750 1136553 AA136666 AW419381 AA984358 AA492073 BE168945 AA8090 101 1362 BE011215 BE011365 BE011363	54 AW238038 BE011212 BE011359 BE011367				
50 55	437214 437240 438993 438993 439780 444163 451844 453823 454789 456034 TABLE 24C Pkey: Raf: Strand:	434730_1 435139_1 467651_1 47673_1 593658_1 88230_1 892526_1 1234742_1 142696_1 Unkque numt Sequence sc	A204995 AWA BE092336 BEE AA747537 BEI AA828995 AA A109688 RZ; A1126098 A118 T81439 A1820 A1.137967 BEI BE156314 BE AW450994 BE BE011368 BE	192259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 1834879 Al926361 18655 R25578 14746 Al148521 1546 Al921336 1554160 BE064186 156316 AW820750 1136553 AA136666 AW419381 AA984358 AA492073 BE168945 AA8090 1011362 BE011215 BE011365 BE011363	54 AW238038 BE011212 BE011359 BE011367				
50 55 60	437214 437240 438993 439780 444163 451844 453823 454789 456034 TABLE 24C Pkey: Ref:	434730_1 435139_1 467651_1 47673_1 593658_1 88230_1 892526_1 1234742_1 142696_1 Unkque numt Sequence sc	AI204995 AWR BE092336 BEI AA747537 BEI AA828995 AAI AL109688 RZ: A1126088 AIRI T61430 AIB20 AL137957 BEI BE156314 BE AW450979 AA BE011368 BE	192259 BE092497 BE092051 AA746682 Al336378 193068 BE098070 1934679 Al926361 19655 R26578 14746 Al148521 15646 Al821336 154160 BE064186 156316 AW820750 1435653 AA136566 AW419381 AA984358 AA492073 BE168945 AA8090 101 1362 BE011215 BE011365 BE011363 Ing to an Eos probesel	54 AW238038 BE011212 BE011359 BE011367				
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50 55 60	437214 437240 438993 438993 439780 444163 451844 453823 454789 456034 TABLE 24C Pkey: Raf: Strand:	434730_1 435139_1 467651_1 47673_1 593658_1 88230_1 892526_1 1234742_1 142696_1 Unkque numt Sequence sc	A204995 AWA BE092336 BEE AA747537 BEI AA828995 AA A109688 R2: A1126088 A118 T61430 A1820 A1.137967 BEI BE16314 BE AW450979 AA BE011368 BE Description of the test	192259 BE092497 BE092051 AA746682 Al336378 193058 BE098070 1934679 Al926361 19655 R26578 14746 Al148521 1546 Al148521 15646 Al821336 154150 BE064186 156316 AW820750 113653 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090 1011362 BE011215 BE011365 BE011363 Ing to an Eos probesel Ing to an Eos probesel Unitary Column are Genbank Identifier (GI) numbers. "Dunham Dunham I. et al., Nature (1999) 402:489-495. Arich exons were predicted.	54 AW238038 BE011212 BE011359 BE011367				
50 55 60 65	437214 437240 437240 437240 437240 449780 444163 451844 453823 454789 456034 TABLE 24C Pkey: Raf: Strand: Nt_position: Pkey	434730_1 436733_1 467651_1 47673_1 593658_1 88230_1 892526_1 1234742_1 142696_1 Unique numb Sequence as human chror Indicates ptx	A204995 AWR BE092336 BE1 AA747537 BE1 AA747537 BE1 AA829995 AA1 A1,109688 RZ: A1126098 A118 T61430 AI820 AL,137957 BEI BE156314 BE AW450979 AA BE011368 BE Der correspondinguce. The 7 dig nosome 22: A strand from w cleotide position	192259 BE092497 BE092051 AA746682 Al336378 193058 BE098070 1934679 Al926361 1965 R28578 14746 Al148521 15464 Al921336 154160 BE064186 156316 AW820750 113653 AA13656 AW419381 AA984358 AA492073 BE168945 AA8090 11362 BE011215 BE011365 BE011363 Ing to an Eos probesel Ing to an Eos probesel Ing to an Eos probesel Outhard I. et al., Nature (1999) 402:489-495. Infinity and the second of the second	54 AW238038 BE011212 BE011359 BE011367				
50 55 60	437214 437240 438993 439780 444163 451834 453823 454789 456034 TABLE 24C Pkey: Raf: Strand: Nt_position: Pkey 400751	434730_1 435139_1 467651_1 47673_1 593658_1 886230_1 982526_1 12247742_1 142696_1 Unique numi Sequence schuman chror Indicates pro	A204995 AWA BE092336 BEE AA747537 BEI AA828995 AAA A109588 R2: A1126098 A118 T61430 A1820 A1137967 BEI BE166314 BE DE166314 BEI DE16631	192259 BE092497 BE092051 AA746882 Al336378 189068 BE089070 1834879 Al926361 1865 R28578 14746 Al148521 1544 Al148521 1544 Al148521 155316 AW820750 113653 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090 11362 BE011215 BE011365 BE011363 1011362 BE011215 BE011365 BE011363 1011362 Be011216 AW800000 1011362 Be011216 BE011365 BE011363	54 AW238038 BE011212 BE011359 BE011367				
50 55 60 65	437214 437240 437240 438993 439780 444163 451844 453823 454789 456034 TABLE 24C Pkey: Ref: Strand: Nt_position: Pkey 400751 400842	434730_1 436733_1 467651_1 47673_1 593658_1 88230_1 892526_1 1234742_1 142696_1 Unique numb Sequence as human chror Indicates ptx	A204995 AWA BE092336 BEE AA747537 BEI AA828995 AAA A109588 R2: A1126098 A118 T61430 A1820 A1.37967 BEI BE166314 BE DE166314 BEI DE16631	192259 BE092497 BE092051 AA746682 Al336378 193058 BE098070 1934679 Al926361 1965 R28578 14746 Al148521 15464 Al921336 154160 BE064186 156316 AW820750 113653 AA13656 AW419381 AA984358 AA492073 BE168945 AA8090 11362 BE011215 BE011365 BE011363 Ing to an Eos probesel Ing to an Eos probesel Ing to an Eos probesel Outhard I. et al., Nature (1999) 402:489-495. Infinity and the second of the second	54 AW238038 BE011212 BE011359 BE011367				
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50 55 60 65 70	437214 437240 437240 438933 439780 444163 451844 453823 454789 456034 TABLE 24C Pkey: Ref: Strand: Nt_position: Pkey 400751 400842 400843 400844 400046	434730_1 435139_1 457651_1 47673_1 593658_1 888230_1 982526_1 1234742_1 142696_1 142696_1 Unique numi Sequence schuman chror Indicates DN Indicates DN Indicates num 7331445 1927148 9188605 9188605	A204995 AWA BE092336 BE1 AAA747537 BEI AAA747537 BEI AAB28995 AAI A109688 RZ; A1126098 A118 TB1439 AIB20 AL137967 BEI BE156314 BE AW450979 BEI BE156314 BE AW450979 BEI BE156314 BE AW450979 BEI BE156314 BE AW450979 BEI BE156314 BEI AW450979 BEI BE156314 BEI AW450979 BEI BE156314	1932259 BE092497 BE092051 AA746682 Al336378 193068 BE098070 1334679 Al926361 19655 R26578 14746 Al148521 15464 Al921336 154160 BE064186 156316 AW820750 1136553 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090 11362 BE011215 BE011365 BE011363 11362 BE011215 BE011365 11362 BE011215 BE011365 11362 BE011365 11362 BE011215 BE011365 11362 BE011365 11362 BE011215 BE011365 11362 B	54 AW238038 BED11212 BE011359 BE011367 14. et al." refers to the publication emittled "The DNA sequence of a sequ				
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50 55 60 65 70	437214 437240 437240 438933 439780 444163 451844 453823 454789 456034 TABLE 24C Pkey: Ref: Strand: Nt_position: Pkey 400751 400842 400843 400844 400846 401486 401747 401780 401781	434730_1 435139_1 435139_1 435139_1 435139_1 457651_1 47673_1 593658_1 888230_1 898230_1 898230_1 1234742_1 142696_1 142696_1 142696_1 Unique numt Sequence schuman chcor Indicates DN Indicates num Ref 7331445 1927148 9188605 9188605 9188605 7341763 9789672 9929699 7249190 7249190	A204995 AWA BE092336 BE1 AA747537 BE1 AAA747537 BE1 AAB2B995 AAA A109688 R2; A1126098 A118 R161439 AIB20 AL137997 BEI BE155314 BE AW450979 AA BE011368 BE DE155314 BEI DE15531	1932259 BE092497 BE092051 AA746682 Al336378 193058 BE098070 1334679 Al926361 1965 R26578 14746 Al148521 15464 Al821336 154160 BE064186 156316 AW820750 1136553 AA136656 AW419381 AA984358 AA492073 BE168945 AA8090 11362 BE011215 BE011365 BE011363 11362 BE011215 BE011365 BE011365 11362 BE011215 BE011365 BE011365 11362 BE011215 BE011365 11362 BE011365 11362 BE011215 BE011365 11362 BE011365 11362 BE011215 BE011365 11362 BE011215 BE011365 11362 BE011215 BE011365 11362 BE011215 BE011365 11362 BE	54 AW238038 BE011212 BE011359 BE011367 1. et al.* refers to the publication entitled "The DNA sequence of ,23827-23958 1-130381,130468-130593,131097-131258,131866-224-30573				

	402034	7684482	Minus	86227-86451
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402230	9966312	Minus	29782-29932
_	402305	7328724	Plus	40832-41362
5	402420	9796339	Plus	129750-129919
	402777	9588235	Plus	126786-126948
	402778	9588235	Plus	128560-128702
	402901	8894222	Minus	175426-175667
4.0	403085	8954241	Pius	165035-165334,165420-165713
10	403381	9438267	Minus	26009-26178
	403478	995B258	Plus	116458-116564
	403715	7239669	Plus	85128-85292
	403903	7710571	Minus	101165-102597
* ~	404148	9863703	Plus	78218-78418,79571-79709
15	404298	9944263	Minus	73591-73723
	404440	7528051	Pius	80430-51581
	404875	9801324	Phus	96588-96732,97722-97831
	404927	7342002	Plus	68690-69563
00	404977	3738341	Minus	43081-43229
20	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40874,42351-42450
	405033	7107731	Minus	142358-142546
	405064	7658416	Plus	81207-81416
	405494	8050952	Minus	70284-70518
0.5	405531	9665194	Plus	35602-35803
25	405646	4914350	Plus	741-969
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
20	406117	9142932	Plus	54304-54584
30	406360	9256107	Minus	7513-7673
	406467	9795551	Plus	182212-182958

35 TABLE 25A: 691 genes upregulated in head and neck center relative to normal body tissues

Table 25A lists about 691 genes upregulated in head and neck cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59560 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogetic function or of bransducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or lon_transporter). Certain predicted protein domains are noted.

Unique Eos probeset identifier number

ExAcon: Exemplar accession number, GenBank accession number

45 UniGenelD: UniGene number

40

Ornetin predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30;276-280). Pred.Prot.Domains:

UnlGene Title:

R1 85th percentile of head and neck cancer Als divided by the 50th percentile of normal tissue Als, where the 10th percentile of all normal tissue Als was 50

subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneiD; Unigene Title; Pred, Prot. Domains; R1

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422168; AA556894; Hs.112408; S100 calcium-binding protein A7 (psorias; efisend, S_100;TM=M;SS=N; 46.25 408522; Al541214; Ns.46320; Small profine-rich protein SPRK [human, ; none, Comitin; 40.37 417366; BE185289; Hs.1076; small profine-rich protein 1B (cornifin); Cornifin;TM=M;SS=N; 38.94 401781; ;; Target Exon; filament;TM=M;SS=N; 29.74 422155; 1.10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.54 401780; ;; NM_005557*;Homo saplens keratin 16 (foca; filament; iffament; 28.58 424068 AC0777374; Hs.193222; small profine-rich synthems & Cornifor TM=M;SS=M; 28.55
55
                                                                                                422168; L10343; Hs.112341; protessa inhibitor 3, ston-centred (strAL; wap; IN=M;SS=Y; 29.54
401780; ; INM_005557*:Homo saplens keratin 16 (foca; filament, filament; 28.58
424098; AF077374; Hs. 139322; small protine-rich protein 3; Comifin; TM=M;SS=N; 28.55
421940; L42583; Hs.334309; keratin 6A; filament, RivoGAP, DUF286;bZIP, Troponyosin, bubulin, DUF164, TBCA, Collegen; TM=M;SS=N; 25.74
428471; X57348; Hs.184510; stratifin; 14-3-3; TM=M;SS=N; 23.65
421940; L42583; Hs.334309; keratin 6A; filament, RivoGAP, DUF286;bZIP, Troponyosin, bubulin, DUF164, TBCA, Collegen; TM=M;SS=N; 25.74
428471; X57348; Hs.184510; stratifin; 14-3-3; TM=M;SS=N; 12.02
421574; AJ000452; Hs.19134; interleukin 1 receptor antagonist; IL1;; 21.02
421574; AJ000452; Hs.195924; detensin, beta 2; Defensin beta; TM=M;SS=M; 20.83
409801; AF237621; Hs.80826; keratin 1 (apidamolytic hyperikeratosis); filament, bZiP, UvrD-helicase, TBCA; TM=M;SS=N; 20.72
433091; Y12642; Hs.3185; lymphocyte antigen 6 complax, bocus D; UPAR_LY6; toxin, Activin_recp; TM=M;SS=N; 19.53
4402783; Al659838; Hs.99923; lectin, galactoside-binding, soluble, 7; Gal-bind_lectin; TM=M;SS=N; 19.13
407788; BE514962; Hs.38991; S100 calcium-binding protein A2; efficand S_100,S_100,effnand; 17.93
416091; AF295370; Hs.283082; defensin, beta 3; Defensin beta; TM=M;SS=M; 17.63
431211; M88849; Hs.323733; gap junction protein, beta 2, 26kD (conn; connexin; TM=Y;SS=M; 16,94
42959; AA420450; Hs.380088; Plakophilin; none,none; 14.92
417515; L24203; Hs.8237; ataxie-tellangiactasia group D-associaled; zf-B_box_zf-UBRt; TTM=M;SS=N; 14.75
423634; AW999990; Hs.181125; Immunoglobulin lambda locus; g, HSP70, Px.49h; Ms.85=N; 12.61
431953; X63829; Hs.181125; Immunoglobulin lambda locus; g, HSP70, Px.49h; TM=M;SS=N; 12.61
431953; X63829; Hs.2877; cadherin 3, type 1, P-cadherin (placents; cadherin,Cadherin _C_ierm; TM=Y;SS=M; 12.45
446921; AB012113; Hs.16630; small inducible cytokine subfamily 4 (Cy; IL8; 11.71
401760; ; Target Exon; none,bromodomain; 11.68
60
65
70
75
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80

44034; AB0121 is, ris. 16300; siteat anticipite cytokine subramay A (x), e.c.; (1.7)
401760; ;; Target Exor; none,bromodomair; 11.68
407839; AA045144; Hs. 161666; E81s; cadherin,cadherin; 11.65
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh;; 11.56
444781; NM_014400; Hs.11950; GPI-anchored metastasis-essociated prote; UPAR_LY6,lactamase_B; 11.31

```
453857; AL080235; Hs. 35861; Ras-Induced senescence 1 (RIS1); none;TM=Y;SS=M; 11.03
424012; AW368377; Hs. 137569; bumor protein 63 kDa with strong homolog; SAM_P53;TM=M;SS=N; 10.75
430530; AW269920; Hs. 2621; cystatin A [stefin A]; cystatin;TM=M;SS=N; 10.58
419683; AA133749; Hs. 301350; FXYD domain-containing lon bransport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 10.30
411274; NM_002776; Hs. 69423; kaliforein 10; trypsin;TM=M;SS=N; 10.25
411633; AW958544; Hs. 112242; normal mucosa of esophagus specific 1; none;TM=M;SS=M; 9.84
446698; AK001898; Hs. 16740; hypothetical protein FLJ11036; none;TM=Y;SS=N; 9.74
402075; ;; ENSP00000251056**Plasme membrane calcium; none;; 9.50
444381; BE367335; Hs. 233713; hypothetical protein BC014245; Callagen;TM=M;SS=M; 9.50
431009; BE149762; Hs. 48966; gap junction protein, beta 6 (connexin 3; connexin;TM=Y;SS=M; 9.48
439310; AF086120; Hs. 102793; ES1s; casein_kappa_pkinase,ig,none; 9.43
414987; AA524394; Hs. 294022; hypothetical protein FLJ114950; SH2;TM=M;SS=M; 9.33
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldeh;TM=M;SS=M; 9.14
409000; L11690; Hs. 198689; bullous pemphigod artigen 1 (230/240kD); ethend,spectrin,GAS2,SH3,Plectin,RA,Xylose_lsom,FIID,bZIP,Tropomyosin,Myo-LZ,MJdh_C,CH,AIP3;TM=M;SS=N; 9.12
4251541; BE279383; Hs. 25557; plakophilin 3; Armadillo_seg;TM=M;SS=N; 9.11
425650; NM_001944; Hs. 1925; desmoglein 3 (pemphigus wigaris antigen; cadherin;TM=M;SS=M; 8.66
452240; Al591147; Hs. 61232; ESTs; none,none; 8.57
42922B; Al553633; Hs. 355822; ESTs; none,none; 8.67
42922B; Al553633; Hs. 355822; ESTs; none,none; 8.67
42922B; Al553633; Hs. 355822; ESTs; none,none; 9.19
413278; BE563036; Hs. 353424; delodinase, lodohyronine, type II; T4_delodinase;TM=M;SS=M; 7.90
413278; BE563085; Hs. 833; Interferon-stimulated protein, 15 kDz; ubiquitin; 7.82
428230; L22524; Hs. 2256; matrix netalloprotelense 7 (nabhlysh; r. Peptidase_M10; 7.82
417308; H60720; Hs. 816822; MAA0101 quene product; none;TM=M;SS=M; 7.77
              5
10
15
20
                                                                                       413276; BE-563095; Hs.833; Interferon-sümulated protein, 15 kDa; ubiquitin; 7.82
428330; L22524; Hs.2256; mainx metalloproteinase 7 (matrilysin, ; Peptidase_M10;; 7.82
417303; H60720; Hs.81892; KJAA0101 gene product; none; TM=M;SS=N; 7.77
413753; U17760; Hs.75517; leminin, beta 3 (nicein (125kD), kalinin; laminin_EGF_taminin_Nterm;; 7.76
423217; NM_000194; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz_BPTI,fn3,wwa_Collagen, beta-lactamase; TM=M;SS=M; 7.71
430686; NM_001942; Hs.2633; desmoglein 1; cadherin_Catherin_C_term; TM=Y;SS=M; 7.69
412270; AC005262; Hs.73797; guanine auclaotide binding protein (G pr; G-alpha,arf; TM=M;SS=N; 7.54
428484; AF104032; Hs.184601; solute carrier family 7 (catloric amino; aa_permeases,pytdoxal_dec.bromodomain,PH0,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.53
418653; AK001100; Hs.41690; desmocylin_3; extherin_Catherin_C term none; 7.30
25
30
                                                                                         aa_permeases,pyriooxa_pec_promountant,rmx,wiopyrt_proc_por_no_pre_prinsec_rx1,1 xxx_por_no
418563; AK001100; Hs.41690; desmocollin 3; cadherin,Cadherin_C_term,none; 7.30
452281; 193500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, done PL; TGFb_propeptide,TGF-beta,none; 7.28
429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 7.26
412719; AW016610; Hs.816; ESTs; none,none; 7.17
35
                                                                                              446519; AUD76643; Hs.313; secreted phosphoprolein 1 (osteopontin; ; Osteopontin; ; 7.10
423961; D13666; Hs.136346; periostin (OSF-2os); Fascklin;TM=M;SS=M; 7.09
427666; Al791495; Hs.180142; calmodulin-like skin protein (CLSP); efhand;TM=M;SS=N; 7.08
431846; BED19924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 7.06
                                                                                  223931; D13666; No. 136346; periocitin (OSF-2ns); Fascolar, That-MySS-M; 7.08
427684; A1791495; No. 180142; calmodulin-like skin protein (CLSP); ethand; TM-MySS-M; 7.08
427684; BED19224; No. 271580; uroplasin 18; bransmernicane4; IM-YySS-M; 7.08
428073; BED03054; No. 5055; matrix metalloproteinase 12 (inacrophage; hemopoxin, Peptidase_M10;TM-MySS-M; 7.03
417471; Homo sapless terratin 17 (KRT177; none, brondomien; 7.01
413859; AW892356; No. 3344; Homo sapless pyruvate debydrogenase kina; SAM_PNT,none; 6.98
429002; AW244843; No. 2404 (punction place)option; Armadile, seg.TM-MySS-M; 6.05
432239; X81334; No. 2936; matrix metalloproteinase 13 (collagenase; hemopoxin, Peptidase_M10; 6.87
417716; AW669587; No. 8536; ESTs; none, none; 6.72
422440; NM_D03812; No. 116724; adio-kato reductase tarrily 1, member 810; ado_kat_red_ROK;TM-MySS-N; 6.50
42339; W00482; No. 2399; matrix metalloproteinase 14 (membrane-in; hemopoxin, Peptidase_M10;TM-MySS-N; 6.39
42039; W00482; No. 2399; matrix metalloproteinase 14 (membrane-in; hemopoxin, Peptidase_M10;TM-MySS-N; 6.39
420039; NM_O0480; No. 376147; author-ansterase family, cytosolic, 25; Sulfohransfer; 8.38
420039; NM_O0480; No. 376147; author-ansterase family, cytosolic, 25; Sulfohransfer; 8.38
42039; APO78037; No. 324051; RelA-associated inhibitor, StR, ank; TM-MySS-N; 6.50
44259; APO78037; Ha. 324051; RelA-associated inhibitor, StR, ank; TM-MySS-N; 6.50
44259; APO78037; Ha. 324051; RelA-associated inhibitor, StR, ank; TM-MySS-N; 6.50
44240; AW383226; Ha. 163834; ESTs, Weakly similar in G01763 attrophin; ras; TM-MySS-N; 6.22
44364; AW383226; Ha. 163834; ESTs, Weakly similar in G01763 attrophin; ras; TM-MySS-N; 6.23
444587; M0307; Ha. 151736; matrix metalloproteinase 9 (galainase B; finally, Est-Nic, 8.24
44587; M0307; Ha. 151736; matrix mishing protein 2 (galainase B; finally, Est-Nic, 8.24
44364; AW383226; Ha. 26399; chromosome 20 open reading fame 1; none; TM-MySS-N; 6.24
44394; AW10470; Ha. 25399; chromosome 20 open reading fame 1; none; TM-MySS-N; 6.61
42397; BEZ7689; Ha. 1639
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429554; NM_012275; Hs.207224; interleukļn 1. delte; IL1;TM=M;SS=N; 5.14
                                                                  429554; NM_012275; Hs.207224; interleuk[n 1, delta; IL1;TM=M;SS=N; 5.14
42150B; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M;SS=N; 5.13
439979; AN\000291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 5.11
427099; AB032953; Hs.173560; odd Ozden-m homolog 2 (Orosophila, mous; NHL;TM=M;SS=N; 5.11
428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 5.08
436369; A1683487; Hs.152213; wingless-type MMTV integration site famit, wnt,none; 5.07
406690; M29540; Hs.20529; carclinoembryonic antigen-related cell act, ig:TM=M;SS=M; 5.05
453905; NM_002314; Hs.35566; LIM domain kinase 1; pklnase,UM;PDZ,zt-PARP;TM=M;SS=N; 5.04
414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibito; serpln; 5.00
413219; AA878200; Hs.118727; Homo saplens CNNA FILJ13692 fis, clone PL; HL/destin,TNFR_e6,Acyl-CoA_hydro; 4.96
4215108; NP=002796; Hs. 105097; Hypodding kinase 1, soluble; TKFULM=M;SS=M; 4.93
              5
10
                                                                    41508; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 4.93
41114B; AA219691; ths.73625; RAB6 interacting, kinasin-like (rabkines; kinasin, Tropomyosin;TM=M;SS=N; 4.92
445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM;; 4.91
428953; AA306510; Hs.348183; tumor necrosis factor receptor superfamil; 60s_ribosomal_Ribosomal_L10,TNFR_c5,DEAD;; 4.90
436555; AW407157; Hs.181125; immunoglobulin lambda locus; [p.HSP70,Ppx-GppA;TM=N;SS=N; 4.89
15
                                                                  43655; AW407157; Hs.181125; immunoglobulin lambda locus; jg.HSP70.Ppx-GppA,TM=M;SS=N; 4.89
447343; AA256641; Hs.236894; ESTs, Highly similiar to S02392 alpha-2-m; none,none; 4.84
430024; Al808780; Hs.227730; Integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 4.81
439706; AWB72527; Hs.59761; ESTs, Wealdy similiar to DAP1_HUMAN DEATH; none,none; 4.80
444371; BE540274; Hs.239; forkhead box M1; Fork_head;TM=M;SS=N; 4.75
42582; BE336699; Hs.185056; BENE protein; none;TM=Y;SS=M; 4.74
419586; BE379320; Hs.91448; MKP-1 like protein; kyrosine phosphatæe; DSPc;; 4.69
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 4.69
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pklnase,fn3,tg; 4.68
418067; Al177958; Hs.63391; ixetable FAM cyratiatr; 4.66
20
                                                                    422510; A4310522; Hs.83393; cystatin EM; cystatin; 4.66
418057; A1127958; Hs.83393; cystatin EM; cystatin; 4.66
414774; X02419; Hs.77274; plasminogen activator, urokinsse; kringle, hypsin, plant_tivonins;; 4.64
456534; X91195; Hs.100623; phospholipase C, beta 3, netghbor pseudo; UM, PDZ, pkinese;; 4.62
410418; D31382; Hs.63325; transmembrane protesse, serine 4; ld_recept_a, hypsin; TM=Y;SS=M; 4.60
417866; AW067903; Hs.82772; collagen, type XI, elpha 1; Collagen, COLFI, TSPN, laminin_G, CorA;; 4.60
25
                                                                      438113; M467909; Hs. 8892; ESTS; 7tm, 1,none; 4.60
418140; BE613836; Hs. 83551; microfibrilar-associated protein 2; none; TM=M;SS=M; 4.57
408360; AF123050; Hs. 44532; diubiquitin; ubiquitin; TM=M;SS=N; 4.55
   30
                                                                      405307, AFT23050; Hs.44532; diubiquor; ubiquor; surquiar; in=m<sub>2</sub>SS=m; 4.55
422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.50
422627; NM_005940; Hs.155324; matrix metalloprobelinase 11 (stromelysin; hemoporin,Peptidase_M10; 4.50
418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domai; death, DED; 4.49
408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 4.48
414166; AVM88941; Hs.75789; N-myc downstream regulated; DEAQ,heficase_C,mm,Ndr,Cys_knot,Tll_vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-
   35
                                                                      414166; AW889341; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,mm,Ndr,Cys_brot,Til_vwe,vwc,vwi beta_DUF139,TPR_DSPc_tsp_1,Riboscmel_S21,rvp;TM=M;SS=N; 4.47
416178; AB06952; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.47
411789; AF245505; Hs.72157; Adilcan; kj_LRR,LRRNT,LRRCT;TM=M;SS=M; 4.47
414561; Allo44813; Hs.195155; Homo sapiens amino acid transport systems Aa_trans;TM=Y;SS=N; 4.47
427765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 4.45
427557; NM_002659; Hs.179657; plasminogen activator, urokinese recepto; UPAR_LY6,ET,PLA2_inh;; 4.43
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 4.42
409041; AB033025; Hs.50081; Hypothetical problin, XP_D51805 (KIAA119; none;TM=M;SS=M; 4.41
408908; Z25437:: ohiH.saotens opticin-brossine kinase gen: none none. 4.40
   40
                                                                       499441; AB033025; Hs.50081; Hypothetical protein, XP_051850 (KIAA119; none;TM=M;SS=M; 4.41
406906; Z25437; ; gb:H.saptens protein-hyrosine kinese gen; none,none; 4.40
459701; H39950; Hs.288457; hypothetical protein XP_088151 (leucine; none,LRRCT,LRR; 4.40
409213; U61412; Hs.51133; PTK6 protein tyrosine kinese 6; SH2,SH3,pkinese;TM=Mt,SS=N; 4.38
429500; X78565; Hs.289114; hexabrechten (tenascin C, cytolectin); EGF,fin3,fixinogen_C,toxin_2,Keretin_B2;TM=Mt,SS=Y; 4.38
429500; X78565; Hs.22486; signal transducer and activator of trans; SH2,STAT,STAT_blnd,STAT_prot;TM=Mt,SS=N; 4.32
423725; AJ403108; Hs.132127; hypothetical protein LOC57622; none;TM=Mt,SS=N; 4.32
411573; AB029000; Hs.70823; KIAA1077 protein; Sulfattase;TM=Mt,SS=N; 4.31
408243; Y00767; Hs.624; interteukin & HLL,PAS,IL8;TM=Mt,SS=N; 4.31
408243; Y00767; Hs.624; interteukin & HLL,PAS,IL8;TM=Mt,SS=N; 4.31
   45
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                                                                41573, AB0029000; Hs.70823; kIAA1077 protein; Sulfatsser,Tha-KSS=N; 4.31
408243; Y00787; Hs.624; Interteukin & HLH, PAS, IL8;TM=M;SS=N; 4.31
418738; AW73661; Hs. 624; Interteukin & HLH, PAS, IL8;TM=M;SS=N; 4.31
418738; AW73661; Hs. 148170; hypothetical protein FL122965; 2:DHHC, none; 4.29
424247; X14008; Hs.234734; Iysozyme (renal amylotiosis); Iys, Ig, FAD_Synth, Idh, Idh_C, pKnase;; 4.29
414821; M33835; Hs.77424; Fe fragment of IgG, high affiritly Ia, re; Ig;TM=Y;SS=M; 4.29
414821; M33835; Hs.77424; Fe fragment of IgG, high affiritly Ia, re; Ig;TM=Y;SS=M; 4.29
414621; M33835; Hs.77424; Fe fragment of IgG, high affiritly Ia, re; Ig;TM=Y;SS=M; 4.29
414621; M33835; Hs.77424; Fe fragment of IgG, high affiritly Ia, re; Ig;TM=Y;SS=M; 4.29
414603; Y07809; Hs.79368; epithelial membrane protein 1; PMP22_Claudin.cxidored_q5_N;TM=Y;SS=M; 4.28
409142; AL136877; Hs.50758; SMC4 (sinuctural maintenance of chromosy, ABC_bran, M;SMC_brand, CDUF;64,none; 4.25
424503; NM_002205; Hs.146170; hypothetical protein FL122935; Armadillo_sep_HEAT;TM=M;SS=M; 4.24
414809; Al434699; Hs.77368; transferrin receptor (pBid_CD71); PA;TM=Y;SS=N; 4.24
414809; Al434699; Hs.77368; transferrin receptor (pBid_CD71); PA;TM=Y;SS=N; 4.24
414909; Al434699; Hs.7727; Inhibit, bata A; Icchin A, actin AB a; TGF-bats,TGFb_propeptida_Tub;; 4.20
439720; Al935202; Hs.9517; differentially expressed in Fanconi's an; none;TM=M;SS=M; 4.23
409958; AW103384; Hs.7727; Inhibit, bata A; Icchin A, actin AB a; TGF-bats,TGFb_propeptida_Tub;; 4.20
417399; BE260984; Hs.82045; mildine (neurite growth-promoting factor; PTN_MIC;TM=M;SS=Y; 4.19
407137; T97307; gbycs53h05.s1 Soares field liver spleen; GOA1_CD39,none; 4.18
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema_PSI,TIG;Integrin_B;TM=Y;SS=M; 4.17
400286; X0426; Hs.14660; historiching; none, none, 4.18
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema_PSI,TIG;Integrin_B;TM=Y;SS=M; 4.17
400286; X0426; Hs.17650; phytin repeat domain 3; ank,pkinese;TM=M;SS=N; 4.00
418929; DA1922; Hs.3050
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414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 4.02
413186; AU077141; Hs.374546; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=M; 4.01
418203; X54942; Hs.83759; CDC28 protein kinase 2; CKS;; 4.01
406906; Z25424; ; gbtH-sepiens protein-serine/threonine ki; none,none; 3.98
450375; AA009647; Hs.352537; a disintegrin and metitoproteinase doma; Reprolysin,Pep_M12B_propep,disIntegrin,Reprolysin,Pep_M12B_propep,disIntegrin; 3.98
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;; 3.96
410342; R31350; Hs.743; Fc fragment of lgf.; high affinity I, rec; ITAM;TM=Y;SS=M; 3.95
425849; AJ000512; Hs.295323; serum/glucocorticoid regulated kinase; pkinase_pkinase_C;TM=M;SS=M; 3.95
427792; M63928; Hs.180841; tumor necrosis factor receptor superfam); SRPLATNFR_CRT;TM=Y;SS=M; 3.95
407792; M63928; Hs.180841; tumor necrosis factor receptor superfam); SRPLATNFR_CR;S=N; 3.91
424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF;; 3.91
423189; M59371; Hs.171596; EphA2; fn3.phinase,SAM,EPH_lbd;TM=Y;SS=M; 3.90
433859; NM_013409; Hs.9914; folistebin; kazal; 3.89
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                                                                                     415999; A1287700; Hs. 351201; ESTE; none,none; 3.90
423899; M23971; hs. 171595; EptAx2, finalphinase, SAM,EPH_Ibd;TM-Y;SS=M; 3.80
423899; MM, 013409; Hs. 9914; foliatedin; kazze;; 3.89
429612; AFD52649; Hs. 252587; pitullarly tumor-branstorming 1; none; 3.89
419073; AV972170; Hs. 183916; Homo sapiems cDNA FLU12797 fis, clone NT; death,ZUS;; 3.88
45068; AAB72505; hs. 25333; interiación 1 recepto; type li; ig;TM-Y;SS=M; 3.88
45068; AAB72505; hs. 25333; interiación 1 recepto; type li; ig;TM-Y;SS=M; 3.88
454506; AAB72505; hs. 25333; interiación 1 recepto; type li; ig;TM-M;SS=N; 3.84
43241; A1929374; Hs. 75367; för-like-adapter; SH2,SH3,TM-M;SS=N; 3.84
43341; A1929374; Hs. 170367; för-like-adapter; SH2,SH3,TM-M;SS=N; 3.84
43763; AA663689; hs. 5331; issue inhibitor of metaloprotelases 1; TIMP, pkinase, DAG_PE-blad,RBD; 3.83
43629; BES68452; hs. 344037; protein regulator of cytokinesis 1; none;TM-M;SS=N; 3.82
417612; A7654; hs. 25256; glycoprotein (transmerbanes) mnix; PMC;TM-Y;SS=M; 3.81
427647; W19744; Hs. 180099; Homo aspiens cDNA FLI,20053 fis, clone K4; none;pkinase; 3.80
434599; AA693667; hs. 1349429; Homo aspiens cDNA FLI,20053 fis, clone K4; none;pkinase; 3.80
434599; AA693667; hs. 1349429; Homo aspiens cDNA FLI,20053 fis, clone K4; none;pkinase; 3.80
434599; AA693667; hs. 1349429; Homo aspiens cDNA FLI 1980 fis, clone His; Nucleoside_ba2,none; 3.80
430778; Z29572; hs. 2555; immor necrosis factor receptor superferni; IL2; 3.79
439167; A743719; hs. 198477; hextokinase 2; hanokinase), becokinase 2, none; 3.77
439257; AW406168; hs. 318953; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Rosap_Ludomain,YLP,none; 3.77
43927; AW406168; hs. 318953; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Rosap_Ludomain,YLP,none; 3.77
43927; AW406168; hs. 36959; receptor temply 7 (catholo amho; as, permesses; M-Y;SS=M; 3.78
413436; AF239035; hs. 88951; sphingosine kinase 1; DAGKE;TM-MSSS-N; 3.75
413436; AF239035; hs. 88951; sphingosine kinase 1; DAGKE;TM-MSSS-N; 3.75
4149018; AV37939; hs. 27959; hs. 2
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                                                                                                    443859; NM_013409; Hs.9914; foliistatin; kazal;; 3,89
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                                                                                                    448316; AW338021; Hs.78531; Homo septens, Similar to RIKEN cDNA 6730; none; TM=M;SS=N; 3.62
438746; Al885815; Hs.184727; Hurman melanoma-associated antigen p97 (m; transfertin, Guanylate_kin,PDZ_SH3; 3.62
446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M;SS=Y; 3.62
452896; Al826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate_kin,PDZ_SH3; 3.60
407634; AW016569; Hs.138414; UDP-GlcNAc:betaGel beta-1,3-N-acetytgluo; Galactosyl_T;TM=M;SS=Y; 3.69
423575; C18863; Hs.163443; intron of periostin
(OSF-2os); Fascician,none; 3.59
421391; AW3034350; Hs. 191958; immunoglobulin superfamily receptor tea; ig,none; 3.68
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pklnase;TM=Y;SS=M; 3.58
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pklnase;TM=Y;SS=M; 3.58
419912; AF249745; Hs.6056; Rho guanine nucleotide exchange factor (; SH3,PH,RhoGEF;TM=M;SS=N; 3.58
419512; AF249745; Hs.205297; Integrin, alpha 11; FG-GAP, wwa;TM=Y;SS=M; 3.57
430379; AF134149; Hs.240395; potassium channal, subfamily K, member 6; log_trans;TM=Y;SS=M; 3.55
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 3.55
441362; BE614410; Hs.23044; RAD51 (S. cerevislee) homolog (E coli Re; none; 3.63
428550; NM_014638; Hs.170156; KfAA0460 gene product; C2;PI-PLC-Y;TM=M;SS=N; 3.53
429506; AW139399; Hs.314807; ESTs; none;TM=M;SS=N; 3.52
449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 3.51
43240; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 3.51
          60
          65
          70
                                                                                                         43256; AA349864; Hs. 278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 3.51
433470; AW980564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 3.51
452203; X77522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 3.49
425566; AW162943; Hs. 250618; UL.16 binding protein 2; IdL_recept_s,PKD,MHC_J;TM=M;SS=Y; 3.48
402447; ;; C1000201;gj;204416[gb]AA002527.1] ([J0519; none;TM=Y;SS=M; 3.48
402447; ;; C1000201;gj;204416[gb]AA002527.1] ([J0519; none;TM=Y;SS=M; 3.48
431183; NM, 005855; Hs. 250696; KDEL (Lya-Asp-Giu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 3.48
448988; Y09763; Hs. 22785; genram-eminobulyric acid (CABA) A receptor, Neur_shan_LBD,Neur_chan_memb;TM=Y;SS=M; 3.48
415323; BE269352; Hs.949; neutrophil cytosolic tactor 2 (65xD, chr.; SH3,TPR;TM=M;SS=N; 3.48
425003; AF119046; Hs.154149; eputrinic/apyrimitainic andonucleese(APEX; Troponin,Exo_endo_phos,IQ;TM=M;SS=N; 3.47
424906; S78187; Hs.153752; cell division cycle 258; Rhodenese;; 3.44
446051; BE049061; Hs.37054; ephrin-A3; Ephrin,A_dearnin,distm,z-elphe; 3.43
418641; BE243136; Hs.86947; a disintegrin and metalloproteinese doma; disintegrin,Reprotysin,Pep_M12B_propep,EGF;TM=Y;SS=M; 3.42
          75
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417426; NM_002291; Hs.82124; taminin, beta 1; taminin_EGF,taminin_Nterm,integrin_B;; 3.42 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 3.42
                                                                                41253, BE25/8027 RS.552812; ESTS; none,none; 3.42
425289; AW133342; Hs. 155530; Interferon, garmma-inductible protein 16; PAAD_DAPIN,HIN; 3.39
425354; U62027; Hs. 155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 3.39
428293; BE250944; Hs. 163556; solute carrier family 1 (neutral amtino a; elF6,SDF; TM=M; SS=N; 3.39
              5
                                                                                43648; Al085377; Hs. 183610; ESTs; Fork_head,none; 3.39
418869; AWS16885; gb:xqD1005.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,WW,IO; 3.38
432179; X75208; Hs. 2913; EphB3; EPH_lbd,fn3,pkinase,SAM;TM=Y;SS=M; 3.38
418918; X07871; Hs. 89476; CD2 antigen (p50), sheep red blood cell; ig;TM=Y;SS=M; 3.38
414368; W70171; Hs. 75935; unidine monophosphale kinase; PRK CoaE;; 3.37
10
                                                                         41831B; X07871; Hs. B9476; CD2 antigen (p50), sheep red blood cell; ig;TM=Y;SS=M; 3.38
414366; W70171; Hs.79539; undine monophosphale kinase; PKK, CoaE;; 3.37
408716; A1567839; Hs. 21672; undine monophosphale kinase; PKK, CoaE;; 3.37
457001; J03258; Hs. 2062; vitamin D (1,25- difrydroxyvitamin D3) re; hormone_rec,zt-C4,Metallothio_5;TM=M;SS=N; 3.37
422283; AW411307; Hs. 114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 3.37
422283; AW411307; Hs. 114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 3.37
422283; AW411307; Hs. 114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 3.37
42283; AW411307; Hs. 114316; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 3.37
421811; AF146074; Hs. 108600; ATP-binding cassette, sub-family C (CFTR; Fasckin,ABC_membrane,GTP_EFTU;TM=M;SS=M; 3.36
400286; AA032279; Hs. 61635; six transmembrane spithelial antigen of; none;TM=Y;SS=N; 3.35
428365; AF112213; Hs. 184052; putetive Rab-5-interacting protein; BH2,SH3;; 3.33
400261; Hs. 1802; Eos Control; ig,MHC; II_beta;TM=Y;SS=M; 3.33
410024; AW191024; Hs. 55016; hypothelical protein FLJ21935; SH3;TM=M;SS=N; 3.32
41584; X54870; Hs. 74085; DNA segment on chromosome 12 (unkque) 24; none,lectin_c; 3.32
416065; BE267931; Hs. 78996; proliferating cell nuclear antigen; PCNA,PCNA_CTM=M;SS=N; 3.31
426840; BE244217; Hs. 172690; discylglyceral kinase, alpha (BtXD); ethand,DAG_PE-bind,DAGKe,DAGKe,DC1;TM=M;SS=N; 3.31
426840; BE244217; Hs. 172690; discylglyceral kinase, alpha (BtXD); ethand,DAG_PE-bind,DAGKe,DAGKe,DC1;TM=M;SS=N; 3.31
42793; AL046606; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;SS=N; 3.31
42793; AL046606; Hs.17064; Hs. 617064; Hs.
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                                                                                      44000; NM_004403; NS. 15303; decaress, addosorina duriniaria o; noris; no-va, 55-in, 5,25
444783; AK001468; Hs. 62180; antilin [Drosophila Screps homolog], act; PH,none; 3.25
422278; AF072873; Hs. 114218; fitzzled (Drosophila) homolog 6; F2, Fritzled, 7m_2; TM=Y;SS=M; 3.25
405932; ;; C15000305;gij3805122[gb]AAC69198.1] (AF0; ras;TM=M;SS=N; 3.25
400205; ; Hs.81846; NM_006265*Homo septems RAD21 (S, pombe); DUF173;; 3.25
    40
                                                                                      400205; ; Hs.81846; NM, Q06265*:Homo saptene RAD21 (S. pomba); DUF173;; 3.25
432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 3.24
412942; AL12044; Hs.76074; mitogen-activated protein kinase-activat; pkinase;TM=M;SS=N; 3.23
435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 3.22
439285; AL133916; Hs.47850; hypothetical protein FLI20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 3.22
410434; AF051 152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 3.22
427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 3.22
436076; 9E090179; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.22
428698; AA852773; Hs.334838; KIAA1856 protein; none;MA;NA; 3.22
448888; AW196663; Hs. 200242; expresse recording nontein 6; CARD:TM=M;SS=N; 3.22
    45
                                                                                    43675; 8E090176; Hs.179902; transporter-like profein; none;TM=Y;SS=M; 3.22
426696; AA852773; Hs.34838; KIAA1866 protein; none;TM=Y;SS=M; 3.22
415149; X12451; Hs.78058; cathepsin L; Peptidase_C1;; 3.21
425393; R37772; Hs.24120; p21-activated protein kinase 6; pkinase,PBD;TM=M;SS=N; 3.22
424518; L29472; Hs.1802; major histocompatibility complex, class; Ig,MHC_JI_beta;TM=Y;SS=M; 3.20
424518; L29472; Hs.1802; major histocompatibility complex, class; Ig,MHC_JI_beta;TM=Y;SS=M; 3.20
438584; AA3315S3; Hs.198253; major histocompatibility complex, class; Ig,MHC_JI_alpha,none; 3.20
456181; L36463; Hs.1030; ras inhibitor; RA_SH2,VPS9;TM=M;SS=N; 3.20
418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase; pkinase,CNH;TM=M;SS=N; 3.19
410682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin_b2IP;TM=M;SS=N; 3.19
410682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin_b2IP;TM=M;SS=N; 3.16
419216; AU076716; Hs.164021; small inducible cytokine subfamily B (Cy; IL8; 3.16
426395; BE151985; Hs.365326; bransmembrane protease, serine 4; trypsin,kii_recep1_a,none; 3.16
426395; BE151985; Hs.355665; hypothetical protein; FLJ23316; pkinase,none; 3.15
433376; Al249361; Hs.74122; caspase 4, apoptosis-related cyslaine pr; CARD,ICE_p10;ICE_p20;; 3.15
410668; BE379794; Hs.196651; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 3.15
432414; U81981; Hs.2794; sodium channel, nonvoltage gated 1 sigha; ASC;TM=Y;SS=N; 3.15
43251; AW972983; Hs.235165; polycythemia rubra vera 1; cell surface; none;TM=M;SS=M; 3.15
407844; AW073716; Hs.6037; ESTs; transmembrane4,none; 3.14
438014; AW407254; Hs.356266; calmodulfin 2 (phosphonylase kinase, delt; none,none; 3.14
438074; AF068816; Hs.6454; chromosome 19 open reading frame 3; PDZ;; 3.13
439336; AB005036; Hs.323949; kangal 1 (suppression of tumorigenticity; transmembrane4,none; 3.13
42930; AB056306; Hs.32939; melanoma cell addension modecule; g,lscdh,ribosomal_L6,F-box;TM=Y;SS
M; 3.12
        50
        55
        60
        65
            70
                                                                                            429336; AB005036; Hs.199270; cytochrome P450, subfamily XXVIIB (25-hy; p450;; 3.13
449230; BE613348; Hs.356392; melaroma cell adhesion molecule; lg.lsodh,Ribosomal_L6,F-box;TM=Y;SS=M; 3.13
429305; AF095727; Hs. 287832; myelin protein zero-like 1; lg.bramembrane4;TM=Y;SS=M; 3.12
419034; NM, 002110; Hs.89555; bemopole@it cell klinase; SHz,SHS,Ribnase; TM=M;SS=N; 3.12
417386; AL037228; Hs.301957; D123 gene product; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 3.11
419138; U48508; Hs.89531; ryanodine receptor 1 (skeletal); lon_trans,SPRY,RYDR_JTPR,RyR,MIR;TM=Y;SS=M; 3.11
440006; AlX0005; TH.5.6844; NALP2 protein; PYRIM-Containing APAF1-II; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 3.10
406467; ;; Target Exxon; efiland,Acytransferase,none; 3.10
422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell transform); BRCT,RhoGEF;TM=M;SS=N; 3.10
417771; AA804696; Hs.82547; retinole acid receptor responder (tezzaro; none,none; 3.09
437016; AU076916; Hs.5398; guardine monphosphate synthetase; PHD,SET,zF-
CXXC,EGF,ank,notch,WW,FCH,GATese,GMP_synt_C,Occludin,YEATS,metalthlo,EB,herne_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT;TM=M;SS=N; 3.09
            75
              80
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441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 3.09
416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 3.09
418498; U33632; Hs.78351; potassium channel, sutbramely K, member 1; ion_brane; TM=Y;SS=M; 3.09
426106; AA622037; Hs.166468; programmed cell death 5; DUF122;Tm=M;SS=N; 3.08
442610; AA622037; Hs. 166468; programmed cell death 5; DUF122;Tm=M;SS=N; 3.08
442610; AA622037; Hs. 166468; programmed cell death 5; DUF122;Tm=AISS=N; 3.08
442610; AA622037; Hs. 166468; programmed cell death 5; DUF122;Tm=AISS=N; 3.08
442233; ;; NM_030760*Homo sapians endothelial dift; 7tm_1;TM=Y;SS=M; 3.07
420367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor 1; none;TM=M;SS=Y; 3.06
434263; N34895; Hs.79187; ES1s; ig.none; 3.06
434263; N34895; Hs.79187; ES1s; ig.none; 3.06
43907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 3.05
439378; U42387; Hs.54426; pancreatic polypeptide receptor 1; 7tm_1;TM=Y;SS=M; 3.05
403778; U42387; Hs.54426; pancreatic polypeptide receptor 1; 7tm_1;TM=Y;SS=M; 3.05
40270; NM_015996; Hs.7120; cytokina receptor-like molecule 9; in3; 3.05
40270; NM_015996; Hs.7120; cytokina receptor-like molecule 9; in3; 3.05
440270; NM_015996; Hs.7120; cytokina receptor-like molecule 9; in3; 3.05
440270; NM_015996; Hs.7120; cytokina receptor-like molecule 9; in3; 3.05
440270; NM_015996; Hs.399; alcohol dehydrogenase 7 {class IV}, mu o; adt_2inc;TM=M;SS=N; 3.05
420189; AW298380; Hs.95821; osteodast stimulating faxlor 1; SH3,ank; 3.05
421541; NM_003942; Hs.10584; ribosomal protein 66 kinase, 90KD, polyp; pkinase,pkinase_C;TM=M;SS=N; 3.04
415444; BE247296; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;SS=N; 3.03
425118; AU076811; Hs.154672; methylene tetrahydrofotate dehydrogenase; myb_DNA-binding,THF_DHQ_CYH_T,CAP_CHY_CAP_CHY_AAA_LON_Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cobransp;TM=M;SS=N; 3.03
449048; Z45051; Hs.2920; similar to 868401 (cettle) glucose induc; Lamp;TM=M;SS=M; 3.02
442675; BE623003; Ns.23625; Homo s
                       5
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                                                                                                  413899; N.M., 00.0078; 1k: 75596; Interieukin 2 receptor, beta; mone; TM-Y;SS=M; 3.02
432675; B425203; N.S. 2655; Horne septems chare TCCCTA0142 mRNA sequ; K_letra, DUF51, none; 3.02
435576; AMSS213; N.S. 17542; ES13; Ym. 1, Dru.P; 3.02
435576; AMSS213; N.S. 17542; ES13; Ym. 1, Dru.P; 3.02
431870; AF147204; Ha.B9414; chemokine (C.X-C molf), receptor 4 (fus; Ym. 1, Ym. 2;TM-Y;SS=M; 3.01
421379; Y15221; Hs. 105982; small inductive cytokine subfamily 16; (C.Y. LE, TM-M-KSS=Y; 3.00)
421379; Y15221; Hs. 105982; small inductive cytokine subfamily 16; (C.Y. LE, TM-M-KSS=Y; 3.00)
4291374; Y15221; Hs. 105982; small inductive cytokine subfamily 16; (C.Y. LE, TM-M-KSS=Y; 3.00)
4291379; Y15221; Hs. 105982; small inductive cytokine subfamily 16; (C.Y. LE, TM-M-KSS=Y; 3.00)
4291379; Y15221; Hs. 105982; small inductive cytokine subfamily 16; (C.Y. LE, TM-M-Y; SS=M; 3.00)
4291374; Y15221; Hs. 105925; brain-derived neurotrophilo factor, NUSF; 2.99
430605; AMS31276; Hs. 59009; ESTS; pklnasa,PP2C_none; 2.98
430605; AMS31276; Hs. 59009; ESTS; pklnasa,PP2C_none; 2.99
430605; AMS31276; Hs. 59009; ESTS; pklnasa,PP2C_none; 2.99
410026; AUS 12051; Hs. 56016; hypothetical protein FLU21935; none,none; 2.97
410026; AUS 12051; Hs. 56016; hypothetical protein FLU21935; none,none; 2.97
43053; AMS51943; Hs. 334; Rho guantine nucleotide exchange factor; none,none; 2.97
427316; AA179949; Hs. 175663; Horne caplens mRNA; CDNA DIACZ-9564ND753 (Jr. none,spection, SH3,PH,CH; 2.97
427316; AA179949; Hs. 175663; Horne caplens mRNA; CDNA DIACZ-9564ND753 (Jr. none,spection, SH3,PH,CH; 2.97
427316; AA179949; Hs. 175663; Horne caplens mRNA; CDNA DIACZ-9564ND753 (Jr. none,spection, SH3,PH,CH; 2.97
427316; AA179949; Hs. 175663; Horne caplens mRNA; CDNA DIACZ-9564ND753 (Jr. none,spection, SH3,PH,CH; 2.97
427316; AA179349; Hs. 175663; Horne caplens mRNA; CDNA DIACZ-9564ND753 (Jr. none,spection, SH3,PH,CH; 2.97
427316; AA179349; Hs. 175663; Horne caplens cDNA FLU21099 fis; clone CO; pklnasa, Furnore; 2.94
42258; AF10000; Hs. 18; 27250; masses cDNA FLU210099 fis
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                                                                                                                            422510; AF153620; Ib. 1547; potassium inwardy-rectifying charues, s; IRK;TM=Y;SS=N; 2.89
402506; ; ; homeodomein-interacting protein kinase 3; hypslm;TM=M;SS=N; 2.89
423804; AW403448; Hs.1706; Interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 2.69
                                                                                                                   403605;;) noneodomin-interacting protein finates 3; hypsin; IM-M;8S=N; 289
423804; AW403448; Hs. 1706; Interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N
425262; D87119; Hs.155418; GS3955 protein; pldnase;; 2.88
422593; BE387202; Hs. 118638; non-meitastatic cells 1, protein (MM23A); NDK,PH,Oxysterol_BP;; 2.88
452888; AW955454; Hs.30942; eptini-B2; Ephrin,fu2;TM=Y;SS=M; 2.88
452888; AW955454; Hs.30942; eptini-B2; Ephrin,fu2;TM=Y;SS=M; 2.88
414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 2.87
444143; AW747996; Hs.160999; ESTs, Moderately slmiter to A56194 throm; Bct-2,none; 2.86
413472; BE242870; Hs.75379; solvite carrier family 1 (glial high afti; SDF;TM=Y;SS=M; 2.88
458039; AAB35884; Hs.130685; leukotriene M4 receptor (chernokine recep; CIDE-N.none; 2.86
434417; AL110157; Hs.3343; Homo saplens mRNA; cDNA DKF2p536F2224 (f; DSPc,none; 2.86
425802; Y14838; ; chemokine-like receptor 1; 7tm_1,none; 2.86
403112; ; Target Exor; efficand, C2;PH,PI-PLC-Y;PI-PLC-X;; 2.86
435663; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_is;TM=Y;SS=N; 2.85
442117; AW664984; Hs.128899; ESTs; hypothetical protein for IMAGE:447; none,none; 2.84
457819; AAD57484; Hs.35406; FL120522 Hypothetical protein for IMAGE:447; none,none; 2.84
456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPasa_c,zf-C2H2,PHD,none; 2.83
448947; AF146747; Hs.236794; histone deacetylase 3; HSP90,HATPasa_c,zf-C2H2,PHD,none; 2.83
448947; AF146747; Hs.236579; hypothetical protein FL122865; myosin_neac, 2.84
447687; AL133017; Hs.21616; KIAA1329 protein; FKD,BNR;TM=Y;SS=M; 2.82
407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC;TM=Y;SS=M; 2.82
        65
           70
              75
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459707; AA631362; Hs. 120866; gb:np86b01.s1 NCL_CGAP_Thy1 Homo sapiens; 7bm_1,none; 2.82 422699; BE410590; Hs. 119257; erns1 sequence (mammary tumor and squamou; SH3,HS1_rep;TM=M;SS=N; 2.82 4381.06; Al471795; Hs. 287776; vaniloid receptor-related csmotically a; ank,ion, brans;TM=Y;SS=N; 2.82 422241; Y00062; Hs. 170121; protein tyrosine phosphatiase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 2.82 422241; Y00062; Hs. 27072; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 2.82 422598; BE247600; Hs. 37795B; ESTs; 7tm_1;TM=Y;SS=M; 2.81 423598; BE247600; Hs. 37795B; ESTs; 7tm_1;TM=Y;SS=M; 2.81 412970; AB026438; Hs. 177534; dual specificity phosphatase 10; Rhodanese, DSPc; 2.81 4141016; Mithige301; brand Federal Company of the phosphatase 10; Rhodanese, DSPc; 2.81
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                                                                            412970; AB026436; Hs.177534; dual specificity phosphalase 10; Rhodanese, ISPc;; 2.81
414198; AW505308; Hs.75812; phosphoenolpyruvate carboxykinase 2 (mit; PEPCK;; 2.81
436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 2.81
432314; AA533447; Hs.285173; ESTs; Xlink, none; 2.81
416207; NM_D14745; Hs.79077; Homo sapiens, clone MGC.2908, mRNA, comp; none;TM=Y;SS=M; 2.80
446985; AL038704; Hs.156827; ESTs, Weakly similar to ALU1_HUMAN ALU S; SAM,SH3,HS1_rep; 2.80
426023; AL038843; Hs.374530; Homo sapiens cDNA; FLIZ3602 fis, clone L;
82_permeasea_pyridoxal_deC,bromodomain,PHD,MBD,AT_bcok,DDT,Pl3_Pl4_kinese,FAT,FATC,BolA,RUN;TM=M;SS=N; 2.80
432866; BE159028; Hs.279704; chromalin accessibility complex 1; none;TM=M;SS=N; 2.80
426006; R49031; Hs.22627; ESTs; pkinese,TBC; 2.79
414217; Al309298; Hs.279898; Homo sariens cDNA; FLIZ3165 fis, clone 1; none;TNA:NA; 2.78
10
15
                                                                            426006; R49031; Hs.22627; ESTs; pklnase,TBC; 2.79
414217; Al309288; Hs.279998; Horno sapiens cDNA: FLJ23165 fts, clone L; none;NA;NA; 2.79
411165; NM_000169; Hs.69089; galactosidese, elpha; Melibiase;; 2.79
450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,Ig,MHC_ll_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 2.78
424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 2.78
421448; AF033850; Hs.104519; phospholipase D2; PH,PLDc,PX;TM=M;SS=N; 2.78
410226; AB31958; Hs.61653; hypothetical protein; SH3;TPR;TM=M;SS=N; 2.78
413253; AF111106; Hs.3382; protein phospholase 4, regulatory subuni; HEAT;TM=M;SS=N; 2.78
415003; AF147078; Hs.375031; p53-responsive gene 6; K_tetra,ton_trans,none; 2.77
413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp7t0H-); TPR,PDZ,WW,Guanytate_kin;TM=M;SS=N; 2.77
454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;SS=N; 2.77
440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 2.77
4425667; H25642; Hs.132821; ESTs; FMO-like; 2.76
415012; NM_004383; Hs.7793; c-src tyrosine kinase; 8142; hs.pkinase;TM=M;SS=N; 2.76
20
25
                                                                                422667; H25642; Hs. 132821; ESTs; FMO-like,FMO-like; 2.76
415012; NM_004383; Hs. 77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 2.76
402316; ;; NM_013447;Horno sapiens egf-like module c; 7tm_2,GPS;TM=M;SS=M; 2.75
425465; £18964; Hs. 1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 2.75
447250; Al878909; Hs. 17883; protein phosphatase 1G (formerly 2C), ma; PP2C;TM=M;SS=N; 2.75
437629; Al187330; Hs.257170; ESTs, Weakly similar to T12515 hypotheti; TNFR_c6,none; 2.75
451144; AN935103; Hs. 61712; pyrturale dehydrogenisse kinase, isoenzyme; HATPase_c,none; 2.74
408543; N78098; Hs. 44289; ESTs; none;TM=M;SS=N; 2.74
408543; N78098; Hs. 495695; hypothetical protein; K_cetra,SAM; 2.74
407722; BE252241; Hs. 436041; ovrificational forded the without and the library file:TM=M;SS=N; 2.73
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  35
                                                                                428345; R11141; Hs. 195995; hypotinetical protein; K_tetra,SAM; 2.74
407722; BE252241; Hs. 38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfkB; TM=M;SS=N; 2.73
420602; AF060877; Hs. 99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 2.73
407217; AA477136; Hs. 105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 2.73
414135; NM, 004419; Hs. 2123; dual specificity phosphatase 5; Rhodanese,DSFe<sub>3</sub>Y_phosphatase;TM=M;SS=N; 2.73
410590; BE615216; Hs. 64746; chloride intracellular channel 3; none;TM=M;SS=N; 2.73
411125; AA151647; Hs. 68877; cytochrome b-245, ghha polypeptide; none;TM=M;SS=M; 2.73
438022; AW617524; Hs. 135201; NOD2 protein; LRR,CARD,GTP_CDC,Viral_helicase1;TM=M;SS=N; 2.72
420929; Al694143; Hs. 326248; programmed cell death 4; MA3;TM=M;SS=N; 2.72
421156; H37879; Hs. 102267; Ivst poldase I varia ovidese Alfose edite Followerser: 2.72
    40
                                                                          431022, AVIS1047, ris.coo77, cycoromore 2-48, spine polyepaus, rune; in-11, 23-74.
438022, AVIS17524, Hs. 135201; NDD2 protein; LRR, CARD, GTP_CC, Viral, Isalicase1;TM-M;SS-N; 2.72
420929, AVIS94143, Hs. 326248; programmed cell death 4; MA3;TM-M;SS-N; 2.72
421155; Baristry, Hs. 102257; lysyl oxidase; Lysyl_oxidase, Adiose_prim_Epimerase;; 2.72
448564; ALD4952; Hs. 21453; inositiol 1,4,5-brisphosphate 3-kinase C; IFX;; 2.71
449561; AW286564; Hs. 133100; EBTs; pkinase, Furth-Ilke, Recep_L_domain, none;; 2.71
449561; AW286564; Hs. 133100; EBTs; pkinase, Furth-Ilke, Recep_L_domain, none;; 2.71
449563; ABT11713; Hs. 12284; junctional adhesion molecule 1; ig; ITM-Y;SS-M; 2.71
419569; AIST1651; Hs. 91143; jagged 1 (Alagille syndrome); DSL.EGF;Iaminin_EGF;wxc,metaltiho;TM-M;SS-M; 2.71
419569; AIST1651; Hs. 91143; jagged 1 (Alagille syndrome); DSL.EGF;Iaminin_EGF;wxc,metaltiho;TM-M;SS-M; 2.70
422616; IBS00330; Hs. 118725; selemophosphate synthetase 2; AIRS,AIRS_C;TM-M;SS-N; 2.70
422124; AABE238; Hs. 91396; ESTS; 71m_1;TM-Y;SS-M; 2.70
422616; IBS00330; Hs. 118725; selemophosphate synthetase 2; AIRS,AIRS_C;TM-M;SS-N; 2.70
422717; H03754; Hs. 152213; winglass-type MMTV integration site famit, wnl,none; 2.70
424717; H03754; Hs. 152213; winglass-type MMTV integration site famit, wnl,none; 2.70
441018; AZB7592; Hs. 7761; SFRS protein Xinase (Tymdykate Nin; none,none; 2.79
441034; L16991; Hs. 79000; deoxythymidylate kinase (Tymdykate Nin; none,none; 2.69
44403; AU07748; Hs. 173624; thymine-DNA glycosylass; UDE;TM-M;SS-N; 2.69
442821; W74048; Hs. 1766; hymphocyte-specific protein tyrosins kin; SH2,SH3,pkinase;TM-M;SS-N; 2.68
42561; AUX07466; Hs. 278441; KUAA0015 gene product; PP2C;TM-M;SS-N; 2.69
424321; W74048; Hs. 1766; hymphocyte-specific protein tyrosins kin; SH2,SH3,pkinase;TM-M;SS-N; 2.68
42561; AUX07466; Hs. 278441; KUAA0015 gene product; PP2C;TM-M;SS-N; 2.69
42686; Au469355; Hs. 15568; receptor tyrosine kinase-like orphan rec; tg, Infinia, Indiase;TM-Y;SS-M; 2.68
427724; NM, 005211; Hs. 174142; colony slimulating factor
    45
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      65
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                                                                                           439730; AL359U5; H8.57654; Horno saplens mRNA full largth insert cDN; IMPDH_N,CBS;Integrin_B,Ricin_B_jectin; 2.66
419745; MAY24725; Hs.75514; mucloselde phosphorylase; Map_PNP; 2.68
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 2.66
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 2.66
449536; Al365582; Hs.57190; Homo septens mRNA for FLJ00016 protein, ; transmembrane4;TM=Y;SS=M; 2.66
434979; Al953054; Hs.89643; transketolase (Wernicko-Korsekoti syndro; ASC,transketolase, transket_pyr,transketolase_C,pkinase; 2.68
408137; ; ; NM_000179*:Homo saptens mulS (E. coti) h; MulS_C,PWWP,MulS_N;TM=M;SS=N; 2.66
          80
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412935; BE267045; Hs.75064; tabulin-specific chaperone c; none;; 2.66
408633; AW963372; Hs.22088; PRO2000 protein; bromodomain,AAA,Sigma64_activat;; 2.66
412817; AL037169; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 2.65
452682; AA456193; Hs.374574; progesterone membrane binding protein; homeobax, none; 2.65
401752; ;; RAN binding protein 3; SH2,STAT,STAT_bind,STAT_prot,lon_brans,PAC,PAS,Orexin; 2.65
450747; Al064821; Hs. 129953; ESTs, Highly similar to 1816357A EWS gen; rm;Z-RanBP,GAS2; 2.65
452774; Al064821; Hs. 129953; ESTs, Highly similar to 1816357A EWS gen; rm;Z-RanBP,GAS2; 2.65
452771; NM_005110; Hs.30332; glutamins-fructose-6-phosphata bransarrin; GATase, 2,SIS;TM=M;SS=N; 2.64
452701; NM_005110; Hs.30532; glutamins-fructose-6-phosphata bransarrin; GATase, 2,SIS;TM=M;SS=N; 2.64
433933; Al764389; Hs.355397; Home sapiens clone TCCCtA00164 mRNA sequ; none;NA;NA; 2.64
421677; H54092; Hs.38282; ESTs; Alpg,Armadillo_seg,IBB; 2.64
423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 2.64
423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 2.64
433712; XU54S8; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyoshn,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 2.63
43712; XU54S8; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyoshn,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 2.63
447217; BE465754; Hs.17778; neuropiin 2; CUB,MAM,FS_F8, type_C;TM=M;SS=N; 2.63
447217; BE465754; Hs.17778; neuropiin 2; CUB,MAM,FS_F8, type_C;TM=M;SS=N; 2.63
44562; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 2.63
44562; AA30770; Hs.288649; hypothetical protein MGC3077; none;; 2.63
44562; AA30770; Hs.288649; hypothetical protein MGC3077; none;; 2.63
44562; AA30770; Hs.287668; linesin ternity member 44; kinesin,DNA_topolsolv,K-box;TM=M;SS=N; 2.63
452012; AA307703; Hs.279766; kinesin ternity member 44; kinesin,DNA_topolsolv,K-box;TM=M;SS=N; 2.63
412182; AA2015588; Hs.73737; Splicing feelor, argininelsedne-rich, 4; mm,hormone_r
                5
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                                                                                                    452012; AA307703; Hs.279766; kinesin family member 44; kinesin,DNA_topcisofV,K-box;TM=M;SS=N; 2.63 412182; AA205588; Hs.73737; Splicing factor, arginine/sedne-rich, 4; rm.,hormone_rec.;2f-C4,sugar_br; 2.63 422887; ALB80207; Hs.134585; DKFZP4346232 proteit; ABC_bran;TM=Y;SS=N; 2.63 417497; AW402482; Hs.82212; CD53 entigen; trensmembrane4;TM=Y;SS=M; 2.62 413407; Al35623; Hs.75339; Inositiol polyphosphates phosphatese-like; SH2,SAM_Exo_endo_phos;; 2.62 413407; Al35623; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 2.62 417890; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushk;TM=M;SS=M; 2.62 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;SS=N; 2.62 401812; ;; sorting nexin 14; AAA,NB-ARC,APS_kinase,cdc48_N,cdc48_2,none; 2.61 417886; A2745848; ESTE_SPRY_7Tm: 3.ANF_excenter_none 2.261
25
                                                                                        444998, NM, 202543; Ha.17773; exidised on density isoprotein (pictrix lediu, c:TM-YiSS-M, 252
474908, E247616; ha.12246); teld: (hymphory) exhabition moleculic (Fell-Line). Lauk/MIM-MiSS-M; 262
472922, 227650; his.22617; H.1 habition family, member 0, hinder, jack-miss-201
472924, 227650; his.22617; H.1 habition family, member 0, hinder, jack-miss-201
472924, A.17260; his.22440; hautile receptor tyrosine kinase subvirus 541
473764, A.17260; his.2440; hautile receptor tyrosine kinase subvirus 541
473764, A.17260; his.2440; hautile receptor tyrosine kinase subvirus 541
473764, A.17260; his.2440; hautile receptor tyrosine kinase subvirus 541
473764, Ha.17260; his.2440; hautile receptor tyrosine kinase subvirus 541
473764, Ha.17260; his.2440; his.2461, his.246
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425966; NM, 901761; Hs. 1973; cyclin F; cyclin,F-box,cyclin_C;TM=M;SS=N; 2.54
446566; H35741; Hs. 17914; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 2.54
412334; R77123; Hs. 79841; Horno sapiens cDNA: FLJ23006 fis, clone L; 7tm_1,none; 2.54
457255; AL133011; Hs. 253920; Horno sapiens mRNA; cDNA DKFZP434P201 (fit, none, none; 2.54
431341; AA307211; Hs. 251531; proteasome [prosome, macropain) subunit; proteasome;TM=M;SS=N; 2.53
417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID_zf-CzHz,SCAN_AMP-binding,KRAB;TM=M;SS=N; 2.53
414331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID_zf-CzHz,SCAN_AMP-binding,KRAB;TM=M;SS=N; 2.53
414570; Y00265; Hs.76473; insulin-like growth factor 2 receptor; frz,CMMR;TM=M;SS=M; 2.53
444836; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 2.53
422609; Z46023; Hs.118721; sialidase 1 (lysosomal stalidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 2.53
450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none,none; 2.53
400702; ;; Target Exon; Ilg_chan,SBP_bec_3,ANF_receptor;TM=Y;SS=M; 2.53
432336; NM_002759; Hs.274382; protein kinase, interferon-Inducble dou; dsrm,pkinase;TM=M;SS=N; 2.53
442643; UB2756; Hs.374973; PRP4/STK/WD spitcing factor; WD40;; 2.52
45200; W26980; Hs.349089, ATP-binding cassette, sub-family F (GCN2,ABC_bran,RK,SWiB; 2.52
443951; F13272; Hs.356035; farrithi, light polypeptide; PMP22_Claudin,none; 2.52
407608; Al928218; Hs.360063; ATPase, Na? transporting, beta 3 polypep; none,none; 2.51
414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 2.51
412663; M68874; Hs.211587; phospholipase A2 group IVA (cytosolic, ; C2,PLA2,B;TM=M;SS=N; 2.51
425644; NM_004954; Hs.157199; ELK, motif kinase; pkinase; µlin-kinase, lib-kina; Brith-M;SS=N; 2.51
439221; AA737106; Hs.32250; ESTs, Moderately similar to 178885 serin; adh_short,Bel-2,BH4,none; 2.51
4034366; BE2243124; Hs.471656; hpsospholipase,none; 2.51
                                                                                           425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M;SS=N; 2.54
              5
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                                                                                        439221; AA737106; Hs. 32250; ESTs, Moderately similar to I78885 sertin; adh_short,Bcl-2,BH4,none; 2.51 403429; ;; Target Exon; Y_phosphatase,none; 2.51 403429; ;; Target Exon; Y_phosphatase,none; 2.51 443468; BEZ43123; Hs. 321045; IKK-related kinase epsilon; inducible lk; pkinase,RIO1;TM=M;SS=N; 2.51 418478; U38945; Hs. 1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 2.50 408056; AA312329; Hs. 42331; ephrin-A4; Ephrin;TM=M;SS=M; 2.50 414419; F06829; Hs. 76900; tumor necrosis factor, elpha-Induced pro; K_letra;TM=M;SS=N; 2.50 408369; ;; NM_005599*:Horno saplens LIM domain kinas; pkinase,LIM,PDZ;; 2.50 418216; AA662240; Hs. 283099; AF15q14 protein; Harnegglutinin,squash;TM=Y;SS=N; 2.50 40321;;; C7001741*:gij2499629jspjC63932/IMPK2_MOUS; none,none; 2.50 403900; U91939; Hs. 284123; G protein-coupled receptor 25; 7m_1;TM=Y;SS=M; 2.49 440861; BE244115; Hs. 7482; KIAA0582 gene product; mm,Guanylate_kin;TM=M;SS=N; 2.49 418741; HB3265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_recp,Pkinase,Activin_rec
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                                                                                                  417034, NM_006183; Hs. 80962; neurotensin; none;; 2.49
400303; AA242758; Hs. 79136; LIV-1 protein, estrogen regulated; none,none; 2.49
408805; H69912; Hs. 48269; vaccinia related kinase 1; pkinase;TM=M;SS=N; 2.49
                                                                                               408B05; Nb:912; Ns.432b5; veccrita retated variese i; prinase; I.M=M;503=v; Z-49
418255; AW135405; Hs.37251; ESTs; pklnase,none; Z-49
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pklnase; TM=M;5S=N; Z-44
417791; AW965339; Hs.44269; ESTs; none,ter2;FAD_binding_5,Aki_Xan_dh_C;fer2_2,Aki_Xan_dh_C2;CO_deh_flav_C; Z-44
453941; U39817; Hs.36820; Bloom syndrome; DEAD,hellcase_C,HRDC;TM=M;SS=N; Z-41
417849; AW291587; Hs.82733; nidogen 2; EGF,id_recept_b,thyroglobulin_1;TM=M;SS=M; Z-39
       40
                                                                                             417849; AW291687; Hs.22733; nidogen 2; EGF,idt_recept_b,ihyroglobulin_1;1M=M;S6=M; 2.39
408908; BE298027; Hs.250802; serine/hrennine kinese 16; pkinese;; 2.32
428513; BE220806; Hs.164697; plexin C1; PSI,none; 2.31
426761; Al015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing ms; none;TM=Y;SS=M; 2.31
427585; D31152; Hs.179729; collagen, type X, siphs 1 (Schmid metaph; C1q,Collagen;; 2.28
412723; A6464859; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=M; 2.28
412723; A6464859; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=M; 2.28
425461; N78223; Hs. 108106; transcription factor; zf-C3HCA,ubiquitin,PHD,YDG_STR,*TM=M;SS=N; 2.26
42547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none,none; 2.15
429486; AF155827; Hs.203963; hypothetical protein FLJ10339; SNF2_N,helicase_C;TM=M;SS=N; 2.15
401486; ;; C4000647*:gij4758508]refilNP_004253.1] at; none;TM=Y;SS=M; 2.15
416209; AA236776; Hs.79078; MAD2 (mitratic arrest deficient, yeast, h; HORMA;TM=M;SS=N; 2.14
424399; Al905667; Hs.348419; A905667: HL-BT095-190199-019 B7095 Homo; none;TM=M;SS=M; 2.14
423761; NM 006194; Hs.132576; calerd box cens 9: PAX*TM=M;SS=M; 2.13
       45
       50
                                                                                                       443939; AUSCOBE; 18,346419; AESCOBE; 11:H3195-190195-019 B1095 Homo; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 1009; 100
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                                                                                                       449448; D60730; Hs.57471; E6Ts; mone, none; 1.92
435243; AW292686; Hs.348932; hypothetical protein dJ434014.3; IRF, none; 1.85
406360; ; ; Target Exon; WID40; TM=M; SS=N; 1.84
                                                                                                       40300;;; rarget extri; vtiD40; N=M,3S=N; 1.64
411388; X72925; Hs.69752; desmocollin 1; cadherin;TM=Y;SS=N; 1.84
453102; NM_007197; Hs.31664; fitzzled (Drosophila) homotog 10; Fz_Frizzled,7tm_2;TM=Y;SS=M; 1.79
419183; U60669; Hs.89663; cytochrome P450, subfamily XXIV (vitamin; p450;; 1.78
420344; BE463721; Hs.97101; puterive G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 1.77
432842; AW674093; Hs.334822; hypothetical protein MGC4495; Ribosomal_L4;TM=M;SS=N; 1.76
           65
                                                                                                       432842; AW674093; Hs.334822; hypothetical protein MGC4485; Ribosome J.A;TM=M;SS=N; 1
419743; AW408762; Hs.5957; Homo saplens clone 24416 mRNA sequence; none,none; 1.73
426427; M86699; Hs.169840; TTK protein kinase; pkinase; 1.62
437915; Al637993; Hs.202312; Homo saplens clone N11 NTera2D1 teratoca; none,none; 1.58
433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz, NTR;; 1.50
434377; AW137148; Hs.306593; Intron of periostin (OSF-2os); Fasciclin,none; 1.47
451592; Al606416; Hs.213897; ESTs; none,none; 1.47
404927; ;; Target Exon; Gelactosy[_T;TM=M;SS=Y; 1.28
421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;; 1.27
427335; Ad448642 Hs.278444; Cardinan 78; none; 1.47
           70
              75
                                                                                                         421552; AF026692; Hs. 105700; secreted fritzied-related protein 4; Fz,NTR; 1.27
427335; AA448542; Hs. 278444; G antigen 7B; none; 1.25
431686; M30703; Hs. 270833; amphiregulin (schwaanoma-derived growth; EGF;TM=Y;SS=M; 1.24
447993; AW139525; Hs. 170362; ESTs; none, none; 1.21
428182; BE386042; Hs. 293317; ESTs; Weakly similar to GGC1_HUMAN G ANT; none;TM=M;SS=N; 1.18
428182; BE38699; Hs. 34073; BH-protocodharin (brain-heart); cadherin;TM=Y;SS=M; 1.14
438274; Al918906; Hs. 55080; ESTs; PAX.cone; 1.14
453968; BE148734; Hs. 63325; transmembrane protease, seriae 4; trypsin,kl_recept_a,none; 1.10
413268; AL039079; Hs. 75256; regulator of G-protein signalling 1; RGS;TM=M;SS=N; 1.07
              80
```

429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, CCLFI, TSPN, Jaminin_G, CorA;; 1.00 452795; AW392655; Hs.18878; hypothetical protein FLJ21620; 2CG-Fell Oxy;TM=N:SS=N; 1.00

				pe XI, alpha 1; Collagen,CCLFI,TSPN,laminin_G,CorA; 1.uu y pro\sin FLJ21620; 2OG-FeIL_Oxy;TM=M;SS≈N; 1.00
5	TABLE 25B			
,	Pkey:		probeset identifi	er number
	CAT number Accession:	: Gene duste Genbank ac	r number cession number	;
10	Pkey	CAT Numbe	er Accession	
	406685	0_0	M18728	
	418869 425802	12789_14 8884_3	AA229762 AA AA122298 AA	
15	417886	1031334_1	AA210987 D5	7294 AA214684 AA207006 D56572
	411133 AW8191987	1070 99 5_1 AW819234	AW819203 AV	V819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AWB19207 AW819220 AWB19208 AW819238
20	TABLE 25C			
20	Pkey:	ກຸນກູ ອນໝີກປັ	ber correspondi	ng to an Eos probeset
	Ref:		ource. The 7 di f human chromo	pit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA some 22." Dunham I. et al., Nature (1999) 402-489-495.
25	Strand: NL position;	Indicates Di	NA strand from v	mich exons were predicted. s of predicted exons.
20	Picey	Ref		
	•			NL position
30	401781 401780	7249190 7249190	Minus Minus	83215-83435,83531-83656,83740-83901,8423 28397-28617,28920-29045,29135-29296,2941
	401760 402075	9929699 8117407	Plus Plus	83126-83250,85320-85540,94719-95287 121907-122035,122804-122921,124019-12416
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
35	402447	9798640	Plus	47605-47729,51698-51821,52070-52257,5330
	405932	7767812	Minus	123525-123713
	406467 402233	9795551 7690102	Pius Pius	182212-182958 90281-91477
	402558	9863760	Plus	19047-19145,21133-21293,33968-34069
40	405556	1552511	Plus	183497-163623,164715-164968,165369-16660
	403112	8980973	Minus	113051-113195
	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
٠,	404891 406137	7329392 9166422	Plus Minus	84974-85125 30487-31058
45	401752	9828651	Plus	144500-144794
	405588	5002511	Plus	46180-46368
	401812	7407975	Minus	55084-55391
	405602	4753260	Plus	44647-44778
50	401751 401218	9828651 9929301	Plus Minus	139165-139322 40793-41031
50	401321	9863631	Minus	104278-104748
	401057	8117645	Plus	158309-159238
	400702	8118856	Minus	11457-11585,26311-26536,27902-28067,3204
55	405429	7321905	Minus	51577-51723
33	405369 404321	2078469 966520 9	Minus Minus	34183-34357,35686-35751 76594-77805
	401486	7341763	Plus	32585-32755,36281-38540,40791-40933,4401
	406360	9256107	Minus	7513-7673
60	404927	7342002	Plus	68690-69563
Ψ.				
	TABLE 26/	A: 834 GENE	ES UP-REGULA	ED IN EWING'S SARCOMA COMPARED TO NORMAL ADULT TISSUES
65	Table 26A	lists about 63	4 cenes up-recu	ated in Ewing's sarcoma compared to normal adult tissues, These were selected from 35403 probesets on the Affymetrix/Eos Hu03
	GeneChip 75th percer	erray such tha title amongst l	at the ratio of "av Ewing sarcomas	orege" kidney cancer to "everage" normal adult tissues was greater than or equal to 1.5. The "everage" kidney cancer level was set to the The "everage" normal adult tissue level was set to the 85% percentile amongst non-malignant tissues, in order to recrove gene-specific zation, the 7.5% percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio
	ANSE BASINS DOCUMENTS			
70	Pkey:		os probesel ideni	Nor nivohor
	ExAcon:	Exemplar	Accession numb	ner number er, Genbank accession number
		: Unigene a	tumber	
75		itte: Unigene g		normal Sauca
13	R1:	LESTING ON F	wing sarcoma to	NOTRAL ESSUE
	Pkey	ExAcon	UniGeneID	UniGene Title R1
	•			
	103447	トノフリ マイル		ah'ikuman aloha satelika and satelika 3

Pkey	ExAcon	UniGenelD	UniGene Title	RI	
101447 115881 110278 121362 101104	AF050147	Hs.184942 Hs.19492 Hs.97932 Hs.169266	gb:Human alpha satellite and satellite 3 G protein-coupled receptor 54 protocadheria 8 chondromodulla I precursor neuropeptide Y receptor Y1	38.4 34.2 32.2 30.3 26.3	

80

	404===	**********		COT IN	
	121792	AW969726	Hs.98381	ESTs, Wealdy similar to serine protease	24.4
	121619 104659	AA528339 AW969769	Hs.178062	ESTs, Weakly similar to phosphatidylseri	23.4 20.2
	106533	AL134708	Hs.105201 Hs.145998	ESTs ESTs	20.2 16.9
5	124006	AI147155	Hs.270016	ESTs	15.0
•	110728	AA737106	Hs.32250	ESTs, Moderately similar to 178885 serin	14.8
	105782	H0974B	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	14.6
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	14,5
4.0	104691	U29690	Hs.37744	Homo sapiens bela-1 adrenargic receptor	13.7
10	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	12.3
	129526	S69681	Hs.177582	surfactant, pulmonary-associated protein	12.1
	119791	AA554907	Hs.58291	ESTs	11.7
	116301	AW969705	Hs.293332	ESTs	11.2
15	123308	C14187	Hs.103538	ESTs	10.9
13	127742	AW293496	Hs.180138	. ESTs	10.8
	131601 127489	NM_007115 AA650250	Hs.29352 Hs,272076	tumor necrosis fector, alpha-laduced pro ESTs	10,7 10.6
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.6
	101063	D54745	Hs.80247	choleckstorgum,	10.6
20	134570	U66615	Hs.172280	SWUSNF releted, matrix associated, ecti	10.5
	100299	D49493	Hs.2171	growth differentiation factor 10	10.1
	127987	AI022103	Hs.124511	ESTs	10.1
	131313	R96290	Hs.336629	rībosomai protein L44	9.2
0.5	126799	AW753865	Hs.74376	ottactomedin related ER localized protel	8.5
25	125847	AW161885	Hs.249034	ESTs	7,0
	100380	D82349	Hs. 18551	newoblastoma (nerve tissue) protein	6.9
	114837	BE244930	Hs.166895	ESTs	6.6
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	6.6
30	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.5
20	127 6 95 125186	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous r	6.5
	118644	AA610620 AA443241	Hs.181244 Hs.336629	major histocompatibility complex, class ribosoma) protein L44	6.4 6.3
	119717	AA918317	Hs.57987	B-cell CLL symphoma 11B (zinc finger pro	6.3
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	6.1
35	113003	AW292315	Hs.7215	ESTs	5.8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.7
	101050	AU077324	Hs.1832	пецгорерії де У	5.7
	116790	AW161357	Hs.101174	microfubule-associated protein tau	5.5
40	119082	AF252297	Hs.91546	cytochrome P450 retinold metabolizing pr	5.1
40	132315	AF091086	Hs.44563	hypothetical protein	5.0
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	4.9
	126077	M78772	Hs.210835	ESTs	4.7
	126426	AA125984	II. Orto	gb:zn27h06.r1 Stratagene neuroepithelium	4.6
45	131307 123619	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	4.5
7.5	128361	AA602964 AW172570	Hs,130246	gb:no97c02.s1 NCI_OGAP_Pr2 Homo sapiens ESTs	4,4 4.3
	127003	AW816515	Hs.173540	ATPase, Class V, type 100	4.3
	100020	74101010	113.113340	ATT 600, Globe V, Upe 100	4.2
	125555	AB033064	Hs.934806	KIAA1238 protein	4.2
50	105316	AJ671245	Hs,24835	hypothetical protein FLJ14594	4.0
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.0
	106516	AL137311	Hs.234074	Homo sepiens mRNA; cDNA DKFZp761G02121 (3.9
	128132			gbmc08a07.rt NCt_CGAP_Pr1 Homo saplens	3.9
66	129012		Hs.336629	ribosomai protein L44	3.9
55	125447	AI582222	Hs.12B686	ESTs	3.8
	134676		Hs.67819	Homo saplens, clone MGC:2492, mRNA, comp	3.6
	119040		Hs.259436	ESTs, Moderately similar to PC4259 ferri	3.6
	128391	AW188326	Hs.170652	ESTs	3.5
60	123829 123949	AF251237 AA621665	Hs.112208 Hs.208957	XAGE-1 protein EST	3.4 3.4
00	126872		FIS.200507	gb:UHH-Bi3-ala-a-12-0-Ut.s1 NCL_CGAP_Su	3.4
	101266		Hs.73964	EphA4	3.3
	121309		Hs.97312	ESTS	3.3
	130637		Hs.17109	integral membrane protein 2A	3.2
65	125464			gb:yz29d09.r1 Soares_multiple_scienosis_	3.2
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	3.2
	107599	AW664072	Hs.60136	ESTs	3.2
	102681		Hs.113503	karyopherin (Importin) beta 3	3.2
70	131688		Hs.30692	p21 (CDKN1A)-activated kinese 2	3.1
70	120147		Hs.155376	hemoglobin, beta	3.1
	110343		Hs.17268	ESIs	3.1
	127664		Hs.116502	ESTs	3.0
	103076		Hs.75319	ribonucleotide reductese M2 polypeptide	3.0
75	126127			gbzb80d09.s1 Soares_senescent_fibroblas	3.0
, ,	125558 100335		He 6702	gbtyh16c10.c1 Soares infant brain 1NIB H	3.0 2.9
	133421		Hs.6793 Hs.7327	platelat-activating factor acetylhydrola claudin 1	2.8 2.8
	102581		ns.7327 Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.8 2.8
	113577		Hs.278937	PRO0470 protein	28
80	118397		Hs.161492	ESTs	2.0
	115773		Hs.38207	Human DNA sequence from clone RP4-530115	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2,8
	127262	AAB28125		gbtod71a09.s1 NCI_CGAP_Ov2 Homo sapiens	2.8

	106472	AJ207162	Hs.3815	stathmin-like-protein RB3	2,7
	125032	T74884	182013	gbtyc58d02.s1 Stratagene liver (937224)	2.7
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	2.7
5	126600	AA699949	Hs.191385	ESTs	2.7
,	120325 127256	AA195651 Al738610	Hs.104196 Hs.267967	ESTs ESTs, Moderately similar to ALU8_HUMAN	2.7 2.7
	117357	N24829	1,0,20,00	gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.7
	126735	M69113	Hs.226795	glutathione S-transferase pi	2.7
10	102745 128040	AW753865	Hs.74376	olfactomedin related ER localized protei	2.7 2.6
10	129706	AW/500486 AA443241	Hs.180610 Hs.336629	splicing factor proline/glutamine rich (ribosomal protein i.44	2.6
	107731	AA016086	Hs.272108	ESTs, Weakly similar to (38022 hypotheti	2.6
	128283	Al076570	Hs.134053	ESTs	26
15	125165 111148	W45350 AB020690	Hs.7782	gb:zc81h08.s1 Pancrestic Islet Homo sapl paraneoplastic antigen MA2	2.6 2.6
13	105577	AW852257	Hs.171391	C-terminal binding protein 2	2,6
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	2.6
	130262	D63216	Hs.153684	frizzled-related protein	2.6
20	132967 102479	AA316181 NM_001991	Hs.61635 Hs.194669	six transmembrane epithelial antigen of enhancer of zeste (Drosophile) homolog 1	2.6 2.6
20	128531	H03721	Hs.2953	ribosomal protein S15a	2.6
	128165	Al741816	Hs.125897	ESTs	2.6
	126086	H75681	11- #4F7FF	gb:yr77g01.r1 Soares fetal liver spleen	2.5
25	118957 120830	A1668670 A156B170	Hs.216756 Hs.96866	ESTs ESTs	2.5 2.5
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.5
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubliquitous TPR m	2.5
	110151	H16B35	Hs.31608	hypothetical protein FLJ20041	25
30	1313B1 133761	M92642 AF041430	Hs.26208 Hs.75922	collegen, type XVI, alpha 1 brain protein I3	2.5 2.5
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2,5
	126693	C05723		gb:C05723 Human pancreatic islet Homo sa	25
	126D21 125905	AA775894 A1678638	Hs.187516 Hs.6456	ESTs chaperonin containing TCP1, subunit 2 (b	2.5 2.5
35	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
	125743	H17151		gb:ym37a05.r1 Soares infant brain 1NiB H	25
	130580	N32368	Hs.334370	uncharacterized hypothelamus protein HBE	2.5
	113119 123110	T47910 AA486256	Hs.193510	gb:yb18b11.s1 Stratagene fetal spleen (9 EST	2.4 2.4
40	113283	T66813	Hs.12947	EST	2.4
	107711	W96141	Hs.220687	ESTE	2.4
	128992	H04150	Hs.107708	ESTs	2.4
	106111 129948	AW875398 A1537162	Hs.6451 Hs.263968	PRO0659 protein ESTs	2.4 2.4
45	125728	AW954565	Hs.57987	B-cell CLL/lymphoma \$18 (zinc finger pro	2.4
	116728	F13687	Hs.227976	EST	24
	103100 124971	NM_005574 T23800	Hs.184585 Hs.151001	LIM domain only 2 (rhombotin-9ke 1) hypothetical protein FLJ14728	2.4 2.4
	131019		Hs.306155	charionic somatomammotropin kormone 1 (p	24
50	128671	AI885045	Hs.211586	phospholnosliide-3-kinase, regulatory s	2.4
	111795		Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.4
	119127 117602		Hs.12248 Hs.44685	ESTs C3HC4-like zinc finger protein	2.4 2.4
	111898		Hs.183475	Homo saplens clone 25061 mRNA sequence	24
55	131916		Hs.34569	ESTS	2.4
	130850		Hs.20237 Hs.78546	DKFZP566C134 protein ATPase, Ca++ transporting, plasma membra	2.4 2.4
	100571 126722	L14561 N66148	Hs.11125	HSPC033 protein	24
70	123720	AA609734	Hs.112755	EST	2.4
60	113609		Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
	131136 129001		Hs.23413 Hs.107812	KIAA1273 protein BPOZ protein	2.4 2.4
	133529		Hs.74571	ADP-ribosylation factor 1	2.4
CE	107593		Hs.60051	ESTs	2.4
65	123910 128B17		Hs.179923 Hs.168640	ESTs, Weakly simiter to S65657 alpha-1C- ankylosis, progressive (mouse) homolog	2.4 2.4
	103080		Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	2.4
	128367		Hs.150742	ESTs	2.4
70	123729		Hs.278672	membrane component, chromosome 11, surfa	2.4
70	112342 114721		Hs.92614 Hs.103822	longevity assurance (LAG1, S. cerevisiae , ESTs	2.3 2.3
	127768		Hs.156187	ESTs	2.3
	127706	A1174238	Hs.186982	ESTs	2,3
75	126029 124 2 50		Hs.169359	ESTs EST, Weakly similar to 2109260A 8 cell	2.3 2.3
, ,	117265		Hs.323875 / Hs.43005	RAB9-like protein	2.3
	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DXFZp434K087 (fr	2.3
	129079		Hs.108502	hypothetical protein FLJ20150	23
80	127252 129228		Hs.94 Hs.239307	OnaJ (Hsp40) homolog, subfamily A, membe tyrosyl-tRNA synthetase	23 23
	114092		Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.3
	10925	2 BE440157	Ha.85944	ESTs	2,3
	12788	A1147408	Hs.144941	ESTs	23

	121202	A A 404002		shareGEH1 st Cooms total fahre NHOLICE	22
	121292 128797	AA401807 NM_002975	Hs.105927	gb:zv65f11.s1 Soeres_total_fetus_Nb2HF8_ stem cell growth factor; tymphocyte secr	2.3 2.3
	132985	AL045579	Hs.62113	KIAA0717 protein	2.3
_	125174	W51835	Hs.231082	EST	23
5	125401	AI204637	Hs.337585	ESTs, Highly similar to KIAA0350 [H.sapi	2.3
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	23
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.3
	123423 123258	AA598484	U= 400074	gb:ae38f04.s1 Gessler Wilms tumor Homo s ESTs, Wealdy similar to RMS1_HUMAN REGUL	2.3 2.3
10	128826	AA490929 Z40313	Hs.105274 Hs.106330	Homo saplens clone IMAGE:23371, mRNA seq	2.3
10	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC	23
	101086	AA382524	Hs.250959	histalin 1	2.3
	110679	AAJ04798	Hs.108311	ESTs, Wealdy similar to T00351 hypotheti	2.3
15	126879	D90391	Hs.1265	branched chain keto acid dehydrogenase E	2.3
15	132317	B£262438	Hs.44592	beta-1,4 mannosyltransferase	2.3
	124691 113474	R05835 R50752	Hs.110153 Hs,23856	ESTs hypothetical protein MGC5297	23 23
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	22
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.2
20	129248	W04606	Hs.171637	hypothetical protein MGC2628	2.2
	100780	BE561958	Hs.302063 -	immunoglobulin heavy constant mu	2.2
	135416	BE281018	Hs.99969	fusion, derived from t(12;16) malignant	22
	129928	Al338993	Hs.134535	ESTs	2.2
25	103319 110256	XB3492 H63947	Hs.82359 Hs.237955	tumor necrosis factor receptor superfami RAB7, member RAS oncogene family	2.2 2.2
20	120734	AA29994B	118.201 800	gb:EST12544 Uterus tumor I Homo sepiens	2.2
	111777	AK001100	Hs.41690	desmocolin 3	2.2
	128963	J03890	Hs.1074	surfactant, pulmonary-associated protein	2.2
20	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
30	134964	Al803516	Hs.272891	hippocalcin-like protein 4	2.2
	127248 125761	AA364195 R68351		gb:EST75015 Pineal gland II Homo saplens gb:yh99b03.r1 Soares placenta NbZHP Homo	2.2 2.2
	101358	M10058	Hs.12056	asialoglycoprotein receptor 1	2.2
	101613	M24283	Hs.168383	Intercellular adhesion molecule 1 (CD54)	22
35	107121	AB015427	Hs.250493	zinc finger protein 219	2.2
	118751	N74210	Hs.50454	ESTs	2.2
	128952	AL043463	Hs.8755	RaP2 interacting protein 8	2.2
	126581 127634	W73306 AA633469	Hs.306668 Hs.193283	Homo sapiens cDNA FLJ14089 fis, clone MA	2.2 2.2
40	130755	BE293520	Hs.18910	ESTs, Weakly similar to unnamed protein prostate cancer overexpressed gene 1	2.2
	132867	AF226687	Hs.58553	CTP synthase II	2.2
	126323	N77584	Hs,68644	Homo sepiens microsomal signal peptidase	2.2
	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bindi	2.2
45	125549	R20215	11- 44Cenn	gb:yg18b09.rt Soares infant brain 1NiB H	2.2
43	128059 132342	AA972446 AW16275B	Hs.145096 Hs.45232	ESTS EST Workly clayler to ALUE WILLIAM ALUE	2.2 2.2
	125722	H29796	Hs.269622	ESTs, Weakly similar to ALU5_HUMAN ALU S ESTs	2.2
	106383	AA447453	Hs.27860	Homo sapisas mRNA; cONA DKFZpS86M0723 (f	2.2
	127644	NB885B	Hs.155101	ATP synthase, H+ transporting, mitochond	2.2
50	128179	AW293689	Hs.127116	ESTs	2.2
	133461	NM_000762	Hs.334345	cytochrome P450, subtemity IIA (phenobar	2.2
	126962 112369	R12014 AW966243	Hs.20976 Hs. <i>4</i> 243	ESTs hypothetical protein FLJ 12650	2.2 2.2
	133582		Hs.75087	Fas-activated serine/threonine kinase	22
55	112276		Hs.26038	ESTs, Weakly similar to 138022 hypothet	2.2
	108743		Hs.71074	ESTs	2.2
•	133726		Hs.252716	exysterol-binding protein-related protei	2.2
	131263		Hs.24950	regulator of G-protein signalling 5	2.2
60	109929 129059		Hs.294027	ESTs	2.2 2.2
v	110724	AW016783	Hs.279583 Hs.30799	CGI-B1 protein Homo saplens cDNA FLI13471 fis, clone PL	2.2
	116962		113.00735	gbyu76g10.s1 Soares fetal liver spleen	2.2
	119232		Hs.117659	ESTs, Wealdy similar to T46481 hypotheti	2.2
15	106711		Hs.143187	hypothetical protein	2.2
65	135191		Hs.301086	cytochrome P450, subfamily IID (debrisog	22
	125822		Hs.268768	ESTs	2.2
	130215 133363		Hs.152707 Hs.71962	glioblastoma amplified sequence ESTs, Weakly similar to B36298 profine-r	2.2 2.2
	126250		Hs.321247	Homo sapiens mRNA; cDNA DKFZo586A181 (fr	2.2
70	103392		140,00,00	gb:H.saplens dbl/acbp gene exon 1 & 2.	22
-	129794	AF161399	Hs.23269	hypothetical protein FLI 13433	2.2
	100253		Hs.157425	double fromeobox, 2	2.2
	130743		Hs.18724	Homo septens mRNA; cDNA DKFZp564F093 (fr	2.2
75	125468 122662		Hs.180461	ESTs ESTs	2.2 2.2
13	133347		Hs.159293 Hs.71475	ecid cluster protein 33	2.2 2.2
	104455		Hs.157211	DKFZP58680621 protein	2.2
	116332		Hs.62620	chromosome 6 open reading frame 1	2.2
00	131163	AAD99524	Hs.23754	ESTs	2.2
80	109592		Hs.26370	ESTs	2.2
	128721 114046		Hs.266175	phosphoprotein associated with GEMs	21 21
	128434		Hs.141003 Hs.143880	Homo saplens cDNA: FLJ21691 fis, clone C ESTs	2.1 2.1
	-20.0				2.7

	103163	AU077018	Hs.3235	keratin 4	2.1
	112379	AK001713	Hs.17860	hypothetical protein FLJ10851	21
	127507	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.1
-	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
5	126153	HB5692	Hs.40730	ESTs	2.1
	122110	Al123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	21
	100554 104799	M95923 AA029703		gb:Human 12-lipoxygenase mRNA, partial c gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.1 2.1
	132664	At740461	Hs.54542	ESTs	2.1
10	114620	AA642974	12101010	gb:nr60h01,s1 NCI_CGAP_Lym3 Homo septens	2,1
		AA281562	Hs.292100	ESTs	21
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	133160	N54958	Hs.66309	hypothetical protein MGC11061	21
15	124656 133576	AW297702 M19850	Hs.102915 Hs.150741	ESTs 2,3'-cyclic nucleotide 3' phosphodieste	21 21
13	132676	N92589	Hs.261038	ESTs, Weakly similar to 138022 hypothet	2.1
	126505	AA2828B1	Hs.190057	ESTs	2.1
	118865	AA736405	Hs.54530	ESTs	2.1
20	134267	A1174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.1
20	134104	1,35253	Hs.79107	mitogen-activated protein kinase 14	21
	133493 112853	AW998046 T02843	Hs.194369	arginine-glutamic acid dipeptide (RE) re gb:FB11H5 Fetal brain, Stratagene Homo s	2.1 2.1
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.1
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, done MA	21
25	134869	AL157518	Hs.90421	PRO2463 protein	21
	128869	AA768242	Hs.80618	hypothetical protein	2.1
	129179	AW969025	Hs.109154	ESTs	2.1
	104857 101651	A)920902 AL037111	Hs.19058 Hs.75641	ESTs, Moderately similar to S65657 alpha	21 21
30	129726	H15474	Hs.132898	galactose-1-phosphate urldylyltransferas fetty acid desalurase 1	2.1
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	126271	AU250773	Hs.270012	EST8	2.1
	116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ce	2.1
35	128468	T23625	Hs.1505B0	putative translation initiation factor	21
33	116031 130724	AA452239 AK001507	Hs.103329	KIAA0970 protein Homo sepiens done FLB6914 PRO1821 mRNA,	2.1 2.1
	121897	AA427419	Hs.306084 Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.1
	123808	AA620552	1101220102	gb:ae58g11.s1 Stretagene lung carcinoma	2.1
40	122333		Hs.98977	ESTs, Moderately similar to T34561 hypot	2.1
40	127841	AW136558	Hs.125246	ESTs	2.1
	100023	DE040540	14. =040	1	2.1
	113002 111567	BE243513 F12628	Hs.7212 Hs.334786	hypothetical protein PP1044 hypothetical protein MGC16040	2.1 2.1
	113697	T97183	Hs.17992	Homo septens mRNA; cDNA DKFZp434J1726 (f	21
45	128033	A1248705	Hs.149321	ESTs	2.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.1
	112370		Hs.167344	Homo saplens clone 23911 mRNA sequence	21
	132786		Hs.56B51	hypothetical protein MGC2668	21
50	113226 117997		Hs.10697 Hs.47420	ESTs EST	2.1 2.1
20	116996		Hs.40535	ESTS	2.1
	127002		Hs.24979	hypothetical protein DKFZp761P1010	21
	122591		Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	21
55	107278		Hs.323910	v-erb-b2 avlan erythroblastic laukernia	2,1
23	103B98 110312		Hs.11896	gb:k3517,seq.F Human fetal heart, Lembde hypothetical protein FLJ12089	2.1 2.1
	127447		Hs.193482	Homo saplens cDNA FLJ11903 fls, clone HE	21
	128352		Hs.169942	ESTs	2.5
CO	113649	N94768	Hs.16400	ESTs, Wealdy similar to KIAA1435 protein	2.0
60	128275		Hs.131240	ESTs .	20
	125976		EI- OCOCO	gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	2.0
	120820 134937		Hs.96869 Hs.171939	EST ESTs	2.0 2.0
	129602		Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	2.0
65	129535		Hs.169965	chimerin (chimaenin) 1	20
	106095		Hs.11713	E74-like factor 5 (ets domain transcript	2.0
	128538		Hs.101189	ESTa	2.0
	105593		Ha.174151	aldehyde oxidase 1	2.0
70	105788 128148		Hs.23965 Hs.126637	solute carrier family 22 (organic anion ESTs	20 20
, ,	125982		113.12.007	gb:yr30e11.r1 Soares fetal liver spleen	20
	125746	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	127839	AA748762	Hs.163113	ESTs, Weakly similar to 138022 hypotheti	20
75	100661		Hs.132748	Homo saplens ribosomal protein 1.39 mRNA,	20
13	124282		Hs.110287 Hs.B32	ESTs ESTs Virghly elemiter to AA1078 integrin	2,0
	126926 100221		FB.532	ESTs, Highly similar to A41029 integrin gb:Human mRNA for ATP synthase 8 chain,	- 2.0
	126053			gb:yu62601.r1 Welzmann Olfactory Epithal	2.0
	10094		Hs.159593	mucin 6, gastric	20
80	12558	AJ272848	Hs.75309	eukaryolic translation elongation factor	2.0
	128604		Hs.102397	GIOT-3 for gonadotropin inducible transc	2.0
	11461		Hs.95456	ESTs PAY temperatura authention domain into	20 20
	13045	3 U80735	Hs.173854	PAX transcription activation domain inte	20

	400000	*******	Lib Droggo		2.0
	135060 114419	AK001887 AJ248013	Hs.259842 Hs.106532	protein kinase, AMP-activated, gamma 2 n ESTs, Wealdy similar to 138588 reverse t	2.0
	126283	N40359	Hs.271896	ESTs	2.0
_	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.0
5	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0 2.0
	127717 126893	F12209 AJ252060	Hs.173380 Hs.26320	CK2 interacting protein 1; HQ0024c prote TRABID protein	2.0
	106798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
10	103760	AA642973	Hs.163842	ubiquilin B	2.0
10	118922	AW206193	Hs.91065	hypothetical protein DKFZp761B2423	20 20
	133195 133424	AI434760 AA350994	Hs.279949 Hs.20281	KIAA1007 protein KIAA1700	20
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.0
4.5	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	2.0
15	126599	H13295	Hs.106135	ESTs	20 20
	114459 128478	AW445217 AA708205	Hs.103362 Hs.100343	ESTs ESTs	2.0 2.0
	127271	H96820	(10.100240	gb:yv99b03.rl Soares melanocyte 2NbHM Ho	2.0
20	111122	N53753	Hs.16492	DKFZP564G2022 protein	2.0
20	130695	T97205	Hs.17998	ESTs, Wealty similar to 2109260A B cell	2.0
	133571 119244	BE515037 AW407564	Hs.177556 Hs.275865	melanoma antigen, family D, 1 ribosomal protein S18	2.0 2.0
	127603	AV447/304 AI016798	Hs.9925	hypothetical protein FLJ20772	2,0
	113626	T9431B	Hs.17359	ESTs, Moderately similar to RLA4_HUMAN 6	20
25	128115	A1435590	Hs.130158	ESTs	20
	117639	AA377165 AF169301	Hs.44833	EST6	20 20
	127033 112411	R43090	Hs.9098 Hs.271510	sulfate transporter 1 ESTs, Moderately similar to ALU1_HUMAN A	2.0
	114601	AA075556	(ICILI (U) U	gb:zm8806.s1 Strategene ovarian cancer	2.0
30	127573	AA594196	Hs.269464	ESTs, Weakly similar to S65657 alpha-1C-	2.0
	125500	AW952654	Hs.244624	ESTS	2.0 2.0
	119416 115487	T97188 Al366784	Hs.48820	gb:ye50h09.s1 Soares fetal liver spleen TATA box binding protein (TBP)-associate	2.0
	126902	AA036637	Hs.107052	ESTs	2.0
35	127684	AA668631	Hs.32556	KIAA0379 protein	2.0
	126288		Hs.89576	Inner mitochondrial membrane peptidase 2	2.0 2.0
	122059 125486		Hs.98749 Hs.190587	EST, Moderately similar to T42671 hypoth ESTs	2.0 2.0
	128895		He,106985	ESTs	2.0
40	105301	AW352357	Hs.7457	MAGE1 protein	2.0
	125536		Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	121387 134126		Hs.131814	gtczu66g06.s1 Soares_testis_NHT Homo sep tankyrase, TRF1-interacting ankyrin-rela	2,0 2.0
	126860		Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.0
45	102907		Hs.202833	heme oxygenase (decycling) 1	2.0
	127804		Hs.292084	ESTs	2.0
	130566 113782		Hs.16073 Hs.311002	ESTs Homo saplens cDNA FLJ10705 fis, clone NT	1.9 1.9
	124119		Hs.248953	solute carrier family 27 (fatty acid tra	1.9
50	132490		Hs.4980	LIM domain binding 2	1.9
	125494		Hs.177543	antigen identified by monoclonal antibod	1.9
	100237 127687		Hs.306333 Hs.300635	Human PAP (pancreatitis-associated prot ESTs	1.9 1.9
	103136		Hs.247936	ollactory receptor, family 1, subfamily	1.9
55	125704		Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	126206		Hs.288548	Homo seplens cDNA FLJ12368 fis, clone MA	1.9
	131902 128860		Hs.34348 Hs.177398	Homo sapiens mRNA; cDNA DKFZp434P0235 (f ESTs	1.9 1.9
	11804		(13.1) / 330	gb:yv55f09.s1 Soares fetal liver spleen	1.9
60	13462		Hs.8700	deleted in liver cancer 1	1.9
	12743		Hs.170311	helerogeneous nuclear ribonucleoprotein	1.9
	126414 12086		Hs.24756 Hs.96952	hepatocyte growth factor-regulated tyros ESTs	1.9 1.9
	12466		Hs.102943	hypothetical protein MGC12916	1.9
65	12609		Hs.283844	similar to ret tricarboxylate cerrier-li	1.9
	10389		Hs.124186	ring finger protein 2	1.9
	12872		Hs,50651	Janus kinase 1 (a protein tyrosine kinas	1.9 1.9
	12683 12536		Hs.79933 Hs.189741	cyclin I ESTs	1.9
70	12427		1100171	gb:ys91a11.s1 Soares retina N2b5HR Homo	1,9
	12652	4 Z45455	Hs.182447	heterogeneous nuclear abonucleoprotein	1.9
	12664		Hs.270502	hypothetical protein FLJ20276	1.9
	12595 12178		Hs.33469B	gb:yo08b06,r1 Soaras adult brain N2b5HB5 Homo sapiens, clone MGC:15203, mRNA, com	1.9 1.9
75	12405		Hs.283713	ESTs, Weakly similar to \$64054 hypotheti	1.9
	13094	5 U20582	Hs.2149	actin like protein	1.9
	12634	B T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	1.9
	10355		Hs.2785	kerafin 17	1.9 1.9
80	12698 12581		Hs.21077	gbczn55g05.s1 Stratagene muscle 937209 H KIAA0532 protein	1.9
	12960		Hs.115726	KIAA1138 protein	1.9
	12600	7 H51097	Hs.143261	ESTs	1,9
	12362	?7 AA909619	Hs.112668	ESTS	1.9

	111587	Al125867	Hs.20734	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLI22237	1.9
	128897	AW979134	Hs.10700	hypothetical protein ·	1.9
5	109891	H04757	Hs.323176	ESTs	1.9 1.9
,	127704 129340	AA679609 H75334	Hs.11050	gb:ag72c02.s1 Gessler Wilms tumor Home s F-box only protein 9	1.9
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	1,9
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	1.9
10	127136	R36277	Hs.7773	Homo sapiens ublquitin conjugating enzym	1.9
IU	110636 128862	H72868 BE250742	Hs.19110 Hs.106673	ESTs eukaryotic translation initiation factor	1.9 1.9
	104689	AA420450	Hs.292911	ESTs, Highly similar to \$60712 band-6-pr	1.9
	130829	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	1.9
15	125768	AI557486	Hs.119122	ribosomal protein L13s	1.9 1.9
12	123613 127506	AA609158 T61039	Hs.291166 Hs.252574	ribosomal protein L10a	1.9
	123546	AA608817	Hs.112597	EST	1.9
	126516	R95872	Hs.117572	chemokine binding protein 2	1.9
20	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9 1.9
20	127426 112339	AA854756 R56570	Hs.124076 Hs.50547	ESTs	1.9
	129101	NM_013403	Hs. 108665	zinedin	1,9
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	1.9
25	118103	AA401733	Hs.184134	ESTs ESTs	1.9 1.9
2.5	125752 102926	AW136622 W28363	Hs.206673 Hs.239752	nuclear receptor subfamily 2, group F, m	1.9
	133975	C18356	Hs.295944	tissue factor pathway Inhibitor 2	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
30	127329	AW160551	Hs.124021	soggy-1 gens	1.8
30	126659 127297	T16245 AW629485	Hs.140720	gb:NIB1005R Normalized Infant brain, Ben GSK-3 binding protein FRAT2	1.6 1.8
	127640	A1557486	Hs.119122	ribosomai protein L13a	1.8
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	1.8
35	127964	F06298	11 00004	gb:HSC13F081 normalized infant brain cDN	1.B
33	122365 128193	AA813546 AJ224442	Hs.99034 Hs.155020	GTP-binding protein Rho? putative methyltransferase	1.8 1.8
	115173	BE612940	Hs.88252	ESTs	1.8
	125532	Al734146	Hs.271800	ESTs, Weakly similar to alternatively sp	1.B
40	126541	AJ271671	Hs.7854	zinc/ron regulated transporter-like	1.8
40	127309 129062	A1669765 AA452970	Hs.133184 Hs.155218	ESTs E1B-55kDa-associated protein 5	1,8 1.8
	126770		Hs.81361	heterogeneous nuclear ribonucleoprotein	1.8
	127775	AA12B808	Hs.179902	transporter-like protein	1.B
45	126994	AA455265	Hs.86686	ESTs, Moderately similar to I54374 gene	1.8
40	130734 114461	AW137091 AA531187	Hs.18624 Hs.126705	KIAA1052 protein ESTs	1.8 1.8
	100842		110.120,00	gb:Human anion exchanger 3 cardiac lacfo	1.8
	127389	T65128	Hs.12743	camitine O-octanoyltransferase	1.B
50	125394		Hs,173772	ESTs, Weakly similar to 178885 serine/th	1.8 1.8
50	107736 125689		Hs.60715 Hs.333256	ESTs ESTs, Weakly similar to ALUB_HUMAN ALU	1.8
	100370		Hs.184884	KIAA0167 gene product	1.B
	113479		Hs.10739	ESTS	1.8
55	105165		Hs.16079	hypothetical protein FLJ10233	1.8 1.8
5.5	120602 112399		Hs.109302 Hs.296770	ESTs KIAA1719 protein	1.8
	123474			gb:eg34b11.s1 Jla bone marrow stroma Hom	1.B
	134212		Hs.17719	EBP50-PDZ interactor of 64 kD	1.8
60	104204 127464		Hs.57655 Hs.292071	hypothetical protein FL310829 ESTs	1,8 1.8
00	116716		Hs.170283	tumor protein p53-binding protein, 1	1.8
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.8
	132380		Hs.46853	ESTs	1.8
65	120087 116356		Hs.79219 Hs.288671	RalGDS-like gene; KIAA0959 protein Homo seplens cDNA FLJ11997 fis, clone HE	1.8 1.B
05	125499		120,200011	gb:ym04c06.r1 Soares infent brain 1NIB H	1.8
	128846		Hs.285753	SCG10-like-protein	1.8
	123869		Hs.112923	EST	1.8
70	108889 126528		Hs.61481	ESTs gb:HSB87F122 STRATAGENE Human skeletal m	1.B 1.8
, ,	127629		Hs.29173	hypothetical protein FLJ20515	1.8
	130004	4 AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	1.8
	13084		Hs.20220	lipase protein	1.8
75	11162/ 13197		Hs.307478 Hs.154938	EST, Wealdy similar to 139058 hypotheti bypothetical protein MDS025	1.8 1.8
	12138		Hs.96854	ESTs, Weakly similar to DYLX_HUMAN CYTOP	1.8
	12770	5 AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	1.8
	12468	7 AA833902	Hs.270745	ESTS	1.8
80	12669 12673		Hs.145088	ESTs, Weakly similar to T15936 hypotheti gb:zv70g02,r1 Soares_total_fetus_Nb2HF8_	1.8 1.8
	12791		Hs.294111	ESTs, Moderately similar to B34087 hypo	1.8
	12840	8 Al183407	Hs.143704	EST	1.B
	12844	0 AW090340	Hs.14337	Homo saplens cDNA FLJ14407 fis, clone HE	1.8

	123783 109152	AA610112 AW380723	Hs.73451	gb:af19g05.s1 Soeres_lotal_fetus_Nb2HF8_ ESTs, Weakly similar to S55024 nebulin,	1.8
	107242	AB020672	Hs.175411	KIAA0865 protein	1,8 1.8
_	132804	A1805943	Hs.326067	hypothetical protein MGC5178	1.8
5	125387	AJ243669	Hs.8127	KIAA0144 gene product	1.8
	121578	AA398791	Hs.178185	ESTs	1.8
	132944 126295	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	1.8
	133335	A1281459 BE251012	Hs.270114 Hs.263812	ESTs	1.8
10	129879	AK001696	Hs.13109	nuclear distribution gene C (A.nidulans) Ren binding protein 11	1.8
	125175	W52355	Hs.303030	EST PARENT P	1.7 1.7
	126919	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 familin	1.7
	127773	AA725863	Hs.120508	ESTs	1.7
15	126495	AB029021	Hs.137732	KIAA1098 protein	1.7
15	126948 126671	AW968535 C03105	Hs.14328	hypothetical protein FLJ20071	1.7
	115428	AA284112	Hs.285847 Hs.94680	CGI-19 protein ESTs, Weakly similar to 178886 serine/t	1.7
	128232	AI830319	Hs.334641	hypothetical protein DKFZp43411916	1.7 1.7
20	126082	H81188	Hs.269571	ESTs	1.7
20	120467	AW292562	Hs.187628	ESTs	1.7
	124041	AW590171	Hs.101413	ESTs	1.7
	105012 123951	AF09B15B ABD12922	Hs.9329	chromosoma 20 open reading frame 1	1.7
	126449	AF223944	Hs.173043 Hs.325443	metastasis-associated 1-like 1 breast cell glutaminase	1.7
25	124554	N65961	110000110	gbza27d03.s1 Soares fetal liver spleen	1.7 1.7
	133651	Al301740	Hs.173381	dihydropyrlmidinasa-like 2	1.7
	126780	R12421	Hs.5811	chromosome 21 open reading frame 59	1.7
	125661	AA491830	Hs.25689	ESTs	1.7
30	125888 127245	H18298		gbtyn48b09.rf Soares adult brain N2b5HB5	1.7
	111223	AA323958 AA852773	Hs.334838	gb:EST26810 Cerebellum II Horno sapiens c KIAA1866 protein	1.7
	115611	R44789	Hs.33191	Homo saplens, Similar to transmembrane r	1.7 1.7
	124846	R59977	Hs.158196	transcriptional adaptor 3 (ADA3, yeast	1.7
35	100397	D84424	Hs.57697	hyaluronan synthase 1	1.7
33	127180 102598	T27097	Hs.22790	ESTs	1.7
	134076	BE250742 AF0B6215	Hs.106673	eukeryotic translation initiation factor	1.7
	115559	W99382	Hs.283709	gb:Homo saplens full length insert cDNA Ilpopolysaccharide specific response-7 p	1.7
40	125555	R19382	Hs.117869	ESTs	1,7 1.7
40	128382	AJ138886	Hs.143243	ESTs	1.7
	127710	AA682867	Hs.191901	ESTs	1,7
	125445 129951	AI452722 AL110282	Hs.7709	WW domain binding protein 1	1.7
	119898	R93325	Hs.268024 Hs.58690	Homo saplens, clone IMAGE:3873720, mRNA ESTs	1.7
45	129703	BE388665	Hs.179999	Homo sapiens, clone (MAGE:3457003, mRNA	1.7 1.7
	133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.7
	119726	AF086289	Hs.234766	skin-specific protein	1.7
	12519 0 121414	W69474 AW291477	Hs.323140 Hs.188763	ESTs	1.7
50	112542	A1458867	Hs.24276	testis expressed sequence 13A ESTs	1.7
	101368	M13058	Hs.73952	profine-rich protein Haelil subtamily 2	1.7 1.7
	125820	AA730136	Hs.75561	teratocarcinoma derived growth factor 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
55	132609 119447	U20165 W31714	Hs.53250 Hs.122856	bone morphogenetic protein receptor, typ	1.7
	113675	T81034	Hs.14841	ESTs, Highly similar to formin 2-like pr	1.7
	113701	T97301	Hs.18026	ESTs	1.7 1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to 138022 hypothet	1.7
60	127133	AA280740	Hs.292072	ESTs, Moderately similar to A45010 X-lin	1.7
UU	113316 123316	T70316 A1290561	Hs.268581	ESTs	1.7
	12263B	AL137476	Hs.155361 Hs.123609	ESTS	1.7
	105053	A1884911	Hs.32989	Homo sapiens mRNA; cDNA DKFZp43410623 (f receptor (calcitonin) activity modifying	1.7
CE	103305	X82279		gh:H.sapiens Fas, Apo-1 gene (promoter a	1.7 1.7
65	110384	H45282	Hs.268798	E8Ts	1.7
	115826 126905	AW630870	Hs.86674	ESTs, Weekly similar to hypothetical pro	1.7
	130820	AW504027 AL353934	Hs.15301 Hs.286798	Homo saplens cDNA FLJ12598 fis, done NT	1.7
	112394	AK00B373	Hs.8358	hypothetical protein FLJ21012 hypothetical protein FLJ20366	1.7
70	129589	AW504292	Hs.11517	ESTs	1.7 1.7
	126446	NM_015670	Hs.118926	sentrin/SUMO-specific protease 3	1.7
	126547	U47732	Hs.84072	transmambrane 4 superfamily member 3	1.7
	120287 129991	AF219946 R28386	Hs.102237	tubby super-family protein	1.7
75	123912	AA621283	Hs.179925 Hs.332855	ESTs, Weakly similar to ALUB_HUMAN ALU EST	1.7
	102071	AL120051	Hs.144700	ephrin-B1	1.7 1.7
	121046	AB033083	Hs.97377	KIAA1257 prolein	1.7
	128403	A1908006	Hs.295362	Homo saplens cDNA FLJ14459 fis, clone HE	1.7
80	104268 111598	AL043864 R11505	Hs.70804	ATPasa, Class II, type 9A	1.7
	128109	AW269421	Hs.268912 Hs.128093	ESTs	1.7
	125435	R08480	Hs.272138	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7 1.7
	133104	Al091195	Hs.65029	growth arrest-specific 1	1.7

	126826	AA099764		objection of Classic and Section 11	4.7
	1064B3	NM_006548	Hs.30299	gb:zn61f12.r1 Stratagene muscle 937209 H 1GF-II mRNA-binding protein 2	1.7 1.7
	129765	M86933	Hs.1238	amelogenia (Y chromosome)	1.7
	115904	Al167560	Hs.61297	ESTs	1.7
5	125514	AB040912	Hs.191098	hypothetical protein FLJ11598	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	133179	U81599	Hs.66731	homeo box B13	1.7
	115167 118036	AA749209 A1471862	Hs.43728 Hs.196008	hypothetical protein Homo sapiens cDNA FLJ11723 fis, clone HE	1.7
10	12454D	N63232	1197130000	gb:yz39a12.s1 Morton Fetal Cochlea Homo	1.7 1.7
	126183	BE018708	Hs.81972	SHC (Src homology 2 demain-containing) t	1.7
	127897	AA773681		gb:af77b12.r1 Soares_NhHMPu_S1 Homo sagi	1.7
	126660	F07097	Hs.133865	transmembrane 6 superfamily member 1	1.7
15	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.7
13	130605	BE514362	Hs.306024	FK506-binding protein 3 (25kD)	1.7
	127541 127392	AA573449 AI816736	Hs.171515 Hs.14896	ESTs DHHC1 protein	1.7
	106B79	Al 190785	Hs.33020	Homo sepiens, clone IMAGE:3939163, mRNA,	1,7 1.7
	128303	Al096444	Hs.7187	hypothetical protein FLJ10707	1.7
20	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.7
	125758	BE174587	Hs.289721	growth arrest specific transcript 5	1.7
	132332	AW978906	Hs.45005	hypothetical protein FLJ12960	1.6
	127142 128416	AW452942	Hs.130393	ESTs	1.6
25	103790	F13166 Al122044	Hs.12549 Hs.331633	ESTs, Weakly similar to 2109260A B cell hypothetical protein DKFZp566N034	1.6 1.6
	134578	AL110193	Hs.224137	hypothetical protein	1.6
	110023	AW294701	Hs.31040	ESTs	1.6
	125511	AJ271379	Hs.76194	ribosomal protein \$5	1.6
20	1114B3	R06569	Hs.269534	ESTs	1.6
30	127363	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	1.6
	126231	AA991766	Hs.300793	ESTs	1.8
	106181 114767	A1803651 A1859865	Hs.191608 Hs.154443	ESTs	1.6
	119929	W86464	Hs.304825	minichromosome maintenance deficient (S ESTs	1.6 1.6
35	132542	AL137751	Hs.263671	Homo saplens mRtNA; cDNA DKFZp43410812 (f	1.6
	127155	AA284993		gb:zt23e10.r1 Soares ovary tumor NbHOT H	1,6
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.6
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.6
40	131330	D13969	Hs.184669	zinc finger protein 144 (Mel-18)	1.6
40	129445 113427	W52452 TB5105	Hs.29797	ribosome) protein L10	1.6
	106124	H93366	Hs.15471 Hs.7587	ESTs Homo sapiens cDNA: FLI21982 fls, clone H	1.6
	128135	AA954381	Hs.269721	ESTs, Moderately similar to ALU1_HUMAN	t.6 1,6
4.5	111460	R02728	Hs.117331	ESTs	1.6
45	125636	H12382	Hs.25119	ESTs, Weakly similar to YEXO_YEAST HYPOT	1.6
	134118	BE336680	Hs.182877	KIAA0116 protein	1.6
	111570	AF059203	Hs.20580	sterol O-acyltransferase 2	1.6
	113511 113296	T89578 AW449560	Hs.189740 Hs.89576	ESTs Inner mitochondrial membrane peptidase 2	1.6
50	109875	H03260	Hs.30385	ESTs	1.6 1.6
	105930	AF016371	Hs.9880	peptidyl prolyl Isomeræse H (cyclophilin	1.6
	105564	BE816694	Hs.288042	hypothetical protein FLJ14299	1.6
	128063	Al377750	Hs.167177	ESTs	1,6
55	109779	AB029396	Hs,3353	beta-1,3-glucuronyltransferase 1 (glucur	1.6
J.J.	125334 127206	TB6569 AW816490	Hs.182118 Hs.337508	ESTs ESTs	1.6
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.6 1.8
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.6
~ 0	114062	A1560984	Hs.272B3	ESTS	1.6
60	122550	AA451859	Hs.99253	ESTs	1.6
	113413	R08872	Hs.186512	ESTs	1:6
	127019 106251	Al929355 R12607	Hs.266128 Hs.35101	hypothetical protein FLJ23329	1.6
	112570	AL138012	Hs.183840	proline-rich Gla (G-carboxyglutamic acid ESTa, Moderately similar to ALU7_HUMAN A	1.6
65	114913		Hs.58940	ESTs, Weakly similar to 138022 hypotheti	1.6 1.6
	126604		Hs.269806	ESTs	1.6
	125324			gbcyf15c06,r1 Soares fetal liver spieen	1.6
	121438		Hs.139389	ESTs	1.6
70	127289		Hs.220752	ESTs, Weakly similar to unnamed protein	1.6
70	126935 132430		Hs.89463 Hs.263105	potassium large conductance calcium acti ESTs	1.6
	133541		Hs.11050	F-box only protein 9	1.6 1.6
	102612		Hs.248124	G protein-coupled receptor 31	1.6
75	12022B	Al192528	Hs.164537	ESTS	1.6
75	122652			gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	1,6
	103456		Hs.9629	papillary renal cell carcinoma (transloc	1.6
	105355 108043		Hs.26938 Hs.160412	Homo sapiens, clone IMAGE:4053044, mRNA,	1.6
	128695		Hs.101299	ESTs callin S	1.6 1.6
80	127984		Hs.193706	ESTs, Weakly similar to ALUS_HUMAN ALU S	1.6
	124405	AA228137	Hs.25005	hypothetical protein MGC3329	1.6
	103934		Hs.134200	DKFZP564C186 protein	1.6
•	124195	H83034		gb:yq48e07.r1 Soares fetal liver spleen	1.5

	440020	N48982	Un 20074	Homo sepiens cDNA FLJ12924 fis, clone NT	1.6
	110938 102687	NM_007019	Hs.38034 Hs.93002	ublguitin carrier protein E2-C	1.6
	121226	AA364109	Hs.177990	ESTs	1.6
_	120415	AA235810		gb:zs41a03.s1 Soares_NhHMPu_S1 Homo sapi	1.6
5	123B64	AA620882		gb:af95g01.s1 Soares_testis_NHT Homo sap	1.6
	125045	A)114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	1.6
	133425	AA444390	Hs.1554B2	hydroxyacyl glutathlone hydrolase	1.6
	126578	AF151861	Hs.107528	andregen induced protein	1.6
10	102406	U43177	ll Then	(NONE)	1.6
10	114126	BE566962	Hs.7063	Homo sepiens cDNA: FLJ20913 fls, clone A	1.6 1.6
	125233 109635	WB5713 F04296	Hs.110092 Hs.169161	ESTs ESTs, Highly similar to MAON_HUMAN NADP-	1.6
	125675	BE294972	Hs.56406	Homo sapiens cDNA FLJ 13549 fis, done PL	1.6
	129707	AW572317	Hs.12082	Homo sepiens mRNA; cDNA DKFZp566L203 (fr	1.6
15	127569	A1765107	Hs.274422	hypothetical protein FLJ20550	1.6
	113302	T66919	Hs.268575	ESTs	1.6
	119705	AI984203	Hs.57874	ESTs	1.6
	127226	AL036559	Hs.3463	ribosomal protein S23	1.6
20	123489	AA599708	11. 04.000	gb:ag11a10.a1 Gessler Wilms tumor Homo s	1.6
20	107468	AA740979	Hs.91389	ESTs	1.6 1.6
	115916 127815	A1052731 AA743490	Hs,91910 Hs.255015	ESTS ESTs	1.6
	100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspert	1.6
	125568	AW615396	Hs.105613	ESTs	1.6
25	105260	N81201	Hs.31755	ESTs	1.6
	125659	T57693	Hs.87929	Horno saplens cDNA FLJ 13707 fis, clone PL	1.6
	111275	N70970	Hs.35006	ES7s	1.6
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.6
20	133423	TB4084	Hs.196008	Homo saplens cDNA FLI11723 fis, clone HE	1.6
30	124770	AA984414	Hs.120429	ESTs	1.6 1.6
	1 1793 6 134385	A)382904 M14660	Hs.47213 Hs.169274	ESTs ESTs, Highly similar to IFT2_HUMAN INTER	1.6
	108367	AW410478	Hs.104019	transforming, acidic colled-coll contain	1.6
	131143	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	1.6
35	105441	N28522	Hs.8935	quinclinate phosphoribosyltransferase (n	1.6
	128215	AA973310		gb:op91e06.s1 Soares_NFL_T_GBC_S1 Homo s	1.6
	127344	A1003929	Hs.80624	hypothetical protein MGC2560	1.6
	126478	BE541249	Hs.109697	ESTs	1.6
40	122053	AI637498	Hs.98745	ESTs	1.5
40	111760		Hs.268754	Homo sapiens cDNA FLJ11949 fls, clone HE	1.5
	112401 103023	R61279 AW500470	Hs.237536 Hs.117950	ESTs, Weakly similar to AF151067 1 HSPC2 multifunctional polypeptide similar to S	1.5 1.5
	125575		LES-1119500	gb:ym19h09.r1 Scares infant brain 1NIB R	1.5
	128765		Hs.143648	Insulin receptor substrate 2	1.5
45	108935		Hs.67991	hypothetical protein DKFZp434G0522	1.5
	121221	Al140708	Hs.97461	ESTs	1.5
	120091		Hs.59558	EST	1.5
	107375		Hs.251064	high-mobility group (nonhistone chromoso	1.5
50	125803		Hs.29852	ESTs	1.5
50	115132 113346		Hs.71433 Hs.14318	ESTs Homo sepiens clone IMAGE:113399 mRNA seq	1.5 1.5
	107357		Hs.103501	modopsin kinase	1.5
	125443		Hs.177592	ribosomal protein, large, P1	1.5
	133803		Hs.76305	surfactant, pulmonary-associated protein	1.5
55	113378	T80738	Hs,14757	ESTs	1.5
	105540		Hs.9265	hypothetical protein FLJ20917	1.5
	127446		11	gb:HSC3HE011 normalized Infant brain cDN	1.5
	134075		Hs.78979 Hs.190632	Golgi apparatus protein 1	1.5 1.5
60	127585 125824		Hs.190032 Hs.286013	ESTs short coiled-coll protein	1.5
	127606		Hs.136552	ESTs	1.5
	126585		Hs.92909	SON DNA binding protein	1.5
	107757		Hs.280792	hypothetical protein FLJ12387 similar to	1.5
~-	109978		Hs.2252B	ESTs	1.5
65	132297		Hs.265317	hypothetical protein MGC2562	1.5
	115784		Hs.54873	tumor necrosis factor (ligand) superfami	1.5
	127880		Hs,73818	ubiquinol-cytochroma c reductase hinge p	1.5
	102305 102866		Hs.90073	chromosome segregation 1 (yeast homolog) plasminogen activator, urokinase	1.5 1.5
70	133457		Hs.77274 Hs.333509	alkaline phosphetase, placental-like 2	1.5
, 4	130339		12000000	gb:zt/9e03.s1 Soares_testis_NHT Homo sap	1.5
	12544		Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.5
	123470	AW303265	Hs.303632	Human DNA sequence from clone RP11-110H4	1.5
75	10002				1.5
75	12706		Hs.331564	Homo saplens mRNA; cDNA DKFZp434H1215 (f	1.5
	12794		Hs.123598	EST\$	1.5
	\$1155. 11600:		Hs.20373 Hs.44238	EST ESTs, Weakly similar to S65657 alpha-1C-	1.5 1,5
	11985		Hs.44238 Hs.46824	ESTs	1.5
80	10650		Hs.64652	hypothetical protein MGC15563	1.5
	12412		Hs.144515	Homo saplens cDNA FLJ11672 ffs, clone HE	1.5
	12671	3 AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	1.5
	12647	5 AW959075	Hs.238797	ESTs, Moderately similar to 138022 hypot	1.5

	400054	D40044	1) 407505	rer-	1,5
	126851 104820	R40611 AW162768	Hs.137565 Hs.22620	ESTs	1.5
	127235	AI817309	Hs.225583	ESTs, Weakly similar to 2004399A chromos	1.5
_	126552	AF168711	Hs.159397	x D10 protein	1.5
5	127523 131692	AA617637	Hs.30736	gb:np34h12.s1 NCI_CGAP_Lu1 Homo sapiens KIAA0124 protein	1,5 1,5
	112974	BE559681 AL353965	Hs.101174	microlubule-associaled protein tau	1,5
	118921	N91914	Hs.54751	ESTs	1.5
10	100676	X02761	Hs.287820	fibronectin 1	1.5
10	127721 115254	T59578	Hs.188440	ESTs, Weakly similar to ALUF_HUMAN !!!! ESTs, Weakly similar to S65657 alpha-1C	1.5 1.5
	128173	AA279024 AI457242	Hs.269316 Hs.127024	ESTS	1.5
	126846	AA663527	Hs,116910	ESTs	1.5
1 5	125294	R40025	Hs.106551	ESTs	1.5
15	127494 134191	AW978730 W26632	Hs.291956 Hs.7979	ESTs, Weekly similar to ALUS_HUMAN ALU S KIAA0736 gene product	1.5 1.5
	107394	AA864798	Hs.186180	Homo saciens cDNA: FLJ23038 fis, clone L	1.5
	131562	NM_903512	Hs.28777	H2A histons family, member L	1.5
20	127310	AW450671	Hs.189284	ESTs	1.5
20	122359	AA523486	U., 402704	gb:ni67f11.s1 NCl_CGAP_Pr12 Homo saplens	1.5 1,5
	100524 128422	M80902 T77794	Hs.183704	ubiquitin C gb:yd20d09.r1 Soares felst liver spleen	1.5
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.5
25	126784	T81887	Hs.108854	HSPC163 protein	1.5
25	123343 105458	AI761902 AW954377	Hs.99597 Hs.26412	ESTs ring finger protein 26	1.5 1.5
	112266	A1652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.5
	127622		Hs.97883	ESTs	1.5
20	113659	R06545	Hs.189781	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.5
30	115892	A1573283	Hs.38458	ESTs	1.5 1.5
	126995 111657	NM_014351 R07364	Hs.189810 Hs.265667	aultortranferase family 4A, member 1 ESTs, Wealdy similer to ALU1_HUMAN ALU	1.5
	100243	AB028125	Hs.77854	regucalcin (senescence marker protein-30	1.5
25	116153	AF107203	Hs.57937	etexin 2-binding protein 1	1.5
35	108892		Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f leptin receptor overlapping transcript-1	1.5 1.5
	113294 126691	A1037922 W03046	Hs.11000 Hs.283664	aspartata beta-hydroxylase	1.5
	106979		Hs.289053	hypothetical protein FLJ14733	1.5
40	125546	H09950		gb:ym01d12.r1 Source intent brain 1NIB H	1.5
40	113990		Hs.83097	hypothetical protein FLJ22955	1.5 1.5
	129295 125431		Hs.110121 Hs.755B4	SEC7 homolog polymyositis/scleroderma autoantigen 2 (1.5
	112558		Hs.15921	hypothetical protein FLI10759	1.5
15	122046		Hs.107319	ESTs	1.5
45	122472 130753		Hs.128652 Hs.189	ESTs phosphodiesterase 4C, cAMP-specific (dun	1.5 1.5
	191714		Hs.31016	putative DNA binding protein	1.5
	101233		Hs.878	sorbital dehydrogenase	1.5
50	109501		Hs.90436	sperm associated antigen 7	1.5
50	126984 125765		Hs.256533 Hs.76941	ESTs, Weakly similar to S11998 finger pr ATPase, Na+/K+ transporting, beta 3 poly	1.5 1.5
	127693		113.10341	gb:zj68b11.s1 Sozies_felel_fiver_spleen_	1.5
	128453	X02761	Hs.287820	fibronectin 1	1.5
55	119418		Hs.221711	ESTs, Weakly similar to ALU1_HUMAN ALU guanine nucleotide binding protein (G pr	1,5 1,6
55	132669 116708		Hs.293981 Hs.70001	ESTs, Moderately similar to JC6169 nucl	1.5
	122420		12010001	gb:zw86f11.s1 Soares_total_fetus_Nb2HF8_	1.5
	100238		Hs.348	calcium/calmodulin-dependent protein kin	1.5
60	109710 105704		Hs.12929 Hs.75431	hypothetical protein FLJ20721 finhogen, gamma polypeptide	1.5 1.5
00	112712		Hs.330761	ESTs	1.5
	10009			gb:Homo saplens delayed rectifier potass	1.5
	11412		Hs.12751	EST's	1.5
65	132397 107881		Hs.4750 Hs.61273	hypothetical protein DKFZp654K0822 hypothetical protein MGC2650	1.5 1.5
05	10630		Hs.18397	hypothetical protein FLJ23221	1.5
	12589		Hs,92287	Homo saplens mRNA; cDNA DKFZp564C2478 (f	1.5
	10495		Hs.10026	mitochondrial ribosomal protein L17	1.5
70	10290 12555		Hs.2693 Hs.279877	glioma-associated oncogene homolog (zinc call division protein FtsJ	1.5 1.5
, 0	10963		Hs.183646	ESTs	1.5
	11660	7 W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.5
	12717			gb:yf54b08.r1 Soares infant brain 1NIB H	1.5
75	11081 12598		Hs.285901	Homo saplens, clone IMAGE:3948563, mRNA, gb:37e10 Human retina cDNA randomly prim	1.5 1.5
, 5	11509		Hs.3542	hypothetical protein FLJ31273	1.5
	12120	7 AA705799	Hs.183714	ESTs	1.5
	11265		Hs.235782	solute cerrier family 21 (organic anion	1.5 1.5
80	12521 12591		Hs.109299 Hs.278712	protein tyrosine phosphatase, receptor t eukaryotic translation initiation factor	1.5
	13304		Ha.63609	Hpall tiny fragments locus 9C	1.5
	12279	1 Al122055	Hs.129836	KIAA1028 protein	1.5

	Table 268		
	Pkey:		Unique Eos probesat identifier number
_	CAT number:		Gene cluster nomber
5	Accession:		Genbank accession numbers
	Pkey	CAT number	Accession
	108451	13766_27	AAD79195 AA084965 AA126308 AA084956
10	124195	2606_3	H83034 H52379
	123619 125165	371681_1 1852047_1	AA602964 AA609200 W45350 W45406
	125324	1692163_1	R07785 T85948 T86972 -
	126053	1601238_1	H64450 H64464
15	126086	1606216_1	H75681 H70975
	126098 125464	1629789_1 168460_1	M79088 N88221 N71807 AA203399
	125499	1562851_1	
20	126127	1205826_1	N95428 W24040 AW751366 H81987
20	125546 125549	356478_1 1702179_1	H09950 R18413 AA570553 AW973425 R20215 R18767
	125558	1703083_1	R59305 R19748
	125575	1566885_1	H14983 R21554
25	125743	5025_5	H17151 H11956 R68351 R68364
LJ	125761 126426	1744008_1 110687_1	AA125984 AA127189 AA065075 AA070377 AA100017
		_	AAD79891 AA113255 AAD75168 AAD82764 AAD83380 NB4829 AAD84752 AAD76512 AAD85119 AAD85208 AAD85045
	127155	200358_1 1695805_1	AA284993 AA478122 AA477923
30	127175 126528		R11937 Z45532 Z24895 AW691336 R01294
-	125957	1583542_1	H41694 H45213
	125976	296453_1	AA436760 AW237453 BE327496 N47347 N56967
•	125982 12598B	1766315_1 1365728_1	
35	127245	226662_1	AA323958 AA370268
	127248	227560_1	A384195 A325029 AW962050 AA909475 AA92407 AA909655
	127262 126659	231725_1 1541209_1	AAB28125 AAB34883 AA330555 T16245 R19694 F13545 H10299 T66048 T65279 H18006
40	126693	87363_1	C05723 AA018342
40	127315 126730	37938_1 297653_1	AF116622 A1114507 AA640834 AA377999 AA442429 T19477
	103898	1872133	AAZABB4
	127446	16001_2	F13008 T75435
45	126826 126872	127356_1 142696_1	AA099764 AA112950 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073, BE168945 AA609064 AW238038 BE011212 BE011359 BE011367
-1.5	123012	142000_1	BE011368 BE011362 BE011215 BE011365 BE011363
	128132	177100_1	AA225632 AI820970 AI820952 AA226472 AI732140 AI732059 AA226307
	127523	351071_1	AA225500 AA617637 AA564963
50	126982	171753_1	AA211419 AA211565
	128215	5303451	AASTS110
	127704 127705	40569Q_1 9662B3_2	AA679609 AA694592 AJ003322 AJ003324
e e	128422	1811283_1	T77794 TB5681
55	127897	446527_1 208882_1	AA773681 AA773857 AA299848 AA299849
	120734 100098	2511713	
	114620	32062_8	AA642974 AA084223
60	122652 100842		2640190 AA454641 Ggr HT4398 U05697
O.	123783		genbank_AA610112
	125032		genbank_T74884
	123808 123864		genbank_AA620552 genbank_AA620882
65	118049		genbank_N53145
	102406		entrez_U43177
	116962 134076	40321_1	genbenk_1479677 AF086215 W02702 AA284288 W25655
70	125888	266863_1	H18296 H46830
70	127271 113119	321389_1	H96820 H79463 oenbank T47910 T47910
	104799		genbank_747910 T47910 genbank_AA029703 AA029703
	127693	790317_1	ÃA676727 AA704704
75	120415 127984	125151 1	genbank_AA235810 AA235810 F06298 R18057
, ,	122359	135151_1	681003_1 AA523486 AW025780 AIB21560 AA443898
	122420		genbank_AA446971
	124276 101447		genbank_H83465 entrez_M21306
80	124540		genbank_N63232
	124554		genbank_N65961
	117357 103305		gentrank_N24829 entrez_X82279

	103392	entrez_X94563
	119416	genbank_T97186
	105225	genbank_AA211777
,	121292	genbank_AA401807
5	112853	genbank_T02843
	121387	genbank_AA405854
	114601	genbank_AA075566
	100221	entrez_D28383
4.0	130339	genbank_AA435746
10	100554	ilgr_HT2241
	123423	genbank_AA598484
	123474	genbank_AA599209
	123489	genbank_AA599708

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TABLE 27A: ABOUT 895 GENES UP-REGULATED IN COMBINED LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 27A lists about 895 genes that are upregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with the normal "body map" samples. These were selected from about 59680 probesets on an Affyredrity/Eos Hu03 GeneChlp array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90* percentile amongst fibrosis samples. The "average" normal adult tissue level was set to the 95* percentile amongst normalignant tissues. In order to remove gene-specific background lavels of non-specific hybridization, the 15* percentile value amongst normalignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

~=		
25	Pkey:	Unique Eos probeset Identifler number
	ExAcen:	Exemplar Accession number, Genbank accession number
	Unigene!D:	Unigene number
	Unigene Title	a: Unigene gene title
30	R1:	Ratto of fibrosis to normal body tissue
211		

30	• • • • • • • • • • • • • • • • • • • •			v.,	
50	Picey	ExAcon	Unigene ID	Unigene Title R1	
	431164	AA493650	Hs.94367	Homo saplens cDNA: FLJ23494 fis, clone L	56.0
	424917	Al636208	Hs.96901	Homo sapiens cDNA: FL123049 fis, clone L	26.5
35	453310	X70697	Hs.553	solute carrier family 6 (neurobransmitte	25.5
	457200	U33749	Hs.197764	thyroid transcription factor 1	22.2
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	21.1
		W25140	Hs.110667	ESTs	19.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitlal	19.1
40	442006	AW975183	Hs.292663	ESTs	18.8
	445885	A1734009	Hs.127699	KIAA1603 protein	18.0
	440452	AJ925138	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	17.8
	422426	W79117	Hs.58559	ESTs, Weakly similar to motekin [M.musc	17.4
	444929	Al685841	Hs.161354	ESTs	16,5
45	440807	AW269421	Hs.128093	EST8	16.3
	408826	AF216077	Hs.4B376	Homo sapiens clone HB-2 mRNA sequence	14.2
	446967	Al699629	Hs.156781	ESTs	13.3
	417801	AA4173B3	Hs.82582	integrin, beta-like 1 (with EGF-like rep	12.3
	437119	Al379921	Hs.177043	ESTs	12.3
50	451103		Hs.25956	DKFZP5640206 protein	11.5
	443450		Hs.133529	ESTs	11.4
	411880			gb:hm30f03.x1 NCI_CGAP_Thy4 Homo septens	11.3
	432519		Hs.130704	ESTs	11.3
EE	414142		Hs.150042	ESTs	11.0
55	433283		Hs.175622	ESTs .	10.1
		AW444B04	Hs.202655	€8Ts	10.1
	452039		Hs.172510	ESTs	10.0
	417204	N81037	Hs.1074	surfectant, pulmonary-associated protein	9.9
60	421952		Hs.98849	ESTs, Moderately similar to AF161511 1 H	9.6
OU	412372 426274		Hs.118615	ESTS	9.8 9.7
	431007		Hs.2007 Hs.248211	lumor necrosis factor (ligand) superfami	. 9.4
	443709		Hs.134662	retinoblastoma-bloding protein 9 ESTs	9.3
	446232		Hs.165547	ESTs	9.2
65	448253		Hs.201591	ESTs	9.2
0.0	432133		Hs.272587	KIAA1262 protein	9.1
	409238		Hs.51515	Homo saciens mRNA; cONA DKFZp564G112 (fr	9.0
	431353		Hs.189076	ESTs	8.8
	450050		Hs.257883	ESTs	6.0
70	458194		Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	0.8
	414968		Hs.297777	ESTs	8.7
	425664		Hs.159003	transient receptor potential channel 6	8.7
	408562		Hs.31141	Homo saplens mRNA for KIAA1568 protein,	8.6
	453672	U73531	Hs.34526	G protein-coupled receptor	B. 5
75	429420	AK001579	Hs.202289	hypothetical protein FLJ10376	8.5
	421478	AI683243	Hs.97258	ESTs	8,4
	404916				8.4
	444396		Hs.4257	ESTs	8.3
90	442275		Ha.54795	ESTs	8.3
80	437479		Hs.101277	ESTs	8.2
	432203		Hs.49	macrophage scavenger receptor 1	8.2
	431433		Hs.253495	surfactant, pulmonary-associated protein	7.9
	406747	A)925153	Hs.217493	annexin A2	7.8

	AAEEOT	AJ245671	Hs.12844	EGF-]Bo-domain, multiple 6	7.7
	445537 450025	AK001875	Hs.24321	Homo saptens cDNA FL/12028 fis, clone HE	7.6
	421798	N7488D	Hs.264330	N-acylsphingosine amidohydrotase (acid c	7.5
5	421155	H87879	Hs.102267	lysyl oxidase	7.5 7.5
5	446917 422798	AL347863 R92347	Hs.156672 Hs.34574	ESTs ESTs	7.3 7.4
	426830	AA385751	Hs.160392	ESTs	7.4
	437157	BE048560	Hs.120655	ESTs	7.4
10	433231	AB040926	Hs.143552	KIAA1493 protein	7.3
10	451561 430656	N52812 AA482900	Hs.177403 Hs.162080	ESTs ESTs	7.1 7.1
	448206	BE622585	Hs.3731	ESTS	7,1
	420209	AA256444	Hs.32295	Homo saplens cONA FLJ12604 fis, clone NT	7.0
1.5	426803	AA382568	Hs.179747	ecotropic viral integration site 5	6.9 6.9
15	427383 409718	NM_005411 D86640	Hs.177582 Hs.56045	surfactant, pulmonary-associated protein src homology three (SH3) and cysteine ri	6.8
	443324	R44013	Hs.164225	ESTs	6.B
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	6.8
20	427356	AW023482	Hs.97849	ESTS	6.7
20	418735 429945	N48769 NM_006729	Hs.44609 Hs.226483	ESTs diaphanous (Drosophila, homolog) 2	6.7 6.6
	407510	V96191	118.22.0100	gb:Human trophoblast hypoxia-regulated f	5.6
	430099	AW194988	Hs.20537	Homo sapiens cDNA FLJ 13942 fis, clone Y7	6.6
25	441835	AB036432	Hs.184	advanced glycosylation end product-speci	6.5 6.5
25	428506 438202	BE252383 AW169287	Hs.184668 Hs.22588	SBBI31 protein ESTs	6.5
	441233	AA972965	Hs.135568	ESTs	6.4
	433384	A\021992	Hs.124244	ESTs	6.3
20	427043	AA397679	Hs.298460	ESTs	6.3
30	425921 438909	NM_007231 AF085839	Hs.162211	solute carrier (amily 6 (neurotransmitte gb:Homo sapiens full tength Insert cDNA	6.3 6.3
	433365	AF026944	Hs.293797	ESTs	6.3
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.2
25	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.2
35	431337	N48107	Hs.292593 Hs.291541	ESTs ESTs	6.1 6.0
	434819 458219	AA650099 H22195	Hs.31874	ESTs	6.0
	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fasciclin	5.9
40	435933	AA805520	Hs.192075	ESTs	5.9
40	436954 445424	AA740151 AB028945	Hs.130425 Hs.12696	ESTs cortactin SH3 domain-binding protein	5.9 5.8
	449108		Hs.98328	ESTs	5.8
	410334		Hs.291993	ESTs	5.7
15	447112		Hs.7154	ESTs	5.7
45	447700 449208		Hs.171077 Hs.48643	ESTs, Weakly similar to similar to serin ESTs	5.7 5.7
	445657		Hs.279575	EST8	5.7
	421554		Hs.97775	ESTs, Weakly similar to Testis-specific	5.7
50	435299		Hs.122614	ESTs, Weakly similar to apoptotic protes	5.6
30	416769 433527		Hs.115436 Hs.133020	ESTs ESTs	5.6 5.6
	452771		113.200020	gb:EST03366 Fetal brain, Stratagene (cat	5.6
	427585		Hs,179729	collagen, type X, alpha 1 (Schmid metaph	5.5
55	411514		Hs.18995	KIAA1304 protein	5.5 5.5
33	424084 444527		Hs,20914 Hs.11383	Homo sapiens cDNA: FLJ23056 fis, clone L small inducible cytokkie subfamily A (Cy	5.4
	429710		Hs.146025	Homo saplens cDNA: FLJ23694 fls, clone L	5.4
	432113		Hs.152365	ESTs .	5.4
60	447997		Hs.29792	ESTs	5.4 5.3
UU	449328 416579		Hs.197647 Hs.38383	ESTs ESTs	5.3
	43200		11220000	gb:Homo sapiens mRNA; cDNA DKFZp761G2123	5.3
	434084	B AF116677	Hs.249270	hypothetical protein PRO1968	5.3
65	44434		Hs.10887	similar to lysosome-associated mambrane	5.2 5.2
UJ	41429 43104		Hs.71730 Hs.105276	ESTs ESTs	5.2
	44810		Hs.178391		5.2
	44527		Hs.22245	ESTs	5.1
70	40897		Hs.49421	Homo sapiens mRNA; cDNA DKFZp434M0728 (f gb:HUM042H10B Clontech human fetal brain	5.1 5.1
70	41509 42824		Hs.42500	ADP-ribosylation factor-like 5	5.1
	45278		Hs.151256		5.1
	45543		Hs.80738	stalophorin (gpl.115, leukoslalin, CD43)	5.1
75	44941		Hs_246311		5.1 5.1
13	42165 40763		Hs.106511		5.0
	44616		Hs.19932		5.0
	41304	8 M93221	Hs.75182	mannose receptor, C type 1	5.0
80	44660		Hs.25784		4.9 4.9
30	41980 44716		Hs.17518	gb:yi75f11.s1 Soares placenta Nb2HP Homo Homo saplens cig5 mRNA, partial sequence	4.9
	4426		Hs.20137	B ESTs, Weakly similar to KIAA0944 protein	4.9
	42949	6 AA453800	Hs.19279	3 ESTs	4.8

	429859	NM_007050	Нь.225952	protein tyrosine phosphatase, receptor t	4.8
		AK001783		hypothetical protein FLJ10921	4.8
	425509	AF079363	Hs.158213	sperm associated antigen 6	4.8
_		H03754	Hs.152213	wingless-type MMTV integration site famil	4.8 4.8
5		AI248584 AF070641	Hs.190745 Hs.10684	Homo sepiens cDNA: FLJ21326 fls, clone C Homo sepiens clone 24421 mRNA sequence	4.0 4,7
		AA709285	Hs.5997	Horno sapiens cDNA FLJ13078 fis, clone NT	4.7
		A)357412	Hs.157601	ESTs	4.7
10		AA810278	Hs.24250	ESTs	4.7
10		AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	4.7 4.7
		A1673025 AA497043	Hs.43874 Hs.115685	ESTs ESTs	4.7
		AI027604	Hs.159650	ESTs	4.7
1.5		AI871833		gb:wm51h09.x1 NCI_CGAP_Ut2 Homo seplens	4.7
15		AI220547	Hs.135223	ESTs	4.7 4.7
	422352 424105	AA766296 Al142336	Hs.99200 Hs.43977	ESTs ESTs	4.6
	439759	AL359055	Hs.67709	Home sapiens mRNA full length insert cDN	4.6
-00	428227	AA321649	Hs.2248	small Inducible cytokine subfamily 8 (Cy	4.6
20	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.6 4.6
	425804 435347	BE501698 AW014873	Hs.258189 Hs.116963	ESTs ESTs	4.6
	446002	A)346468	Hs.145789	ESTS	4.6
	452883	X80031	Hs.150318	ESTs	4.6
25	442176	AA983764	Hs.128910	ESTs	4.6
	443253	AJ041212 U29615	Hs.132117 Hs.91093	ESTs chilfnase 1 (chitotriosidase)	4.5 4.5
	419556 439920	H05430	Hs.144455	ESTs	4.5
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	4.5
30	434424	Al811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L	4.4
	408625	AW243323	Hs.266785	ESTS	4.4 4.4
	449299 450656	AA299919 AA010539	Hs.18912	gb;EST12592 Uterus tumor 1 Homo sapiens ESTs	4.4
	433815	AI696602	Hs.112757	ESTs	4.4
35	416879	H98899	Hs.42599	ESTs	4.3
	432182	AW607789	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.3 4.3
	445386 450478	AJ422005 AW451709	Hs.160380 Hs.271200	ESTs	4.3
	453080	A1423056	Hs.23921	Homo saplens cONA FLJ12482 tis, clone NT	4.3
40	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	4.3
	443257	A1334040	Hs.11614	Homo sapiens cDNA: FLJ23555 fis, clone L	4.3 4.3
	453921 419721	A1824009 NM_001650	Hs.44577 Hs.288650	ESTs aquaportn 4	4.2
	432316	AW973235	Hs.293697	ESTs	4.2
45	435202	AI971313	Hs.170204	KIAA0551 protein	4.2
	440320	AA879294	11 40000	gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	4.2
	438796 400269	W67821	Hs.109590	genethonin 1	4.2 4.2
	447724	AW298375	Hs.24477	ESTs	4.1
50	446509	AF169693	Hs.132892	protocadherin 20	4,1
	451620	AW449888	Hs.257224	ESTs	4.1 4.1
	451963 456408	A1825440 A1288348	Hs.224952 Hs.23450	ESTs mRNA for FLJ00023 protein	4,1
	425895	A1269484	Hs.161427	zinc finger protein 215	4.1
55	447048	080666MA	Hs.228320	Homo sapieля cDNA: FLJ23537 fls, clone L	4.1
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	4.0
	415929 426625	AA724373 T78300	Hs.295306 Hs.171409		4.0 4.0
	434334		Hs.116750		4.0
60	437138		Hs.271245	ESTs	4.0
	455024	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo	4.0
	436246		Hs.119991	ESTs ESTs	4.0 4.0
	416030 459267		Hs.21948	gb:AJ003631 Selected chromosome 21 cDNA	3.9
65	445122		Hs.147377		3.9
	414812		Hs.77367	monokine induced by gamma interferor	3.9
	421160		Hs.102301		3.9 3.9
	425734 429208		Hs.159396 Hs.190478		3.9
70	442957		Hs.49397	ESTS	3.9
	444050	AW138295	Hs.135024	ESTS	3.9
	444078		Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.9 3.9
	451024 442832		Hs.253569	gb:zw63b0Br1 Soares_lolal_felus_Nb2HF8_) ESTs	3.9
75	423377		المردي ا	gb:Homo sagiens mRNA; cDNA DKFZp586H0718	3.9
• •	451895	5 T93573	Hs.16970	ESTs	3.9
	442353		Hs.49136	ESTs	3.8
	421464		Hs.190080	6 ESTS	3.8 3.8
80	404043 407053			gb:H.saplens DNA for endogenous retrovir	3.8
	41000			gb:zm20h12.s1 Strategene pancreas (93720	3.B
	41024	7 AF181721	Hs.61345	RU2S	3.8
	41746	1 R38403	Hs.13305	ESTs	3,8

	102000	4 4 0000 10	U- Admon		20
	423609 440444	AA328348 AA885221	Hs.218269 Hs.156984	ESTs ESTs	3.8 3.8
	446254	BE179B29	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT	3.B
	447505	ALB49266	Hs.1B724	Homo sapiens mRNA; cDNA DXFZp564F093 (fr	3.8
5	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	3.8
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	3.8
	444271	AW452569	Hs.149B04	ESTs	3.B
	434217	AW014795	Hs.23349	ESTs -	3.8
10	452571	W31518	Hs.34665	ESTs	3.7
10	423575 408771	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	3.7 3.7
	431322	AW732573 AW970622	Hs.475B4	polassium voltaga-gated channel, delayed gb:EST382704 MAGE resequences, MAGK Homo	3.7
	445034	AW293376	Hs.160323	ESTs	3.7
	438842	AA827176	Hs.124316	ESTs	3.7
15	424906	Al566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	415025	AW207091	Hs.72307	ESTS	3.7
	420313	AB023230	Hs.96427	KIAA1013 protein	3.7
	423448	AK000776	Hs.128753	Homo saplens cDNA FLJ20769 fls, clone CO	3.7
20	433492	AW605849	11 044001	gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.7
20	434636 435747	AA083764 A1079519	Hs.241334	ESTs	3.7
	45B158	AW29677B	Hs.134398 Hs.300357	ESTs ESTs, Highly similar to d3416F21.2 [H.sa	3.7 3.7
	419261	X07876	Hs.89791	wingless-type MMTV Integration site famil	3.7
	410060	NM_001448	Hs.58367	glypican 4	3.7
25	426116	AA868729	Hs.144694	ESTs	3.7
	409203	AA780473	Hs.687	cytochrome P460, subfamily IVB, polypept	3.7
	414259	W44633	Hs.25044	Home saplens cDNA: FLJ23131 fis, clone L	3.7
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.6
30	431889	AA521277	Hs.124946	ESTs	3.6
50	430414 433426	AW365665 H69125	Hs.120388 Hs.133525	ESTs ESTs	3.6 3.6
	421764	A)681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.6
	410785	AW803341	110,000 72	gb:IL2-UM0079-090300-050-D03 UM0079 Homo	3.6
	455235	AW875951		gb:CM1-PT0013-131299-067-109 PT0013 Homo	3.6
35	408399	NM_005426	Hs.44585	turnor protein p53-blnding protein, 2	3.6
	429784	MB9796	Hs.30	membrane-spanning 4-domains, subfamily A	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	3,6
40	432837 452166	AA310693 Al948607	Hs.279512 Hs.264680	HSPC072 protein	3.6
40	458154	AW816379	115.204000	ESTs gb:QV4-ST0234-181199-035-g01 ST0234 Homo	3.5 3.5
	420352	U79734	Hs.97206	huntingtin interacting protein 1	3.5
	424202	BE350295	Hs.15032	ESTs, Weakly similar to RAN binding prot	3.5
	410658	AW105231	Hs.192035	ESTs	3.5
45	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	419503	AA243642	Hs.137422	ESTs	3.5
	439479	AI734258	Hs.245367	ESTS, Weakly similar to ALU1_HUMAN ALU S	3.5
	448404	BE089973	13- 444000	gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.5
50	424268 420637	AA397653 AW976153	Hs.144339	Human DNA sequence from clone 495010 on gb:EST388262 MAGE resequences, MAGN Homo	3.5
50	450715	AJ266484	Hs.31570	ESTs, Weekly similar to KIAA1324 protein	3.5 3.5
	428927	AA441837	Hs.90250	ESTs	3.5
	422544	AB018259	Hs.118140	KIAA0716 gene product	3.4
	431207	AA495925	Hs.9394	ESTe	3.4
55	42450B	AL080103	Hs.149770	Homo saplens cONA FLI13658 fis, clone PL	3.4
	441484	AA9354B1	Hs.56972	ESTs	3.4
	425916	NM_006786	Hs.162200	urotensin 2	3.4
	401793 431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.4 3.4
60	438038	Al732629	Hs.194161	ESTs, Weakly similar to TAZR HUMAN, BETA	3.4
	439619	AW975998	Hs.58595	ESTs	3.4
	446577	AB040933	Hs.15420	KIAA1500 protein	3,4
	450445		Hs.194563	EST8	3.4
C 5	459482		Hs.237052	EST, Weakly similar to ALU1_HUMAN ALU SU	3.4
65	445495		Hs.38489	ESTs	3.4
	428743		Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.4
	426320 432869		Hs.169300	transforming growth factor, beta 2	3.4
	419235		Hs.288433	gb:EST386197 MAGE resequences, MAGM Homo neurotrimin	3.3 3.3
70	429703		Hs.28705	ESTS	3.3
	413499			gb:CMO-HT0182-041099-065-e11 HT0182 Hamo	3.3
	406182			-	3.3
	417307		Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	3.3
75	430140		Hs.221999	ESTs	3.3
75	435111		Hs.157212		3.3
	449729 457620		Hs.29235	ESTs gb:np03b06.s1 NCt_CGAP_Pr2 Homo sapless	3.3
	428434		Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	3.3 3.3
	406554		110,000001	Cold trough agrice ford, 117350 11 COMO	3.3 3.3
80	451381			gb:TCAAP2E0011 Pediatric acute myelogeno	3.3
	443113	AI040686	Hs.132908	ESTs	3.3
	421470		Hs.1378	annexin A3	3.3
	446428	AW082270	Hs.210617	ESTs, Westly similar to ALU4_HUMAN ALU S	. 3.3

	435031	A1632091		ESTs	3.3
	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	3.2
	429228	A1553633		ESTs	3.2 3.2
5	420252 423629	AW270404 AW021173	Hs.193161 Hs.18612	ESTs Homo sapiens cDNA: FLJ21909 fis, clone H	3.2
•	444339	T96555	Hs.31562	ESTs	3.2
	434164	AW207019	Hs.148135	ESTs	3.2
	404599	A A2027E4	Un 122121	ESTs	3,2 3.2
10	426920 453736	AA393351 AL118674	Hs,132121 Hs.34871	KIAA0569 gene product	3.2
	408923	H73881	Hs.255436	ESTs	3.2
	430919	AA489041	Hs.29544B	ESTs	3.2
	431622 433584	AW979271 AW295399	Hs.293184	ESTs gb:UI-H-BI2-ehv-h-03-0-UI.st NCI_CGAP_Su	3.2 3.2
15	437073	A1885608	Hs.94122	ESTs	3.2
	438394	BE379623	Hs.27693	CGI-124 protein	3.2
	446242	N66336	Hs.7360	ESTs	3.2 3.2
	452542 454009	AW812256 AW015927	Hs.233071	gb:RCO-ST0174-191099-031-a07 ST0174 Homo ESTs	3.2 3.2
20	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN AL	3.2
	415652	179213	Hs.272073	ESTs	3.2
	453931 439382	AL121278 BE247684	Hs.25144 Hs.103070	ESTs ESTs	3.2 3.2
	420077	AW512260	Hs.87767	ESTs	3.2
25	430437	A176B801	Hs.169943	Homo sepiens cDNA FLJ13569 fis, clone PL	3.2
	446745	AW118189	Hs.156400	ESTs	3.1 3.1
	408308 450320	AL033377 AW291775	Hs.44197 Hs.213793	hypothetica) protein DKFZp564D0462 ESTs	3.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.1
30	449523	NM_000579	Hs.54443	chemokine (C-C molif) receptor 5	3.1
	451110	A)955040	Hs.301584	ESTs ESTs	3.1 3.1
	431745 410781	AW972448 Al375672	Hs.163425 Hs.165028	EST8	3.1
0.5	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapians	3.1
35	444330	Al597655	Hs.49265	ESTs	3.1
	406761 409026	AA057264 AL137554	Hs.238936 Hs.49927	ESTs Homa sepiens mRNA; cDNA DKFZp434H1720 (f	3.1 3.1
	432055	AW972359	Hs.293334	ESTs	3.1
40	432441	AW292425	Hs.163484	ESTs	3.1
40	408045	AW138959	Hs.245123	ESTS	9.1 3.1
	427191 41 6 965	BE221825 N26223	Hs.97691 Hs.160436	ESTS ESTS	3.1
	441594		Hs.208765	ESTs	3.1
15	406992			gb:beta-pol=DNA polymerase beta (exon a	3.0
45	431941 438323	AKD00106 A1985394	Hs.272227 Hs.123369	Homo saplene cDNA FLJ20099 fis, clone CO ESTs	3.0 3.0
	427698		Hs.294140	ESTs	3.0
	424296	A)631874	Hs.169391	ESTs	3.0
50	450522 407942		Ma cond	gbcwd31f02.x1 Soares_NFL_T_GBC_S1 Homo s hypothetical protein FL110305	3.0 3.0
30	417991		Hs.5894 Hs.190008	ESTs	3.0
	422589		Ha.179725	EETs	3.0
	437583		Hs.244627	ESTS	3.0
55	452019 449494		Hs.27552 Hs.288650	Homo seglens mRNA; cDNA DKFZp586N2424 (f aquaporin 4	3.0 3.0
	444188		Hs.19175	ESTs	3.0
	400297	Al127076	Hs.288381	hypothetical protein DKFZp564O1278	3.0
	410811 450584		Hs.300648 Hs.60371	ESTs ESTs	3.0 3.0
60	428043		Hs.2240	uteroglobin	3.0
	436120	AJ248193	Hs.119860	ESTS	3.0
	442324		Hs.28426 Hs.228320	ESTs Home sapiens cDNA: FLJ23537 fis, clone L	2.9 2.9
	448693 425555		Ha.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.9
65	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	2.9
	408427		Hs.177236	ESTS	29
	459587 438128		Hs.122049	gb:zk15e04.s1 Soæes_pregnant_uterus_NbH ESTs, Weakly similar to U4/U6 small nucl	2.9 2.9
	408938		Hs.22607	ESTS	2.9
70	419270	BE165909	Hs.134682		2.9
	42202		Hs.200442		2.9 2.9
	426891 42 73 74		Hs.41294 Hs.143686	ESTs ESTs	29
7.	43420	B T92641	Hs.127648	hypothetical protein PRO2176	2.9
75	44646		Hs.308	arrestin 3, retinal (X-arrestin)	2.9
	45122 41551		Hs.48473 Hs.182362	ESTs ESTs	2.9 2.9
	40877		Hs,63356	ESTs	2.9
PΛ	42111	0 AJ250717	Hs.1355	cathepsin E	2.9
80	45363 43657		Hs.169872		29 29
	43657 42608		Hs.134859 Hs.126712		2.9 2.9
	41923		Hs.136245		2.8

	******	1.00.000		N	
	408171 445189	AA301228 Al936450	Hs.43299 Hs.147482	Homo sepiens cDNA FLJ12890 fis, clone NT ESTs	2.8 2.8
	419150	T2961B	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.B
_	427457	AW779105	Hs.164682	ESTs, Wealdy similar to ORF2 consensus s	2.8
5	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	2.8
	446932	AA961459	Hs.125644	ESTs	28
	439140 405041	W85737	Hs.290830	ESTs	2.8 2.8
	421306	AAB06207	Hs.125889	EGTs	2.8
10	427514	AA640773	Hs.209224	ESTs	2.8
	427939	T92459	Hs.16886	ESTs	2.8
	429127	AA749382	Hs.107233	ESTs	28
	429590 433163	AI219490 R40468	Hs.44445 Hs.163582	ESTs, Weakly similar to Keich motificant ESTs	2.B 2.8
15	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone H	2.8
	448015	A1458065	Hs.23196	ESTs	28
	456761	D59899	Hs.127842	CGI-142	28
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
20	449540 447020	AAD01713 T27308	Hs.16986	gb:zh86e08.s1 Soares_fetal_liver_spleen_ hypothetical protein FLJ11046	2.8 2.8
20	412610	X90908	Hs.74126	fatty acid binding protein 6, Ileal (gas	2.8
	433515	AA595800	Hs.190246	ESTa	2.8
	424450	AL137526	Hs.147472	dynein intermediate chain 2	2.B
25	438122	A1620270	Hs.129837	ESTs lysyl oxidase	2.8 2.8
23	424086 438885	A1351010 A168655B	Hs.102267 Hs.184987	ESTs	2.8
	412903	BE007967	Hs.155795	ESTs	28
	454111	AW081681	Hs.269064	ESTs	2.8
20	439398	AA284267	Hs.221504	ESTs	2.8
30	449802	AW901804 AA649860	Hs.23984 Hs.189496	hypothetical protein FLJ20147 ESTs	2.8 2.8
	434812 432583	AW023624	Hs.162282	ESTS	28
	428104	AA421350	Hs.191604	ESTs	28
25	408217	A1433201	Hs.279860	hypothetical protein FLJ20030	2.8
35	438018	AJ949638	Hs.109150	8H3-domain binding protein 5 (BTK-assoc)	2.8
	436396 430887	AJ683487 N66B01	Hs.299112 Hs.260267	Homo sapiens cDNA FLH1441 fis, clone HE ESTs. Weakly similar to ALU7_HUMAN ALU S	2.7 2.7
	446311	AW007294	Hs.149795	ESTS, Weakly similar to ALU1_HUMAN ALU 8	2.7
40	4161B5	AW975861	Hs.291995	ESTs	2.7
40	408613	AW242086	Hs.253967	ESTs	2.7
	442510	AF150179	Hs.249890	ESTS	2.7 2.7
	433293 413875		Hs.32417	ESTs gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.7
	4044BB			Boulton Ittiana Ittana et i Geo till too till too	2.7
45	408936		Hs.293549	ESTs	2.7
	431980		Hs.222695	Homo saplens cDNA: FLJ20986 fis, clone C	27
	436738 451797		Hs.152913 Hs.56120	ESTs ESTs	2.7 2.7
	452163		1000120	gb:tz43h12x1 NCI_CGAP_Bm52 Homo saplen	2.7
50	452778	R71338	Hs.5921	Homo saplena cDNA: FLJ21592 fis, clone C	2.7
	459366			gbzn92605.r1 Stratagene lung carcinoma	2.7
	431448 430733		Hs.286381 Hs.283361	hypothetical protein DKFZp564O1278 ESTs	2.7 2.7
	453652		Hs.28368	ESTs	2.7
55	453616	NM_003462	Hs.33846	dynein, accremal, light intermediate pol	27
	411905			gb:601193893F1 NIH_MGC_7 Home saplans cD	2.7
	408729 450726		Hs.72639 Hs.264330	ESTs N-acylephingosine amidohydrolase (acid c	2.7 2.7
	447720		Hs.161304	ESTs	2.7
60	451497		Hs.284122	Wint inhibitory factor-1	2.7
	442074		Hs.128430	EST8	2.7
	424115 417728		Hs.293965 Hs.24790	ESTs KIAA1573 protein	2.7 2.7
	433803		Hs.27688	EST8	2.7
65	419247		Hs.89764	fregle X mental retardation 1	2.7
	424910		Hs.50334	ESTs	2.6
	43B504		Hs.224625	ESTS	2,6 2.6
	426486 430417		Hs.170058 Hs.50701	Homo saplens mRNA; cDNA DKFZp58680220 (f ESTs	2.6
70	438297		Hs.258238		2.6
	42250	5 AL120862	Hs.124165	ESTs	26
	45728		Hs.226780		2.6 2.5
	428657 431750		Hs.74407 Hs.283705	mudeolar protein p40; homolog of yeast ESTs	2.6 2.6
75	43557		Hs.44234	triggering receptor expressed on myeloid	2.6
	41338	6 M34455	He.840	indoleamine-pyrrole 2,3 dloxygenase	26
	40390		Un denne	Shmonetis loveles dah kanamankana a	2.6
	407910 42342		Hs.41296 Hs.128433	fibronectin leucine rich transmembrane p prostagiandin D2 synthase, hematopoletic	2.6 2.6
80	43604		Hs.168830		2.6
	43664	5 AW023424	Hs.158520	ESTs	26
	40838 40262		Hs.44532	d]ubiquitin	2.6 2.6
	10202	ə			2.0

	406594				2.6
	415122	D60708	Hs.22245	ESTs	2.6
	416747	AW876523	Hs.15929	Homo saplens cDNA FLJ12910 fis, clone NT	26
5	420159	AJ572490 W76027	Hs.99765 Hs.23920	Homo sapiens cDNA: FLJ21245 fls, clone C Homo sapiens cDNA FLJ13124 fls, clone NT	2.6 2.6
	444361 446609	BE395090	Hs.15535	Human gene from PAC 886K2, chromosome 1	2.6
	449260	AA7411B0	Hs.29879	ESTs	26
	452311	AW304029	Hs.252744)	ESTs ST	2.6
10	413802 417318	AW964490 AW953937	Hs.32241 Hs.12891	ESTs ESTs	2,6 2.6
10	440028	AW473675	Hs.125843	ESTs	26
	437960	AI669586	Hs.222194	ESTs	2.6
	433687	AA743991	11- 100045	gb:ny57g01.s1 NCI_CGAP_Pr18 Hamo sepiens ESTs	2,6 2.6
15	430573 439737	AA744550 A1751438	Hs.136345 Hs.41271	Homo sapiens mRNA full length insert cON	2.6
	453204	R10799	Hs.191990	ESTs	26
	436751	AA732217	Hs.294054	ESTS	26
	408165 431120	AL137573 AA492588	Hs.43143	Homo saplens mRNA; cDNA DKFZp564A2463 (f gb:ng99c08.s1 NCI_CGAP_Thy1 Homo saplens	2.6 2.5
20	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	2.5
	43845B	AW975186	Hs.162875	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	446063	A1720140	Hs.151079	ESTs	2.5 2.5
	430499 450496	AW969408 AW449251	Hs.231991 Hs.257131	ESTs ESTs	2.5
25	441330	AI692984	Hs.129354	ESTs .	2.5
	424433	H04607	Hs.9218	ESTs	2.5
	434677 445779	AW444575 A)253104	Hs.130834 Hs.189267	ESTs ESTs	2.5 2.5
	444649	AW207523	Hs.197628	ESTa	2.5
30	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	25
	432222	AI204995		gb:an03c03.x1 Strategene schizo brain S1	2.5 2,5
	404288 408572	AA055611	Hs.22556B	ESTs, Moderately similar to ALU4_HUMAN A	2.5
~ ~	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	25
35	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	2.5
	410095 410947	AW589638 AK000305	Hs.258947 Hs.67055	ESTS hypothetical protein FLJ20298	2.5 2.5
	418343	AA216372	Hs.159501	ESTs	2.5
40	423401	NM_001992	Hs.128087	coegulation fector II (thrombin) recepto	25
40	428637 429846	AW979268 AB023021	Hs.225945	gb:EST391378 MAGE resequences, MAGP Homo fucosyltransferase 9 (alpha (1,3) fucosy	2.5 2.5
	432507	BE391093	113.225570	gb:601286042F1 NIH_MGC_44 Homo sapiens c	25
	433858	N69243	Hs.192974	Homo seplens cDNA FLJ12735 fis, clone NT	2.5
45	438851 443830	H64500	Hs.123646 Hs.143273	ESTs ESTs	2.5 2.5
43	446800		Hs.156486	ESTs	2.5 2.5
	450262		Hs.271166	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451343		Hs.293353	ESTs	2.5
50	451539 452412		Hs.218933 Hs.61373	ESTs ESTs	2.5 2.5
	454288		Hs.279458	ESTs, Highly similar to c380A1.1b (H.sap	2.5
	445745		Hs.13245	KIAA0455 gane product	2.5
	424943 440106		Hs.153924 Hs.127699	deatit-associated protein kinase 1 KIAA1603 protein	2.5 2.5
55	45B429		Hs.12346	Home saplens cDNA; FLJ21399 fis, clone C	2.5
	415261		Hs.8346	ESTs	2.5
	420026 431806		Hs.166676 Hs.270737	ESTs turner necrosis factor (Ilgand) superfami	2.5 2.5
	458722		Hs.282B32	ESTs	25
60	419449		Hs.57483	Homo sapiens cDNA FLJ14294 fls, clone PL	2.5
	436260 433644		Hs.292710 Hs.256112	ESTs, Weakly similar to ALU5_HUMAN ALU S ESTs	2,5 2.5
	419172		Hs.22120	ESTs	2.5
15	437982	N93486	Hs.121764		2.5
65	443348		Ks.67572 Hs.285754	ESTs	2.5 2.5
	417218 419236		Hs.135159		2.5
	448030	N30714	Hs.20161	HDCME31P protein	2.5
70	417203		Hs.269908		2.5
70	449275 436198		Hs.205457 Hs.300922		2.4 2.4
	452281	T93500	Hs.28792	Homo sepiens cDNA FLJ11041 fis, clone PL	2.4
	44219	W95186	Hs.8136	endothelial PAS domain protein 1	2.4
75	428571 453142		Hs.2291 Hs.7473	Probe hTg737 (polycystic kldney disease, ESTs	2.4 2.4
, 5	42565		Hs.119471		2.4
	452822	2 X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone H	2.4
	416778		Hs.79876 Hs.220491	steroid sulfatase (microsomal), aryisulf ESTs	2,4 2,4
80	458333 44814		Hs.20450	SCM-like membrane protein precursor	2.4 2.4
	45964	4			2.4
	42912		Hs.271004 Hs.3782		2.4 2.4
	44833	7 AW206453	1 13,31 02	ESTs	44

	197770	A A 44 22 22	Un 105323	COT-	2.4
	427778 425371	AA412323 D49441	Hs.105323 Hs.155981	ESTs mesothelin	2.4
	44B299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.4
c.		AW296286	Hs.255534	ESTs	24
5	409519	AA075368	11- 7697	gb:zm86h10.r1 Stratagene ovarian cancer	24 . 24
	441006 440817	AW605267 Al341423	Hs.7627 Hs.270165	CGI-60 protein ESTs	2.4
	420020	BE295866	Hs.94382	adenosine kinase	2.4
.	435395	AA729235	Hs.117907	ESTs	2.4
10	424144	AA454033	Hs.41644	Homo sapiens cDNA: FLJ23003 fis, clone L	2.4
	405494	A1920.467	U= 120704	ECT.	2.4 2.4
	458145 408547	Al239457 AA574291	Hs.130794 Hs.57837	ESTs ESTs	2.4
	408941	Al452469	Hs.165221	ESTs	2.4
15	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276 Homo	2,4
	417137	U46265	Hs.81281	hypothetical protein	24
	418950 420756	T78517 AA411800	Hs.13941 Hs.189900	ESTs ESTs	2.4 2.4
	420788	Al860775	Hs.98506	ESTs	24
20	432896	NM_014097	Hs.279778	PRO1693 protein	2.4
	43614B	BE005252		gb:CM1-BN0116-030400-171-g02 BN0116 Homo	2.4
	436284	AA708016	Hs.190389	ESTS	24 24
	437327 442611	AL353942 BE077155	Hs.177537	gb:Homo saptens mRNA; cDNA DKFZp761L2312 ESTs	24
25	456062	AI866286	Hs.71962	ESTs	2.4
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.4
	401335				24
	428771	AB028992	Hs.193143	KIAA1069 protein ESTs	2.4 2.4
30	419140 454693	Al982647 AW813428	Hs.215725	gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.4
-	427785	X81053	Hs.180828	collagen, type IV, atpha 4	24
	407339	AA777542	Hs.132670	ESTs	2.4
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	2,4
35	427019 431089	AA001732 BE041395	Hs.173233 Hs.283676	hypothetical protein FLJ10970 ESTs, Weakly similar to unknown protein	2.4 2.4
55	452561	AI692181	Hs.49169	KIAA1634 protein	24
	427878	C05766	Hs.181022	CGI-07 protein	2.4
	419752		Hs.152618	ESTa	2.4
40	430073	UB6136	Hs.232070 Hs.29352	telomerase-associated protein 1 tumor necrosis factor, alpha-induced pro	24 24
40	452401 430345	NM_007115 AK000282	Hs.239681	hypothetical protein FLJ20275	23
	407905	AW103655	Hs.252905	ESTs	2.3
	427660		Hs.114121	Homo saplens cDNA: FLJ23228 fis, clone C	23
45	422355		Hs.140	Immunoglobulin heavy constant gamma 3 (G	2.3
40	453049 438568		Hs.30343 Hs.11135	ESTs mejor histocompatibility complex, class	2.3 2.3
	453445		Hs.91453	ESTs	2.3
	424711		Hs.152175	calcitonin receptor-like	2.3
50	446346		11- 400045	gb:qi79g06.x1 Soares_NhHMPu_61 Homo sapi	2.3
50	441974 444805		Hs.128245 Hs.12017	ESTs KIAA0439 protein; homolog of yeast ubiqu	2.3 2.3
	424027		He.201591	ESTs	2.3
	419606		Hs.198529	ESTs, Weakly similar to similar to acyl-	2.3
55	428613		Hs.186928	KIAA1328 protein	23 23
33	434340 450297		Hs.128685 Hs.38592	ESTs Homo sapiens cDNA: FLJ23342 ffs, clone H	2.3 2.3
	432779		113.00002	gb:EST391351 MAGE resequences, MAGP Homo	2.3
	433650		Hs.28456	ESTS	2.3
60	419086		Hs.89591	Kallmann syndrome 1 sequence	23
60	428758 430153		Hs.98502	Homo seplens cDNA FLJ14303 fis, clone PL gb:EST380338 MAGE resequences, MAGJ Homo	2.3 2.3
	418883		Hs.1211	acid phosphatase 5, tartrate resistant	2.3
	427669		Hs.255938	ESTs, Moderately similar to KIAA1200 pro	2.3
65	400610				23
65	402222 407162		Hs.142634	nian Ennanmentale	2.3 2.3
	415250		Hs.27319	zinc finger protein ESTs	2.3
	421751		Hs.159153		2.3
70	428557		Hs.129520		2.3
70	43265		Hs.162319		23 23
	434742 436588		Hs.291695 Hs.167028		2.3
	44167		Hs.5461	ESTs	2.3
75	44203	9 AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicu	23
75	44316		Hs.36053	ESTS	2.3 2.3
	44876 44957		Hs.182112 Hs.134014		2,3 2.3
	43981		Hs.B556B	EST	23
oΔ	41371	4 A1560944	Hs.71428	ESTs	2.3
80	40028		Hs,225B	matrix metalloproteinase 10 (stromelysin	2.3 2.3
	41338 43867		Hs.75334 Hs.123428	exosioses (multiple) 2 3 ESTs	2.3 23
	41999		Hs.94210	eyes absent (Drosophila) homolog 1	23

	100700				2.3
	459702 414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	2.3 2.3
	438474	AW865B18		KIAA0764 gene product	23
	453037	AA045175		ESTs	2.3
`5	428467	AK902121		hypothetical protein FLJ11259	23
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	23 23
	422429 415083	AA310527 A)632683	Hs.27179	gb:EST181333 Jurket T-cells V Homo sapie Homo sapiens cDNA FLJ12933 fis, clone NT	2.3
	417015	M83772	Hs.80876	flavin containing moneoxygenase 3	2.3
10	406506				23
	448330	AL036449	Hs.207163	ESTs	23
	409719	AT769160	Hs.108681	ESTs	2.3 2.3
	423354 425188	AB011130 AK002052	Hs.127436 Hs.155071	calcium channel, voltage-dependent, alph hypothetical protein FLI11190	23
15	427961	AWZ93165	Hs.143134	ESTs	2.3
	447357	A1375922	Hs.159367	ESTs	2.3
	412642	BE244598	Hs.809	hepstocyte growth factor (hepspoietin A;	2.3
	453716 437370	AA037675 AL359567	Hs.152675 Hs.161962	ESTs Homo sapiens mRNA; cDNA DKFZp547D023 (fr	23 23
20	407949	W21874	Hs.247057	ESTs	2.2
	427972	AA864870	Hs.181304	putative gene product	2.2
	453313	BE005771	Hs.153746	Homo saplens cDNA: FLJ22490 fis, clone H	2.2
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	2.2 2.2
25	424238 452930	AA337401 AW195285	Hs.137635 Hs.194097	ESTs ESTs	2.2
<i></i>	424527	AW138558	Hs.267158	ESTs	2.2
	453095	AW295660	Hs.252756	ESTs	2.2
	449161	N53431	Hs.47647	ESTs, Weakly similar to KIAA0423 [H.sapl	2.2
30	429586	T73510 A1472209	Hs.209153 Hs.288369	angiopoietin-like 3 ESTs	2.2 2.2
50	4237B2 458124	AW005548	Hs.124590	ESTs	2.2
	450109	A)539295	Hs.17967	ESTs	2.2
	421461	AW291023	Hs.97255	ESTs	2.2
35	412222	AA528283	Hs.292737	ESTs	22 22
33	418882 441736	NM_004996 AW292779	Hs.89433 Hs.169799	ATP-binding casselte, sub-family C (CFTR ESTs	2.2
	401049	Allege 15	113.100700	2018	2.2
	440727	Al073991	Hs.134268	ESTs	2.2
40	419751	AW195581	Hs.93121	KIAA0761 protein	2.2
40	445640 421379	AW969626 Y15221	Hs.31704 Hs.103982	ESTs, Wealdy similar to KIAA0227 [H.sapi small inducible cytokine subfamily B (Cy	22 22
	422109	573265	Hs.1473	gastrin-releasing peptide	2.2
	410292	AA843087	Hs.124194	ESTs	2.2
15	434265	AAB46811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.2
45	449695		Hs.34550	ESTs ESTs	. 22 . 22
	429399 444042		Hs.16727 Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.2
50	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	2.2
50	428784		Hs.193470	purinergic receptor P2X, ligand-gated to	2.2 2.2
	445268 402481	AJ218358	Hs.175048	ESTs	2.2
	412608	AA247995	Hs.4489B	Homo saplens clone TCCCTA00151 mRNA sequ	2.2
EE	416521		Hs.44197	hypothetical protein DKFZp564D0462	2.2
55	416624		LI= 077ED:	gb:y/77h05.s1 Sogres fetal liver spicen	2.2 2,2
	419780 421211		Hs.87752 [,] Hs.266308	ESTs ESTs, Weekly similar to AF216312 1 type	22
	427541		Hs.97961	ESTs	2.2
70	432013		Hs.162102	ESTs	2.2
60	436461		Hs.293261	ESTS	2.2 2.2
	438002 440312		Hs,20164B Hs. 724 75	ESTs, Wealdy straiter to ZN42_HUMAN ZINC ESTs	2.2
	440479		Hs.208161	ESTs	2.2
~-	441178	W90769	Hs.153976	ESTs	2.2
65	441235		Hs.135570	Homo saplens cDNA: FLJ21268 ffs, clone C	2,2
	443314 422165		Hs.54646 Hs.1481	ESTs Ns6dine decarboxylase	2.2 2.2
	450696		Hs.16026	Homo saplens cDNA: FLJ23191 fis, clone L	2.2
	432974			gb:ht/70g02.x1 NCt_CGAP_Lu24 Homo sapiens	2.2
70	404200				22
	435990 421309		Hs.131793 Hs.270449		2.2 2.2
	45155		Hs.26630	ATP-binding cassette, sub-family A (ABC1	22
	416643	2 T96118	Hs.226313	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.2
75	40667		Hs.198253		22
	417819		Hs.133540	ESTs endothalin receptor type B	2.2 2.2
	41735 45957		Hs.62002 Hs.101810		2.2
	40427	4	10 10 10		2.2
80	41508	8 Al597963	Hs.118726		2.2
	41821		Hs.13337	ESTs, Weakly similar to unnamed protein ESTs	2.2 2.2
	41922 44431		Hs.291759	gb.cw76b09.s1 Spares_fetal_liver_spleen_	2,2
				215	.,_

	451050	A1A(027470	De cocco	ESTs	2.2
		AW937420 X16895	Hs.69662 Hs.82112	Interleukin 1 receptor, type 1	22
		ALD49980	Hs.184216	DKFZP564C152 protein	2.2
_		AI089319	Hs.179243	ESTs	2.2
5		Al859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	22
		R36207	Hs.25092	ESTs 12 Mb	2.2 2.2
		M34996	Hs.198253	major histocompatibility complex, class qb;zh85d01.s1 Socres_fetal_liver_spleen_	2.2
		AA002071 AA001150	Hs.132937	ESTs	2.2
10		BE140602	Hs.246645	ESTs	2.2
		H47867	Hs.34024	ESTs	2.2
		AI472078		gb:lj89h03.x1 Soares_NSF_FB_9W_OT_PA_P_S	2,2
		AA281279	Hs.23317	ESTS	2,2 2.2
15		AB009303	Hs.297790 Hs.279525	Human clone 23734 mRNA sequence hypothetical protein PRO2605	2.2
13	446999 457447	AA151520 X78261	Hs.272177	H.sapiens mRNA for TRE17 5 extremity an	2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.1
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	21
20	410048	W76467	Hs.274550	profine oxidase homolog	2.1
20	400880	D.15454	II. Ancona	FAT.	2.1
	418092	R45154	Hs.106694	ESTs ESTs	21 21
	428780 431067	AJ478578 AW574823	Hs.50636 Hs.200413	ESTs	2.1
	432803	AA565398	16.200710	gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	2.1
25	412104	AW205197	Hs.240951	ESTE	2.1
	422819	AL122084	Hs.121073	hypothetical protein FLI10466	2.1
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	21
	424806	AA382523	Hs.105689	EST ₈	2.1 2.1
30	434445 442994	Al349306 Al026718	Hs.11782 Hs.16954	ESTs ESTs	2.1
20	410371	AA084482	Hs.115850	ESTs	2.1
	450232	BE300815	Hs.201326	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	21
25	430899	BE018217	Hs.183528	ESTs, Weakly similar to Bern46-like prote	2.1
35	431814	BE256242	Hs.270847	delta-lubulin	2.1
	417543 444542	AA203620 Al161293	Hs.110153 Hs.146862	ESTs, Weakly similar to BCGF_HUMAN B-CEL ESTs, Weakly similar to KIAA0525 protein	2.1 2.1
	404593	AU 10 1293	FS. 340002	CO15, 1469rd Salina in Javanosca hotella	2.1
	434803	AW974640		gb:EST386744 MAGE resequences, MAGM Homo	2.1
40	451623	H77818	Hs.268991	ESTs	21
	452466	N84635	Hs.29684	Human DNA sequence from done 682J15 on	2.1
	402046	1) zcczn	11- 000045	News portons USBCOOK mDNA partial ada	2.1 2.1
	434927 436192	H46612 W93847	Hs.293815 Hs,24139	Homo saplens HSPC285 mRNA, partial cds Homo sapiens cDNA: FLJ23137 fis, cione L	21
45	401987	1755041	110,24100	TOTAL SUPPORT SUPERIOR IN SUPERIOR E	2.1
	423119	AA322201	Hs.131976	EST	2.1
	427112	Z32867	Hs.290951	ESTs .	21
	414464	Al870175	Hs.13957	ESTs	2.1
50	447829	A1433029	Hs.164104	ESTs Homo saplens cDNA FLJ11846 fls, clone HE	2.1 2.1
50	449679 405472	Al823951	Hs.296668	HUMB SEPTEM CONA CONTROL HOS COME THE	21
	413621	A180864B	Hs.184158	ESTs	21
	432212	AW137742	Hs.293451		2.1
	404289				2.1
55	415362	F06735		gb:HSC1JB091 normalized Infant brain cDN	2.1
	427739	AW198755	Hs.98105 Hs.98123	ESTs ESTs	2.1 2.1
	427772 430B44	AA412289 T94960	FIS.:30123	gbtye38d07.r1 Stratagene lung (937210) H	2.1
_	434335	AA630107	Hs.213220		21
60	436052	AJ021983	Hs.271432	ESTs	2.1
	442773	AB037722	Hs.8707	Homo sapiens mRNA; cDNA DKFZp434N1131 (f	21
	445799	AW978373	Hs.49221	ESTs, Wealdy similar to zinc finger prot	21 21
	450221 455673	AA328102 BE065939	Hs.24641	cytosketeton associated protein 2 gb:RC3-BT0319-100100-012-c11 BT0319 Homo	21
65	458624		Hs.181801		21
•	405095		(,,_,_,_	20.10	2.1
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	2.1
	433589		Hs.188912		2.1
70	438398		Hs.130277		2.1 2.1
70	447233 447197		Hs.17901	Homo saplens cDNA: FLJ21974 fis, clone H gb:yh88b01.s1 Soeres ptacenta Nb2HP Homo	2.1
	431087		Hs.290791		2.1
	409064		Hs.141883	B ESTs	21
75	427558	D49493	Hs.2171	growth differentiation factor 10	2.1
75	426457		Hs.16996		2.1
	438118		Hs.25941;		21 21
	427621 452114		Hs.17988 Hs.8236	2 Homo saplens cDNA FLJ12437 fis, clone NT ESTs	21
	448782		Hs.30155		2.1
80	403937			• 1	2.1
	416402		Hs.1012	complement component 4-binding protein,	21
	452416		Hs.11477		2.1 2.1
	451609	AL046019	Hs.20927	6 ESTs	Z. l

		R19382		ESTs	21 21
		AI992108		ESTs Homo sapiens cDNA FLI 12807 fis, clone NT	2.1
		AA045847 AA742697		ESTs, Weakly similar to S59856 collegen	21
5		AW827419		ESTs	21
3		R256B5		collegen, type XIII, alpha 1	2.1
		UBB967		protein tyrosine phosphatase, receptor-t	2,1
		AA813745	Hs.123446	ESTs	2.1
10	40584B				21
10		N75620		ESTs	21
	442381	A1185136	Hs.48650	ESTS	2.1 2.1
	420036	R60336	Hs.52792 Hs.120969	Homo saplens mRNA; cONA DKFZp586H823 (f Homo saplens cDNA FLJ11562 fis, clone HE	21
	436252 413450	AI539519 Z99716	Hs.75372	N-acetylgalectosaminidase, alpha-	2.1
15	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.1
~~	439425	AF086244	Hs.114659	ESTS	2,1
	42116B	AF182277	Hs.1360	cytochrome P450, subfamily I/B (phenober	2.1
	449611	AJ970394	Hs.197075	ESTB	2.1
20	404548				2.1
20	416734	HB1213	Hs.14825	ESTS	2.1 2.1
	435865 439072	AA883552 AF085930	Hs.16810 Hs.269123	ESTs ESTs	2.1
	447482	AB033059	Hs.18705	KIAA1233 protein	2.1
	457292	A1921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	2.1
25	444974	AI203500	Hs.151612	ESTs	2.1
	456034	AW450979		gb:UI-H-BI3-de-e-12-0-UI.s1 NCI_CGAP_Su	21
	430634	A1860651	Hs.26685	ESTs	2.1
	426782	R14614	Hs.191254	ESTS	2.0 2.0
30	452943	BE247449	Hs,31082	hypothetical protein FLJ10525 ESTs	2.0
50	445326 421247	AI220072 BE391727	Hs.165893 Hs.102910	general transcription factor IIH, polype	2.0
	409994	D86864	Hs.57735	acetyl LDL receptor, SREC	20
	443268	Al800271	Hs.129445	hypothetical protein FLJ12496	20
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.0
35	417321	N68722	Hs.191368	ESTs	2.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.0 2.0
	404323 448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	421047	AW514772	Hs.104473	ESTs	2.0
40	425497	AA524596	Hs.188844	ESTs	20
	444623	AI183829	Hs.202111	ESTs	2.0
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.0
	433563	A1732637	Hs.277901	EST8	20
A.C	406485			and the second of	20
45	428330	1.22524	Hs.2256	metrix metalloproteinsse 7 (matrilysin, qb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.0 2.0
	455807 425465	BE141140 L18964	Hs.1904	protein kinese C, iata	20
	449424	AW448937	Hs.197030	ESTs	2.0
	427940		Hs.38775	ESTs	2.0
50	411502	AW946605	Hs,250154	Homo septens cDNA FLJ12973 fis, clone NT	2.0
	411365	M76477	Hs.278242	tubulin, alpha, ubiquitous	20
	412369	H80456	Hs.205243	Homo saplens cDNA: FLJ22029 fls, clone H	2.0
	452959		Hs.189674 Hs.79385	ESTs Human clone 23574 mRNA sequence	2.0 2.0
55	416680 428775	T61572 AA434579	Hs.143691	ESTs	2.0
25	420000		Hs.180726	Homo saplens cDNA FLJ13543 fis, clone PL	20
	408321	AW405BB2	Hs.44205	cortistatin	2.0
	410011	AB020641	Ha.57856	PFTAIRE protein kinase 1	2.0
60	411050			gb:MR1-8T0205-120400-022-f08 ST0206 Homo	20
60	452453		Hs 125445	gb:QV-BT009-101198-051 BT009 Homo sapien FSTs	2.0 2.0
	428978 458682		Hs.145268	ESTS	2.0
	425527		Hs.15B258	Homo sepiens mRNA; cDNA DKFZp434B1272 (f	2.0
	403760		10114000	, ionio copinio inicia, con contrata de localeste (20
65	424368		Hs.146085	KJAA1345 protein	2.0
	421229	A1056590	Hs.7086	Homo saplens cDNA: FLJ23000 ffs, clone L	2.0
	436304		Hs,108887	ESTs	2.0
	453498		Hs.23245	Homo sapiens cONA FLJ11767 fis, done HE	20
70	439018 453280		Hs.26638 Hs.32913	ESTs, Weakly similar to unnamed protein Homo szolens mRNA; cDNA DKFZp781C082 (fr	2.0 2.0
10	420193		Hs.202869		20
	444810		, ,	gb:HA2501 Human fetal liver cDNA library	2.0
	401575			-	2.0
-	419092	2 J05581	Hs.89603	mucin 1, transmembrane	20
75	430129		Hs.233955		20
	410763		Hs.8968	tumor endothelial marker 8	2.0
	414783 411492		Hs.75839 Hs.70337	zinc finger protein 6 (CMPX1) Immunoglobulin superfamily, member 4	2.0 2.0
	405963		(15.70337	many department of the man of the	2.0
80	418378			gb:EST374154 MAGE resequences, MAGG Homo	2.0
	420831		Hs.190035		2,0
	42415	2 AL133591	Hs.301405	Homo saplens mRNA; cONA DKFZp434N079 (fr	20
	424641	1 AB001106	Hs.151413	glia maturation factor, beta	20

	ATTG1C	Aleggesia	st- poopo	FOT.	
		A1698684 A1821726	Hs.98028 Hs.116603	ESTs ESTs	2.0 2.0
	437636	AA764781	Hs.291844	ESTs	2.0
5		AI394151 AF124250	Hs.37932 Hs.6564	ESTs	2.0
_	445386	Al925280	Hs.236B42	breast cancer anti-estrogen resistance 3 EST	2.0 2.0
	447101		Hs.44189	ESTs	2.0
		AA147829 C00719	Hs.33193 Hs.120440	ESTs, Highly similar to AC007228 3 BC372 ESTs	2.0
10			Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	2.0 2.0
	456613	R19992	Hs.106620	Homo sepiens clone 23950 mRNA sequence	2.0
		Al355009 AA501760	Hs.221698 Hs.18075	ESTs chromosome 9 open reading frame 3	2.0
1.5		AW971364	110,10010	gb:EST3B3453 MAGE resequences, MAGL Homo	2,0 2.0
15					
	TABLE 2	7B			
20	Pkey:	Unique Fos r	mobeset ident	iter number	
	CAT num	iber: Gene duster	number		
	Accessio	n: Genbank acc	ession numb	ers	
0.5	Pkey	CAT number	Accession		
25	409457			AW392887 AW514700 AW392881	
	409519 410008	113722_1 116812_1	AA075368 A AA079552 P	AU75369 IE142525 BE142527	
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30	411050	1230330_1	AW814902 (3E156666 BE156667 BE156590 BE156441 BE156447	
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	413136 413499	1350379_1		E066911 BE066979 BE066929 BE066925	
35	413875	1396766_1	BE144884 F BE176776 F		
	415094	1522103_1	D59513 D59	9515 D80174 D69514	
	415362 415624			1896 R12110 H08697 1867 H75691 T50292	
40	418378	174656_1		AA218925 AA354237	
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	430844 431120	324570_1 328264_1		187679 T95013 NA492498 AA492571	
50	431169	328799_1		AA493843 AA493723	
	431322	331543_1		AA503009 AA50299B AA502989 AA502805 T92188	
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60	433492 433584	367934_1 370400_1	AVV295399	AW262898 N41060 AA594852 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 /	AA776832
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	437327	41500_1 43610_1	AL353942 /		
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	449299	80436_1	AA299918 /	AW957012 AA001107 T83631 BE156389	
	449540 449677	80945_2 81270_1	AA0017131	H63836 AAD02232 T99209	
75	450522			04002232 199299 1909260 Af909259	
	451024	85565_1	AA442176	AA259181	
	451381 452163	867770_1 902067_1		AW249135 BE548847 AW250245 /80703 R43474	
90	452293	9091951	A!871833		
80	452453			1902518 A1902516 ANNOTES A1006422 A1005420	
	452542 452771	921410_1 930983_t		AW812257 Al906423 Al906422 7855 Al917711	
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AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
AW851309 AW850888 AW851419 AW851412 AW851299
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AW875951 AW875950 AW875936 AW875948 AW875939 AW875957
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                          1265634_1
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           455673
                          1370914_1
                                         BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
           455807
                                         142696_1 AW450979 AA136653 AA13655 AW419381 AA9B4358 AA492073 BE168945 AAB09054 AW238038 BE011212 BE011369 BE011367 BE011368 BE011362 BE011365 BE011365 BE011363 BE011364 AA526021 AA570759
                          456034
           457471
                          340916 1
10
                                         AA602711 BE078290
           457620
                          371514_1
           458154
                          491768_1
                                         AW816379 AA888282 AA879046 AA879195
           459267
                          966605_1
                                         AJ003631 AJ003650 AJ003651
15
           TABLE 27C
                          Unique number corresponding to an Eos probeset
                          Sequence source: 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I, et al," refers to the publication entitled "The DNA sequence of human
20
            chromosoma 22." Dunham I. et al., Nature (1999) 402:489-495.
                          Indicates DNA strand from which exons were predicted.
            Nt_position:
                          Indicates nucleotide positions of predicted exons.
                                                        Nt position
            Pkey
                                         Strand
25
            400610
                          9887671
                                                        117605-117928,124040-124147
                                          Minus
            4008B0
                          9931121
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                                          Plus
            401049
                           7232177
                                          Plus
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            401335
                           9684881
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76253-76364
30 -
                          7229R04
            401575
                                          Minus
            401793
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                                                         102945-103083
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3261-3834,3939-4269
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                           8072415
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                                          Pine
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             404200
404274
                                                         7066-7210
104127-104318
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                                          Plus
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                                          Minus
                                                         110443-110733
91057-91188
121230-121714
             404599
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                                          Plus
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                                           Plus
                                                         106297-106447,108462-108596
70284-70518
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                            7651809
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                                                         28256-28935
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             406554
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                                           Plus
             406594
                            8248611
                                                         35543-35B45
                                           Minus
             TABLE 28A: ABOUT 796 GENES DOWN-REGULATED IN LUNG FIBROSIS COMPARED TO NORMAL BODY
  65
             Table 28A lists of about 796 genes that are downregulated to lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetriz/Exx Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues sample expression was less than or equal to 0.1. The "average" normal lung tissue level was set to the 75° percentile amongst normal lung tissues. The "average" fibrosis
             expression level was sat to the 95th percentile amongst fibrosis samples. In order to remove gene-specific background levels of non-specific bybridization, the 15th percentile value
  70
             amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated,
                            Unique Eos probeset identifier number
              Pkey:
                            Exemplar Accession number, Genbank accession number
              ExAcon:
              UnigenelD: Unigene number
  75
              Unigene Title: Unigene gene title
              R1:
                             Ratio of normal lung to fibrosis
              Pkey
                          ExAcca
                                           Unigene ID Unigene Title
                                                                                                                           Rt
  80
              414002
                           NM_006732
                                           Hs.75678
                                                          FBJ murine osteosarcoma viral encogene h
                                                                                                                            18.18
              421218
                           NM_000499
                                           Hs.72912
                                                          cytochrome P450, subfamily I (aromatic c
                           AIR15601
                                                          CD83 antigen (activated B lymphocytes, I
              404518
                                           Hs.79197
                                                                                                                            8.30
                                                                                                                            5.56
              404795
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	100034				F 40
	403211 417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	5.46 5.43
	400489	00274310	113,1113	Marie receptor something of all coops of the	5.19
	425571	AJ007292	Hs.158306	ephrin-A2	5.19
5	406357	, = 05, 505		-pixiiii	5.08
	407979	AA046306	Hs.62927	ESTs	5.08
	452378	AA025855	Hs.19597	ESTs	4.7B
	408053	AW139474	Hs.246862	ESTs	4.62
10	421770	AA374192	Hs.108124	rībosomal protein L41	4.52
10	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	4.49
	402386				4.39 4.37
	402448	Alngorra	N= 470042	COT-	4.31
	448245 413778	A1923551 AA090235	Hs.170843 Hs.75535	ESTs myosin, light polypeptide 2, regulatory,	4.29
15	419968	X04430	Hs.93913	interleukin 6 (Interferon, bela 2)	4.24
15 -	44776B	X8640D	Hs.19520	FXYD domain-containing fon transport reg	4.21
	405163	7100 700		this animal animalia an addate and	4.19
	437120	Al356125	Hs.157767	ESTs, Weakly similar to human HOXA2 [H.s	4.19
	409020	AA062549	Hs.21162	ESTs	4.09
20	431073	BE254470	Hs.249186	cone-rad homeobax	4.07
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	4.05
	403716				3.99
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.94
25	404348	******		-t-NiDNA for ODDMI-i-	3.90
23	407070	Y10209	Hs.816	gb:)1.sapiens mRNA for CD301, protein SRY (sex determining region Y)-box 2	3.82 3.81
	412919 402409	Al368680	U2'0 10	SAT (SEX DESTINATING TORONT 1)-DOX 2	3.80
	456150	Z42308		gb:HSC0FB121 normalized Infant brain cDN	3.79
	427030	AA397600	Hs.97531	ESTs	3.76
30	42632B	AW631296		gb:hh83c09.y1 NCI_CGAP_GU1 Homo sapiens	3.74
	429307	AU076592	Hs.198951	Jun B proto-ancogene	3.71
	400172			• •	3.70
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	3.68
3.5	433863	A1925688	Hs.222312	ESTs, Weakly similar to B24264 proline-r	3.68
35	446850	R71245	Hs.174303	ESTs	3.67
	405147			MOT IN IT THE ALERS HEREALT TRACT	3.64
	406821	AA977896	Hs.128873	ESTs, Highly similar to ALFA_HUMAN FRUCT	3.57
	402762				3.55 3.50
40	401496 421201	AW241940	Hs.102500	hypothetical protein FLJ20481	3,50
70	402911	A11241540	1 102,000	Hypothesical protestivi cosco-rovi	3.49
	425330	D25216	Hs.155650	KIAA0014 gene product	3.49
	438004	AA774984	Hs.220649	ESTs, Weakly similar to FCE2 MOUSE LOW A	3.46
	448185	A1633040	Hs.172730	ESTS	3.46
45	433367	AA584930	Hs.269451	ESTs, Weakly similar to XAP-5-like prote	3.43
	416596	H67669	Hs.38564	ESTs	3.41
	400545				3.39
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB5	3.37
50 .	426507	AA380285		gb:EST93491 Supt cells Homo sapiens cDNA	3.35
<i>3</i> 0 .	403479	047022	Hs.82927	adosacina mananharahata dasminana 7 lina	3.34 3.34
	4060B2 4019 1 9	S47833	136.02327	adenosine monophosphate deaminase 2 (iso	3.33
	449031	Al867502	Hs.271462	ESTs	3.33
	400115	74031002	HOLET FROM	2010	3.31
55	401590				3.29
	401007				3.28
	404610	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.25
	408641	AW245207	Hs.5555	Homo sapiens cDNA FLJ13170 fis, clone NT	3.25
60	407196	D11747	Hs.177415		3.23
ΟU	410258	X52838	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	3,23
	433232	AI658621 AW976930	Hs.127769 Hs.128760		3.23 3.23
	457937 406101	MINITOSOU	175.120100	Luis	3,18
	407080	Z38133	Hs.113973	mypain, heavy polypeptide 8, skeletal mu	3.18
65	419947	AW298744	Hs.118894		3.18
	421905	A1660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein (H	3.16
	454019	D31846	Hs.37025	aquaporin 2 (collecting duct)	3.16
	428674	AAA31734	Hs.104915	ESTs	3.14
70	402056				3.06
70	425182	AF041259	Hs.155040		3.06
	425393	NM_000218			3.06
	433657	A1244368	Hs.8124	PH domain containing protein in retina 1	3.05
	402158 404938				3.03 3.02
75	404938				3.01
,,,	418828	AF020774	Hs.88844	Homo saplens hair and skin epidermal-typ	3.00
	402423		1 10-1101-14	- ming ankings time area attentioned the	2.99
	416253	BE250659	Hs.15463	ESTs	2.99
	435265		Hs.185932		2.99
80	425655	BE614551	Hs.158674	5 rfbosomal protein L14	2.98
	428704		Hs.249484		298
	425439		Hs.15742		2.97
	445613	BE550889	Hs.15849	1 ESTs	2.97

	402714				2.96
	403526 403605				2.96 2.95
	441852	ABD28968	Hs.7989	KIAA1045 protein	2.95
5	417629	176945	Hs.64211	ESTs, Weakly similar to similar to acyl-	2.94
-	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgra	2.91
	419821	AW967486	Hs.189119	ESTs	2.90
	446993	A)570964	Hs.164257	ESTs	2.89
	414580	BE386918	1 101101201	gb:601275386F1 NIH, MGC_20 Homo saplens c	2.68
10	423379	A1985349	Hs.157492	Homo sapiens cDNA FLI 14079 lis, clone HE	2.8B
~ ~	440206	AI762232	Hs.46794	EST8	2.88
	402212	AW502761	Hs.30909	KIAA0430 gene product	2.87
	406059				2.86
	423548	AF007194	Hs.129782	mucin 3A, Intestinal	2.B6
15	402051				2.85
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	2.85
	455446	AW947749		gb:RCO-MT9005-130300-031-b01 MT9005 Homo	2,85
	442428	BE464988	Hs.298302	EST8	2.84
20	403247				2.83
20	404825				2.83
	459184	L35001	Hs.95669	ESTs	2.83
	402968			-4-	2.82
	417575	R00382	Hs.191199	ESTs	2.82
25	404668	*C40Dac4	[]- DD420	IY- when Carea makely	2.81 2.81
23	420619 447241	AF130255 BE382838	Hs.99430 Hs.19322	lastis zinc finger protein ESTs	2.80
•	448793	A1864581	Hs.215477	ESTB	2.79
	453014	AI937242	Hs.176590	ESTs	2.79
	446775	Al792836	Hs.232273	ESTS	2.78
30	455075	AW854850	113.202270	gb:QV2-CT0261-201099-011-h03 CT0251 Homo	2.78
	406704	M21865	Hs.929	myosin, heavy polypeptide 7, cardiac mus	2.75
	457546	AA568484	Hs.153632	ESTs	2.75
	410197	NM_00551B	Hs.59889	3-hydroxy-3-mathylglularyl-Coenzyme A sy	2.74
	433677	A1791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN A	2.74
35	405703				2.73
	408840	AW277132	Hs.254880	ESTs	2.73
	413958	BE277913	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.73
	454421	BE409759	Hs.59563	Homo saptens mRNA for FLJ00007 protein,	2.73
40'	406702	Z20656	Hs_278432	myosin, heavy polypeptide 6, cardiac mus	2.72
40'	40B664	R56362		gb:yg93c07.r1 Soares Infant brain 1Ni8 H	2.72
	402457				271
	403612	1770000		MAIN	271
	407049	X72632	11- 400047	(NONE)	2.71
45	415423	AA164743	Hs.187617	Homo sapiens cDNA FLJ13941 fis, clone Y7	2.70
7.7	402862 403540				2.69 2.69
	431465	AW293178	Hs.180086	ESTs	2.69
	406563	A11233170	NS. 100000	E01\$	2.68
	417003	AL038170	Hs.B0756	betaine-homocysteine methyltransferæse	2.6B
50	426220	Al3B3475	Hs.171697	ESTs, Weakly similar to immunoglobulin s	2,68
	446707	Al591214	Hs.156336	ESTB	2.68
	447557	AW028809	Hs.229570	ESTs	2.68
	413529	U11874	Hs.846	interleukin 8 receptor, beta	2.67
	403997				2.66
55	408704	AA056635	Hs. 5366	Homo sapiens cDNA: FLJ21522 fis, clone C	2.66
	407005	U20230		gb:Human guanyi cyclase C gene, partial	2,65
	405075				2.64
	430728	AW968522		gb:EST380598 MAGE resequences, MAGJ Homo	2.64
60	405327	05444545	N 00.474	WOW IN IN I I DAMAGE I I	2.63
UU	409419	8E207219	Hs.20474	ESTs, Highly similar to S17112 interfero	263
	434300	AA740944	Hs.116295	ESTs	2.63
	405895 431929	AW294163	Hs,146127	ESTs	2.62 2.61
	405217	A44254100	[B,140121	COIS	260
65	437569	AA760849	Hs.294052	ESTs	2.60 2.60
Q.D	419822	AW968864	Hs.255780	ESTs	2.59
	445918	AW014139	Hs.145656	ESTs	2.59
	446149	BE242960	Hs.203181	ESTs	2.59
	457829	AJ742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.ca	2.58
70	404282				2.53
	409778	AW499705		gb:U1-HF-9R0p-ajk-b-05-0-U1.r1 N1H_MGC_5	2.53
	445353	BE551465	Hs.175211		2,53
	458764	BE619386		gb:601473204F1 NIH_MGC_68 Home saptens c	2.53
a -	402195				2.52
75	404247				2.52
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	. 2.52
	402588	hte			2.50
	432301	U34249	Hs.167075		2.50
80	424958	AA984420	Hs.283559		2,49
GU.	442197 415003	AW837912	LIA 77744	gb:QV3-LT0048-260100-068-c02 LT0048 Homo	2.49
	420767	M11437 AF072711	Hs,77741 Hs.99918	kininogen carboxyl estar lipase (bile salt-stimula	2.48 2.48
	422885	BE244088	Hs.121544		2.40 2.47
		WELTTOOD	110.12.1077		241
				201	

	440424	AJ991125	Hs.189109	Homo sapiens cDNA: FLJ21458 fis, clone C	2.47
	402153			1. 1. m. 1. m. 1000000 5 1 - 500	2.46
	432152	AK000245	Hs,272790	Homo sapiens cDNA FLJ20238 fis, clone CO	2.46
5	454414	R55574	Hs.164675	ESTs	2.45 2.44
2	401603	DICTORDE A	14- 40000	should be a subsect of the subsect o	2.44
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle) ESTs	2.43
	408513	AW206468	Hs.103118	hypothetical protein FLJ23412	2.42
	409826 400672	AW501112	Hs.34487	hypothetical protein resesting	241
10	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	241
10	449748	H23963	Hs.32043	ESTB	2.41
	453756	AW139415	Hs.61906	ESTs	2.41
	400624	7111 105410	10.01000		2.40
	403125				2.40
15	405118				2.39
	402165				2.38
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.38
	425515	W26609		gb:35f12 Human relina cDNA randomly prim	2.38
	402951				2.37
20	427886	AA417083	Hs.104789	ESTs	2.37
	447173	AW449385	Hs.157294	ESTs	2.37
	448703	BE613942	Hs.170890	Homo saplens cDNA: FLJ21129 fis, clone C	2.37
	425344	H41821	Hs.169393	transcriptional activator of the o-fos p	2.36
25	401840				2.35 2.34
25	403731				2.34
	405378 405555	Y09306	Hs.30148	homeodomain-Interacting protein kinase 3	2.34
	416559	A1039195	Hs.128060	ESTs, Weakly similar to cDNA EST yk481g5	2.34
	438216	ZB3952	Hs.252815	ESTs	2,34
30	448427	BE395250	1 10.202010	gb:601311130F1 NIH_MGC_44 Homo sepiens c	2.34
	4515BB	AW072057		gb:ws58g05.x1 NCI_CGAP_Bm25 Homo saplen	2.34
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA	2.33
	451172	AW206465	Hs.207423	ESTs	2.33
	401015				2.32
35	414705	BE464157	Hs.201455	aT83	2.32
	439894	AAB53077		gb:NHTBCae03e05f1 Normal Human Trabecula	2.31
	446305	AW270149	Hs.254515	ESTs, Moderately similar to AF248953 1 g	2.31
	453512	ALD40160	Hs.209542	ESTs, Weakly similar to B cell linker pr	2.29
40	418556	T02850	13 40-446	gb:FB12A9 Fetal brain, Stratagene Homo s	2.28 2.28
40	457197	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	2.28 2.2B
	457275 458766	AA463422 AW183618	Hs.209431 Hs.168417	ESTs ESTs, Weakly similar to ZnT-3 [H.saptens	2.28
	414075	U11862	Hs.75741	amlloride binding protein 1 (amine oxida	2.27
	430210	AL157426	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (fr	2.27
45	442614	Al269030		gb:qj73c12x1 NCI_CGAP_Kid3 Homo saplens	2.27
	402538				2.26
	439891	AL389940	Hs.109968	ESTs	2.26
	440056	BE294828	Hs.13323	hypothetical protein FLJ22059	2.26 2.25
50	406150	A 5 4C7 4D0		physiol 7-11 at Coome Toolle MUT Llema page	2.25 2.25
20	426880 447129	AA4534B2 AW014123	Hs.161402	gb:zx47a11z1 Soeres_tests_NHT Homo sap ESTs	2.25
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25
	458778	Al458309	Hs.117408	ESTS	2.24
	401728		1,2,1,1,1,00	2010	2.23
55	404139				2.23
	414095	BE293546		gb;601186671F1 NIH_MGC_15 Homo sapiens c	2.23
	432037	AW450592	Hs.300459	ESTs	2.23
	451965	AA021163	Hs.22287	ESTs	2.23
60	416768	AA363733	Hs.1032	regenerating Islat-derived 1 alpha (panc	2.22
60	427586	AA609681	Hs.190592		2.22
	454108	AA161071	Hs.71465 Hs.22293	squalene epoxidase	2,22 2,21
	429749	A%85174 AW511138	Hs.256581	ESTs ESTs	2.21
	434507 436652	AA724543	Hs.168824		2.21
65	437433	R74016	Hs.121581		2.21
05	4016B8	14,4014	112.12.1001	20.0	2,20
	441748	R14439	Hs.209194	ESTs	2.19
	453072	BE251845	Hs.221516		2.19
 -	400535			•	2.18
70	417176	AW974475	Hs.143467	ESTs	2.18
	427858	NM_001971	Hs.21	elastase 1, pancreatic	2.18
	454886	AW837063		gb:CV1-LT0037-150200-069-g08 LT0037 Homo	2.18
	458232	BE217872	Hs.279537		2.18
75	408922	R87388	11. 46444	gb:ym88g04.r1 Soares adult brain N2b4HB5	2.17
75	423668	Y10148	Hs.13113		2.17 2.17
	440338		Hs.12758	ESTs	2.17
	403115 409125		Hs.301560	D ESTs	2.18
	426887		Hs.21289		216
80	413811	BE168828	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:QV1-HT0517-020400-145-f04 HT0617 Homo	215
	442962		Hs.13161		2.15
	403921				2.14
	413140	T06507	Hs.6846	hypothetical protein FLJ13055	214
				200	

	421996	AW583807	Hs.1460	glucagon	2.14
	436130 407243	AA341497 AA058357	Hs.31408 Hs.74466	ESTs carcinoembryonic antigen-related cell ad	2,14 2,13
	407708	AF019968	Hs.37936	suppressor of varience in 3-9 (Drosophil	213
5	442792	Al352340	Hs.131194	ESTs	2.12
	454406	AA213605	Hs.267861	ESTs	2.12
	424648	AA344576		gb:EST50478 Gall bladder I Homo saplens	2.11
	433963	A1218808	Hs.187778	ESTa	2.11
10	400736				2.10
10	406343				2.10
	409702	AI752244	Hs.285749	Human DNA from chromosome 19-specific co	2.10
	432092	AF135026	11-007000	gh:Homo sapiers kallikrein-like protein	2.10
	441915 453147	A1566116	Hs.207066	ESTs, Weakly similar to FOG [M.musculus] CGI-05 protein	2.10
15	415604	AA733098 Z44177	Hs.279909 Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.10 2.08
1.5	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.08
	401211	AJ004832	Hs.5038	neuropathy target exterese	2.07
	413808	J00287	Ha.182183	caldesmon 1	2.07
	414433	BE407755	Hs.169100	Homo sapiens cDNA FLJ12529 fis, clone NT	2.07
20	421978	AJ243662	Hs.110195	NICE-1 protein	2,07
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	207
	433605	Al378012	Hs.147953	ESTs	2.06
	4493B3	AW444712	Hs.196573	ESTs	2,06
25	455652	BE054675		gb:RC1-BT0313-301299-012-h11 BT0313 Homo	2.05
25	402382	4 14 Page 114	h	ware.	2.04
	407282	Al345597	Hs.254727	ESTs	204
	457273 459073	AI167145	Hs.165538	ESTs	2.04
	402394	AW968616	Hs.296234	ESTs, Highly similar to mitogen-activate	2,04 2.03
30	428875	AW451624	Hs.178202	ESTs	2.03
_0	456634	AA609911	Hs.109012	ESTs	2.03
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.02
	439281	AA100768	Hs.48485	ESTs	2.02
	444153	AK001610	Hs.10414	hypothetical protein FLJ 10748	2.02
35	401122				2.01
	444340	A1143198	Hs.143561	ESTs	2.01
	455104	BE064863		gb:RC1-BT0313-110300-015-106 BT0313 Homo	2.01
	415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	2.00
40	440144	AW082297	Hs.88523	ESTs	2.00
40	403183	490000700		- Lab to the ploton is 07 of the shirt become	1.99
	409802 430144	AW500732 AJ732722	Hs.187694	gb:Ui-HF-BN0-akm-b-07-0-Ul.r1 NIH_MGC_50 ESTs	1.98 1.98
	444580	AI152722 AI168365	Hs.268663	ESTs	1.98
	401704	A 100303	1820000	Lois	1.97
45	401810				1.97
	424473	AK001405	Hs.148584	Homo sapiens cDNA FLJ10543 fis, clone NT	1.97
	438573	AW135084	Hs.299865	ESTs	1.97
	412921	BE009345	Hs.128942	ESTs	1.96
	422233	AB00205B	Hs.113275	purinergic receptor P2X-like 1, orphen r	1.96
50	425352	NM_000939	Hs.1897	prooplomelanocortin (adrenocorticotropin	1.96
	410285	AA083609		gb:zm53d05.r1 Stratagene fibroblast (937	1.95
	414323	NM_014759	Hs.239500	KIAA0273 gene product	1,94
	428119	AW298211	Hs.255737	ESTs	1.94
55	424510 425280	AK001841	Hs.149797	hypothetical protein FLJ 10979	1.92
55	429785	U31519 HB2114	Hs.1872	phosphoenolpyruvate carboxykinese 1 (sol	1,92
	437344	R90921	Hs.301769 Hs.6846	ESTs hypothetical protein FLJ13055	1.92 1. 9 2
	451819	AI819096	Hs.249260	ESTs	1.92
	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein	1.92
60	422664	AA315933	Hs.120879	ESTs	1.91
-	432247	AA531287	Hs.105805	ESTs	1.91
	453B Z 0	R77494	Hs.75416	DAZ associated protein 2	1.91
	400675				1.90
65	405556	Y09306	Hs.30148	homeodomaki-interacting protein kinase 3	1.90
65	407099	M94891	Hs.278423	pregnancy specific beta-1-glycoprotein 4	1.90
	440297	BE560553	Hs.205450	Homo sapiers cONA: FLJ22570 fis, clone H	1.90
	443104	AA088470	Hs.83135	p53-responsive gene 6	1,90
	444329 402590	W79753	Ha.5B330	ESTs	1.90
70	432354	AW137262	Hs.192713	ESTs	1.89
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.89 1.88
	443322	Al825817	Hs.143272	ESTs	1.88
	45B185	A)762757	Hs.129869		1.88
-	459072	AI815978	Hs.160427	ESTs	1.58
75	402534				1.87
	409689	AA078492		gb:7P04D11 Chromosome 7 Placental cDNA L	1.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	1.87
	430176	AL161995	Hs.234775		1.87
80	430631	AJ003147	Hs.278464		1.87
οU	433114	AA121579	11-004-	gb:zn77f02r1 Stratagene NT2 neuronal pr	1.87
	439254	U57352	Hs.6517	amiloride-sensitive cation channel 1, no	1.87
	448461 450675	AW166358 AA010662	Hs.124979 Hs.188639		1.87 1.87
	7,0073	1010 1000Z	1 to. 100000	2075	1.0/
				200	

	401767				1.85
	449891 400527	N64867	Hs.37848	ESTs	1.85 1.84
	428581	AA430570	Hs.104881	ESTs	1.84
5	443647	AV653846	Hs. 126261	Homo sapiens Chromosome 16 BAC clone CIT	1.84
5	444785	AV651441	Hs.282475	ESTs	1.84
	449566	AADD1778	Hs.288156	Homo sepiens cDNA: FLJ21819 fis, clone H	1.84
	436752	AW298529	Hs.255774	ESTs	1.83
	437405	AA338837	Ha.42547	Homo saplens cDNA FLJ13975 fis, clone Y7	1.83
10	449174	T66136	Hs.12880	ESTs	1.83
	449887	AW080B43	Hs.200275	ESTs	1.83
	453261	AA034116	Hs.118494	ESTs	1.83
	454243	AW241901	Hs.250683	ESTs	1.63
	459188	AA216382	Hs.30002	SH3-containing protein SH3GLB2	1.83
15	424334	AA393460		gb:zt71e05.r1 Soares_testls_NHT Homo sap	1.82
	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	1.82
	408123	AW163377		gb:au94e02.y1 Schneider fetal brafn 0000	1.81
	428722	U76456	Hs.190787	Essue inhibitor of metalloproteinase 4	1.80
20	442196	AI902646	Hs.31844	Homo saplens cDNA FLJ12586 fis, clone NT	1.80
20	421419	M99587	Hs.104134	homeo box (H6 family) 1	1.79
	405420				1.78
	405737	44404-03			1.78
	414016	AA134594	Hs.71528	ESTs	\$.78
25	415744	AW964850	Hs.279307	ESTs	1.78
25	420375	AF182077	Hs.97244	glioma tumor suppressor candidate region	1.78
	426322 421592	J05068 AF009801	Hs.2012 Hs.105941	transcobalamin 1 (vitamin B12 binding pr	1.78 1.77
	401743	AFGGS001	FIS. 100841	bagpips homeobox (Drosophila) homolog 1	1,75
	405187				1.75
30	442763	A)017037	Hs.131121	ESTs	1.75
50	451621	A)879148	Hs.26770	failty acid blooking protein 7, brain	1.75
	413248	T64B58	Hs.21433	ESTs	1.74
	423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti	1.74
	439999	AA115B11	Hs.6838	ras homolog gene family, member E	1.74
35	440185	AW104546	Hs.270929	ESTs	1,74
	450482	Al697844	Hs.221720	ESTs	1.74
	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYD	1.73
	420476	AW575863	Hs.136232	ESTs	1.73
40	428748	AW593206	Hs.98785	ESTs	1.73
40	431148	AA502653	Hs.28621	ESTs	1.73
	447205	BE617015	Hs.11006	ESTs	1.73
	455994	BE179190		gb:RC0-HT0613-210300-032-07 HT0613 Homo	1,73
	401039				1.72
45	403251	1111400004	11-053830	FOT.	1.72
45	409762	AW498884	Hs.257970	ESTs	1.72
	440914	AA909552	Hs.143884 Hs.21333	ESTS	1.72
	448507 409605	AL133109 AW444477	Hs.258507	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	1.72 1.71
	441212	AW242447	Hs.146182	ESTs ESTs, Weakly similar to lactese phlorizi	1.71
50	445624	AVV140103	Hs.78880	IVB (bacterial acelolactate synthase)-1	1.71
-	458619	AAB72064	Hs.301218	ESTs, Weakly similar to Unknown gene pro	1.71
	401969		1101001210	more troons on the production by	1.70
	403327				1.70
	407245	X90568	Hs.172004	tiün	1.70
55	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1,70
	436034	AF2B2693	Hs.150185	Inflammation-related G protein-coupled r	1.70
	442682	AI014545	Hs.231027	EST	1.70
	458494	Al380906	Hs.158436	ESTs .	1.70
4 0	404682				1.69
60	407402	AF035303		gb:Homo saplens clone 23943 mRNA sequenc	1.69
	409368	AA071059	14 405500	gb:zm66a10.r1 Stratagene neuroepithellum	1.69
	440362	AA883812	Hs. 125508	ESTs	1.69
	448868	BE297743	Hs.284203	myogenic factor 3	1.69
65	402201 426230	AA367019	tio 244205	contagns rusine 4 (trunsle 4)	1,6B
US	403186	MAGOIDIS	Hs.241395	prolease, serine, 1 (trypsln 1)	1.68 1.67
	409543	AW410200		gbtfn05b12.x1 NIH_MGC_17 Horse sepiens cD	1.67
	443672	AA323362	Hs.9667	butyrobelaine (genma), 2-oxoglutarate di	1,67
	450391	Al694522	Hs.202280	ESTs	1.67
70	408919	AW295352	Hs.251836	ESTs	1.66
-	416136	H45027	Hs.181770	ESTs	1.66
	416865	H97863	Hs.42456	ESTs	1.68
	419582	H13139	Hs.92282	paired-like homeodomain transcription fa	1.66
=-	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo saptens c	
75	429134	AA446953	Hs.99004	ESTs	1.65
	445041	T64183	Hs.11398	ESTs	1.65
	453240	A1969564	Hs.284249	Homo sapians cDNA: FLJ22334 fis, clone H	1.65
	405243	Gy*****	10 40-00-	r and AD	1.64
80	426039	BE265133	Hs.217493	annexin A2	1.64
00	430135	NM_000035			1.64
	435942 448106	R06285 A1800470	Hs.191215 Hs.171941		1.64 1.64
	408591	AF015224	Hs.46452	mammaglobin 1	1.63
	100001	1444	1 NITURAL		1.03

	410881	AW809157		gb:RC0-ST0118-041099-031-c07_1 ST0118 Ho	1.63
	417743	R14738	Hs.8312	ESTs, Weekly similar to AF170723 1 prote	1.62
	430632	AC004597	Hs.248088	olfactory receptor, family 10, subfamily	1.62
5	448651	BE246440	Hs.93728	pre-B-cell leukemla transcription factor	1,62 1.62
3	453718	AL119317	Hs.120360 Hs.28355	phospholipase A2, group VI (cytosolic, c Homo sapiens cDNA: FLJ22402 fis, clone H	1.62
	459499 412374	AW402653 X01388	Hs.73849	apolipoprotein C-III	1.61
	419113	Al446586	Hs.21835	ESTs	1.61
	426795	A\810474	Hs.196945	ESTs	1.61
10	426998	BE274360		gb:601121068F1 NIH_MGC_20 Homo saplens c	1.61
	428407	NM_003963	Hs.184194	transmembrane 4 superfamily member 5	1.61
	444475	C75571		gb:C75571 Human pancreatic Islet Homo sa	1.61
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	1.61
1 "	456275	AW976183	Hs.88414	ESTs, Weakly similar to dJ512E2.1 [H.sep	1,61
15	414050	BE246327		gb:TCBAP1E1967 Pediatric pre-B cell acut	1.60
	418004	U37519	Hs.87539	aldehyde dehydrogenasa 8	1.50
	428651	AF196478	Hs.188401	annexin A10	1.60
	443853	A1089064	Hs.250644	ESTs qb:Human mRNA clone with similarity to L	1.60 1.59
20	407007	U22981		gb:noman narray clone wan samany to c gb:yy78d01.r1 Soares_multiple_sclerosis_	1,59
20	412067 419080	N45697 AW150835	Hs.18878	hypothetical protein FLJ21620	1,59
	448619	A1867182	Hs.202255	ESTs	1.59
	403665	HIDO7 TOL	102202200		1.58
	407524	X64985		gh:H.sapiens mRNA HTPCRX11 for olfactory	1.58
25	424286	AA338285	Hs.90744	proteasome (prosome, mecropain) 26S subu	1.58
	412056	T28160	Hs.778	guanylate cyclese activator 18 (retina)	1.57
	430218	AW998865	Hs.186703	ESTs	1.57
	431882	NM_001426	Hs.271977	engralled homolog (1,57
20	450797	Al761930	Hs.205127	ESTs	1.57
30	455366	AW947563		gb:RC0-MT0004-140300-031-g11 MT0004 Homo	1.57
	408421	AW193734	Hs.253067	ESTs	1.58
	421907	BE018556	Hs.10935B	ATPase, Class V, type 108	1.56 1.56
	432742	AA564453 T64297	Hs.162339 Hs.5241	ESTs fatty acid binding protein 1, liver	1.56
35	436624 439543	W75935	Hs.146083	ESTs	1.56
55	443317	AI051601	Hs.200191	ESTS	1.56
	449097	BE271708	Hs.95110	ESTs, Weakly similar to PIP6_HUMAN 1-PHO	1.56
	457127	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	1.56
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1,	1.55
40	418837	U48263	Hs.89040	prepronociceptin	1,55
	436749	AA584890	Hs.5302	lectin, galactosida-binding, soluble, 4	1.55
	458475	AI650322	Hs.143249	EST8	1.55
	402561				1.54
45	411187	AW821291	**	gb:PM3-ST0307-241299-002-103 ST0307 Homo	1.54
43	419224	NM_012189	Hs.252716	fibroushealthin II	1.54
	414657	AA424074	Hs.76780	protein phosphalase 1, regulatory (inhib	1.53 1,53
	41542 6 421428	Z41991 U26726	Hs.23197 Hs.1376	ESTs hydroxysterold (11-bata) dehydrogenase 2	1.53
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.53
50	428489	Al807459	Hs.98582	ESTs	1.53
	437728	AA766719	IDDUUGE	gb:ca39c09.s1 NCI_CGAP_GCB1 Homo sapiens	1,53
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.52
	414932	C14577	Hs.194517	ESTS	1.52
	433500	AF064255	Hs.111401	very long-chain acyl-CoA synthetase homo	1,52
5 5	439688	AW445181	Hs.209837	Homo septens cDNA FLJ12921 fis, clone NT	1.52
	453391	AW600302	Hs.232655	ESTs	1.52
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	1.51
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.51
60	443012	A1566813	Hs,13227B Hs,78871	ESTs	1,51 1.50
UV	415824 445152	D42039 AI214567	Hs.283597	mesoderm developmeat candidate 2 ⊏stre	1.50
	440152 455941	BE160011	Hs.203097 Hs.129998	ESTs Homo sapiens cDNA FLI14267 fis, clone PL	1.50
	457889	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.50
	458503	AL133933	Hs.64310	Interleukin 11 receptor, alpha	1.50
65	400694				1.49
•	420937	AW966719	Hs.1340	colipase, pancreatic	1.49
	426752	X69490	Hs.172004	titien	1.49
	426784	U03749	Hs.172216	chromogrania A (parathyroid secretory pr	1.49
70	428874	W32133	Hs.194366		1,49
70	444287	A1033077	Hs.10755	dihydropyrimidinase	1.49
	450684	AA872605	Hs.25333	Interlaukin 1 receptor, type II	1.49
	425747	AI457620	Hs.205360		1.48
	432378	A(493046	Hs.146133		1.48 1.48
75	447999 452888		Hs.201778 Hs.252819		1.48
7.5	453888 406667		Hs.252818	appniju E218	1.40
	418129		Hs.1144	glycoprotein IX (platelet)	1.47
	426309		Hs.157195		1.47
	426755			gb:601108143F1 NTH_MGC_16 Horno septens c	1.47
80	414258		Hs.294141		1.46
	417421	AL138201	Hs.82120	nuclear receptor subternity 4, group A, m	1.46
	420562		Hs.190048		1.46
	425011	T51986	Hs.283100	hemoglobin, gamma G	1.46
				205	

	-100	*****			
	443050	AI612788	Hs.132348	ESTs, Weakly similar to diaphanous 1 (H.	1.46
	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.45
	434680	T1173B	Hs.127574	ESTs	1.45
	454771	AW819939	Hs,273629	ESTs	1,45
5	415672	N53097	Hs.193579	ESTs	1.44
•	418141	AWB45738	Hs.171118	Homo sapiens mRNA for FLJ00026 protein,	1.44
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.43
	418197	AA214253		gb:zn58g02,r1 Stratagane muscle 937209 H	1.43
10	431821	AW452256	Hs.271221	hypothetical protein FLJ20064	1.43
10	455433	AW939463		gb:QV1-DT0072-310100-056-g02 DT0072 Homo	1.43
	407743	AW814118		gb:MR3-ST0203-151199-011-d09 ST0203 Homo	1,42
	418888	AU076801	Hs.89436	cadherin 17, Li cadherin (liver-Intestin	1.42
	434001	AW950905	Ha.3697	serine (or cysteine) proteinase inhibito	1.42
16	441031	AI110684	Hs.7645	fibrinogen, B bela polypeptide	1.42
15	452456	BE080763		gb:QV1-BT0631-150200-071-f09 BT0631 Homo	1.42
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.42
	408349	BE546947	Hs.44276	homeo box C10	1,41
	420391	AA456891	Hs.79123	KIAA0084 protein	1.41
	421126				
20		M74587	Hs.102122	insulin-like growth tector binding prote	1.41
20	449329	AW752783		gb:ll.3-CT0219-221199-029-F03 CT0219 Homo	1.41
	453515	AA195712	Hs.132696	ESTs .	1.41
	417296	L36198	Hs.818B4	sulfoiransferase family, cylosolic, 2A,	1.40
	420287	AA740907	Hs.88297	ESTs	1.40
	427583	MB2962	Hs.179704	meprin A, alpha (PABA peptide hydrolese)	1.40
25	418787	AW296134	Hs.86999	ESTs	
23					1.39
	422072	AB018255	Hs.111138	KIAA0712 gene product	1,39
	425988	BE045897	Hs.274454	ESTs	1.39
	426087	AA100573	Hs.182421	troponin C2, fasi	1.39
	438136	NM_002390	Hs.6088	a disintegrin and metalloproteinase doma	1.39
30	455579	BE011320		gb:PM3-BN0218-090500-002-d09 9N0218 Horso	1.39
	402316			San um pueste despre ses cueste i tento	1,38
	417084	1100270	Un 22007	FCT-	
		H09370	Hs.33067	ESTs	1.38
	423276	AC003034	Hs.126261	Horno sapiens Chromosome 16 BAC clone CIT	1.3B
25	433767	A1472951	Hs.173688	ESTs	1.38
35	413830	BE263439	Hs.13144	HSPC160 protein	1.37
	423576	NM 000383	Hs.129829	autoimmune regulator (automimmune polyen	1.37
	401886				1.35
	412688	AW583062	Hs.74502	observatora de D4	
		ATTOMOG	11974905	chymotrypsinogen 81	1.36
40	401238				1.34
40	421511	AA488940	Hs.105216	hypothetical protein FLJ11125	1.34
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	1.34
	425450	U14755	Hs.157449	LIM homeobox protein 1	1.34
	427333	AF067797	Hs. 176658	aguaponin 8	1.34
	430937	X53463	Hs.2704	glulathione permidase 2 (gastrointestin	1.34
45	445204				
73		AW195523	Hs.245853	ESTs	1.34
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	1.34
	456379	W22206		gb:63E10 Human relina cDNA Tsp509I-cleav	1,34
	457416	BE142052		gb:CM3-HT0137-150999-011-b05 HT0137 Homo	1.34
	415741	AI902761	Hs.272087	ESTs	1.33
50	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	1.33
	429188	AB011171	Hs.198037		
				KIAA0599 protein	1.33
	442776	AW959498	Hs.8709	chymotrypsin C (celdectin)	1.33
	454748	AW862014		gb:RC3-CT0347-160200-013-d09 CT0347 Homo	1.33
	437744	AW290905	Hs.300288	ESTs, Weakly similar to CGHU2E collagen	1.32
55	451997	AAD21351	Hs.158497	KIAA0724 gene product	1.32
	452340	NM 002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.32
	411879	BE145354	Hs.273758	Homo sapiens cDNA: FLJ23112 fis, clone L	1.31
	424304				
		NM_001395	Hs.144879	dual specificity phosphatase 9	1.31
60	401442				1.30
UU	403942				1.30
	443687	F13040	Hs.182937	peptidylprolyl isomerase A (cyclophilin	1.30
	401624				1.29
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	1.29
	418575	AA225313	Hs.222886	ESTs	1.29
65	419818	A\657122	Hs.301931	ESTS	1,29
00					
	429845	AB020337	Hs.225943	UDP-GaltbetaGlcNAc beta 1,3-galactosyltr	1.29
	447586	Al0B1980	Hs.285829	solute certier family 25 (milochondrial	1.29
	407013	U35637		gb:Human nebulin mRNA, partial cds	1.28
	428470	AC002301	Hs.184507	Homo saplens Chromosome 16 BAC clone CIT	1.28
70	429780	AL137518	Hs.300388	ESTs	1.28
	453539	AW731886	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.eleg	1.28
	400846		17000130	weed anima a trootes frach	
		AASETONE	Lin doon to	C07a	1.27
	420257	AA257035	Hs.190042	ESTs	1.27
75	429184	AF095735	Hs.198003	sarcosine dehydrogenase	1.27
75	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	1,27
	444412	AI147652	Hs.216381	Homo saplens clone HH409 unknown mRNA	1.27
	451139	AW293316	Ha.205558	ESTs	1.27
	431284	AA570148	Hs.126783	Homo sapiens cDNA: FLJ22610 fis, clone H	1.26
80	431969	AA366217	Hs.2679	carboxypeptidase A1 (pancreatic)	1.26
OU	406158	transco.			1.25
	419648	773661	Hs.91877	ESTs, Highly similar to THIH_HUMAN THYRO	1.25
	430681	AW969675	Hs.291232	ESTs	1.25
	434880	1102388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.25

	436217	T53925	Hs.107	fortnagen-like t	1.25
	4400B9	AA864468	Hs.135646	ESTS	1.25
	446787 448207	U67167 A\475490	Hs.315 Hs.170577	mucin 2, inlestinal/tracheal ESTs	1.25 1.25
5	454869	AW836004	18.1103/	gb:PM0-LT0019-170200-001-d11 LT0019 Homo	1.25
	413271	AA127873	Hs.114949	ESTs	1.24
	422619	AA313322		gb:EST185218 Colon cardnoma (HCC) cell	1.24
	422796 427530	AW897265 AA405093	Hs.126519	gb:CM0-NN0057-150400-335-a04 NN0057 Homo ESTs	1.24 1.24
10	437727	AA766707	Hs.153039	ESTs	1.24
	426435	Al827946	Hs.189118	ESTs	1.23
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	1.22
	407964 430B28	AW130334 A1763257	Hs.281111 Hs.86327	ESTs Homo saplens cDNA: FLJ22431 fis, clone H	1.21 1.21
15	432029	D31628	Hs.2899	4-hydroxyphenylpyrsvate dioxygenase	1.21
	457843	AW138211	Hs.128746	ESTE	1.21
	413242	BE074165		gb:PM3-BT0564-030300-002-e12 BT0564 Homo	1.20
	446057 447198	Al420227 D61523	Hs.149358 Hs.283435	ESTS ESTs	1.20 1.20
20	449513	AI653232	Hs.195059	EST	1.20
	415566	F12119	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:HSC35H091 normalized infant brain cDN	1.19
	423315	R54109	Hs.26096	ĒSTs	1.19
	455817	BE142384		gb:CM2-HT0144-210999-011-d04 HT0144 Homo	1.19
25	459354 408432	BE514778 AW195262		gb:601317094F1 NIH_MGC_9 Homo sapiens cD gb:xn67b05.x1 NCL_CGAP_CML1 Home sapiens	1.19 1.18
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.18
	419251	NM_001486	Hs.89771	glucokinase (hexokinase 4) regulatory pr	1.18
	456702	AI684534	15. 444004	gb;wa72f10.x1 Soares_NFL_T_GBC_S1 Homo s	1.18
30	458009 410193	AJ221409 AJ132592	Hs.144983 Hs.59757	ESTs zlac finger protein 281	1,18 1 . 17
20	417779	AA829526	Hs.124977	ESTs	1,17
	435101	AJ743156	Hs.131064	ESTs	1.17
	445360	A)798776	Hs.158029	ESTs	1.17
35	414160 418078	BE257021 AA52126B	Hs.86508	gb:601117426F1 NIH_MGC_16 Homo saplens c ESTs	1.15 1.15
23	425133	NM_002613	Hs.154729	3-phosphoinositide dependent protein kin	1.15
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	1.15
	446377	AW014022	Hs.170953	ESTs	1.15
40	420097 446591	AA700127 H44186	Hs.190504 Hs.15456	ESTs PDZ domain containing 1	1.13 1.13
40	451477	A1798425	Hs.42710	ESTs	1.13
	459197	BE244587		gb:TCBAP2E0851 Pediatric pre-B cell scut	1.13
	428934	AF039401	Hs.194659	chloride channel, calcium activated, fem	1.12
45	431191 424403	AW972118	Hs,100002 Hs.1799	HSPC162 protein	1.12
45	433546	F05183 Al075877	Hs.125461	CD1D antigen, d polypeptide Homo sapiens cDNA FLJ11539 fis, clone HE	1.11 1.11
	451179	W05469	Hs.31818	ESTs	1.11
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	1.10
50	420774	AA280209	Hs.165270	ESTS	1.10
50	428887 430582	AA437009 A1215509	Hs.98954 Hs.143964	ESTs ESTs	1.10 1.10
	453642	Al370936	Hs.34074	dipeptidylpeptidase VI	1.10
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.09
55	41799B	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	1.09
33	456387 427965	W28876 D00306	Hs.183864	gb:52h7 Human retina cDNA randomly prime elastase 38	1.09 1,08
	447388	AW630534	Hs.78277	ESTs, Weakly similar to TB2 [H.saplens]	1.08
	413841	M34276	Hs.75576	plasminogen	1.07
60	429201	X03178	Hs.198246	group-specific component (vitamin D blnd	1.07
OU	433313 439450	W20128 R51613	Hs.298039 Hs.125304	ESTs ESTs	1.07 1.07
	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	1.07
	405161			· · · · · · · · · · · · · · · · · · ·	1.06
65	405741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	1.06
03	424294 424544	BE299311 M88700	Hs.150403	gb:801119256F1 NIH_MGC_17 Homo saplens c dopa decarboxylase (aromatic L-amino aci	1.06 1.06
	444687	AW972109	Hs.135107		1.06
	444754	TB3911	Hs.11881	transmembrane 4 superfamily marriber 4	1.06
70	421243	AW873803	Hs.102876		1.05
70	- 444290 407984	AA262496	Hs.29280	ESTs ESTs	1.05
	439706	AW134708 AW872527	Hs.243569 Hs.59761	ESTS	1.04 1.04
	402194	,	-		1.03
75	427506	AK000134	Hs.179100		1.03
75	428819	AL135623	Ha.193914		1.03
	434590 416378	T47232 AW044457	Hs.73708	gb:yb64b06.s1 Stratagene ovary (937217) ESTs, Waskly similar to A57291 cytokina	1.03 1.02
	431912	A\660552	Hs.154903		1.02
00	443316	A1478463	Hs.18443	ESTs	1.02
80	42B585	AB007863	Hs.185140		1.01
	400440 404819	X83957 BE514535	Hs.83870 Hs.77171	nebulin minichromozome malntenance deficient (S.	1.00 1.00
	407168	R45175		gbyg40f01.s1 Soares intent brain 1NiB H	1.00

	408052	AW501117	Hs.283585	ESTs	1.00
	409187	AF154830	Hs.50966	carbamoyi-phosphate synthelase 1, mitoch	1.00
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.00
_	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	1.00
5	410319	R23413	Hs.71935	putative zinc finger protein from EUROIM	1.00
	411D00	N40449	Hs.201619	ESTs, Weakly similar to SEB4B [H.saplens	1.00
	412098	AI493054	Hs.158968	ESTS	1.00
	412446	A1768015	Hs.92127	ESTs	1,00 1.00
10	412637 413147	AA115097 BE087271	Hs.261313	ESTs gb:PM2-BT0349-161299-001-b05 BT0349 Homo	1.00
10	413597	AW302885	Hs.117183	ESTs	1.00
	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzhache	1.00
	414523	AU076633	Hs.76353	serine (or cystelne) proteinase intribito	1.00
	417074	249878	Hs.81131	guanidinoacetate N-methyltransferase	1.00
15	418390	AF133820	Hs.84665	litin immunoglobulin domein protein (myo	1.00
	419768	T72104	Hs.93194	apolipoprotein A-l	1.00
	420182	Z44245	Hs.22999	ESTs	1.00
	420923	AF097021	Hs.273321	differentially expressed in hemetopoieti	1.00
20	421100	AW351839 AW081587	Hs.124660 Hs.165051	Homo sapisna cDNA: FLJ21763 fis, clone C ESTs	1.00 1,00
20	421204 422189	AF252292	Hs.112933	Tax interaction protein 40	1,00
	422792	AI95154B	Hs.135163	ESTs	1.00
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	1.00
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.00
25	424922	BE386547	Hs.217112	ESTs, Weekly similar to Similarity to Ye	1.00
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.00
	425545	N98529	Hs.158295	Huchan mRNA for myosin light chain 3 (MLC	1.00
	425983	AK000226	Hs.165619	mucin and cadherin-like	1.00 1.00
30	426004 427627	AW500300 R87582	Hs.124123 Hs.179915	ESTs, Weakly similar to syncollin [R.nor guanine nucleotide binding protein (G pr	1.00
50	428848	NM_000230	Hs.194235	leptin (murine obesity homolog)	1.00
	429027	AL022314	Hs.194750	Human DNA sequence from clone 1170K4 on	1.00
	429231	AAB13214		gb:a[32e09.s1 Soares_testis_NHT Homo sap	1.00
	429441	AJ224172	Hs.204098	lipophilin B (uteroglobin family member)	1.00
35	429930	A1580809	Hs.99569	ESTs	1.00
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1.00
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	1.00
	431845 433084	AA516469	Hs.270554 Hs.282265	ESTs fatty actd binding protein 2, intestinal	1.00 1.00
40	433839	M18079 F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00
	434452	AA634333	Hs.116822	ESTs	1.00
	435499	R89344	Hs.14148	ESTs	1,00
	438433	AB018274	Hs.6214	KIAA0731 protein	1.00
4	442403	AW207724	Hs.129516	ESTs	1.00
45	442803	A)67529B	Hs.199917	ESTa	1.00
	443266	Al277101	He.25890	ESTs, Weakly similar to transducin [H.sa	1.00
	444656	A1277924	Hs.145199	ESTS	1.00
	445573 446163	A1439646 AA026880	Hs.157494 Hs.25252	ESTs, Weakly similar to KIAA0676 protein Homo sapiens cDNA FLJ13603 fis, clone PL	1.00 1.00
50	447359	NM_012093	Hs.18268	edenylate kinase 5	1.00
•	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac mus	1.00
	448657	BE147657	Hs.293841	ESTs, Weakly similar to KIAA0672 protein	1.00
	449238	AA426229	Hs.85524	muscle-specific RING-finger protein homo	1.00
<i></i>	450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 ffs, clone C	1.00
55	450390	N93227	Hs.98403	ESTS	1.00
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AAS4_HUMAN 64 KD	1.00
	452093 452528	AA447453 AA742457	Hs.27860 Hs.291479	Homo sepiens mRNA; cDNA DKFZp586M0723 (f ESTs	1.00 1.00
	452624	AU076606	Hs.30054	coagulation factor V (proeccelerin, lab)	1.00
60	453754	AW972580	Hs.172753	ESTs	1.00
_	453991	AW014915	Hs.273741	ESTs	1.00
	454517	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	1.00
	459367	BE148877		gb:CM4-HT0244-111199-040-h12 HT0244 Homo	1.00
65	408021	AW137133	Hs.245B67	ESTs	0.99
U.J	417435 437206	NM_005181	Hs.82129 Hs.283382	carbonic anhydrase III, muscle specific	0.99 0.99
	437200 422890	AW975934 ZA3784	Hs.78713	ESTs, Weakly similar to Protein sequence solute carrier family 25 (mitochondrial	0.98
	425878	AW964806	Hs.38085	ESTs, Weakly similar to pulative glycine	0.9B
	441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.98
70	42306B	M25829	Hs.123107		0.97
	453534	NM_014796	Hs.33187	KIAA0748 gene product	0.97
	457787	AA683268		gb;as92b04.s1 Strategene schizo brain S1	0.97
	421285	NM_000102		cytochrome P450, subfamily XVII (steroid	0.96
75	422069	AJ010063	Hs.111110		0,96
13	425260 418406	1.47726 X73501	Hs.1870 Hs.84905	phenylalanine hydroxylase cytokaratin 20	0.96 0. 95
	425870	AW968536	Hs.190146		0.95
	416373	AA195845	Hs.73680	ESTs. Weakly similar to AF19B455 1 epith	0.94
	452243	AL355715	Hs.28555	programmed call death 9	0.94
80	411908	L27943	Hs.72924	cytidine deaminase	0.93
	415067	A1264969	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.93
	437156	A)916600	Hs.121194		0.93
	450685	L15533	Hs.423	pancrealitis-associated protein	0.92

	427450	AB014526	Hs.178121	KIAA0626 gene product	0.91
	432440	X63597	Hs.2996	sucrase-leomaliase	0.91
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.90
5	414910 423317	X12662 AJ272204	Hs.29679 Hs.64616	cofactor required for Sp1 transcriptiona chromosome 12 open reading frame 3	0.89 0.89
_	424735	U31875	Hs.152677	Homo saplens cDNA FLJ20338 fis, clone HE	0.89
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cON	0.89
	452689 446240	F33868	Hs.284176	transferin	0.89
10	449110	A1535736 H56112	Hs.170165 Hs.277053	ESTs ESTs	0.88 0.88
10	453817	AW755253	Hs.61920	ESTs	0.88
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.87
	438461	AW075485	Hs,286049	phosphosenne aminotransferase	0.87
15	446525 453341	AW967069 Al758912	Hs.211556 Hs.296341	Homo caplens cONA: FLJ23378 fis, clone H adenylyl cyclase-associated protein 2	0.87 0.87
	403740	22212			0.86
	420156	AW44925B	Hs.6187	ESTs	0.86
	430304 421142	AL122071 AW503944	Hs.238927 Hs.130822	Homo sapiens mRNA; cDNA DKFZp434H1235 (f ESTs	0.86 0.85
20	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.85
	419415	AW451692	Hs.192036	ESTs	0.84
	423321	AB013885	Hs.126926	beta-ureidopropionese	0.84
	432938 433447	T27013 U29195	Hs.3132	steroidogenic acute regulatory protein	0.84 G.84
25	403047	Q23133	Hs.3281	neuronal pentraxin II	0.83
	406707	S73840	Ha.931	myosin, heavy polypeptide 2, skeletal mu	0.81
	407782	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje	0.81
	405232 437776	AA768037	Hs.291671	ESTs	08.0 08.0
30	415505	R39870	Hs.12548	ESTs	0.66
	444436	N25871	Hs.177337	ESTs	0.78
	409096	AA194412	Hs.50550	sarcomeric muscle protein	0.77
	432134 437066	A1816782 AA743570	Hs.122583 Hs.200935	Homo sapiens cDNA: FLJ21934 fis, clone H ESTs	0.76 0.76
35	427003	U19487	Hs,2090	prostaglandin E receptor 2 (subtype EP2)	0.75
	423634	AW959908 .	Hs.1690	heparin-binding growth factor binding pr	0.73
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	0.71
	420567 447145	AK000812 AA761073	Hs.98874 Hs.192943	similær to proline-rich protein 48 ESTs	0.71 0.71
40	452103	R42764	Hs.3248	mutS (E. coli) homolog 6	0.71
	410929	H47233	Hs.30643	ESTs	0.70
	400301	X03635	Hs.1657	estrogen receptor 1	0.69
	415702 411396	F28877 C04646	Hs.85428	gb:HSPD18414 HM3 Homo sapiens cDNA clone ESTs	0.67 0.65
45	431706	AI816066	Hs.296341	adenylyl cyclase-associated protein 2	0.65
50	TABLE 2	BB			
50	(Name	Dalaira Can		KE	
	Pkey: CAT num	Onique Ecs ber: Gene cluste:	probesetiden r number	idliet unuper	
	Accession		cession numb	pers	
55					
33	Pkey 407743	1012151_1	Accession	AW814257 AW072376	
	408123	1040435_1		AW160398	
	40B432	1058667_1	AW195262	R27868 AW811262	
60	408664	1073340_1		V248096 R07162 R07285	
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70	412067 413147	1275641_1 1350637 1		15540 AW890595 BE067266 BE067286 BE067278 BE067299 BE067286	
, 0	413242	1355323_1		BE075001 BE075009	
	413811	1391117_1	BE168828	9E168830 BE168823 BE168928 BE168820 BE168826	
	414060	1413697_1	BE246327		
75	414095 414160	1416521_1 1422273_1	BE293546 BE257021	BE258316 BE257099	
	414580	1463848_1		9E408B33 BE385437	
	415011	15132B_1	AW963089	5 AA159005 AW963073	
	415566 415702	1539861_1		5475 T64832	
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	418197	172884_1	AA214253	AA214259 Z28472 Z28881 Z17828	
	418464	17590382			
	418556	1767866	102850		

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AW631296 AA375484
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          426507
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 55
            TABLE 28C
            Pkey:
Ref:
                          Unique number corresponding to an Eos probeset
                          Sequence source. The 7 digit numbers fit this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 60
                          indicates DNA strand from which exons were predicted.
            Strand:
            Nt_position:
                          indicates nucleotide positions of predicted exons.
            Pkey
                                                      Nt_position
                                        Strand
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                          8954013
                                        Phis
                                                      131475-131652
 65
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400545
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9800107
                                        Plus
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                          722B177
                                        Minus
                          8567750
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	401840	7684597	Plus	56283-56439
	401886	7229913	Minus	79215-79393
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10	401969	3126777	Plus	44863-45366
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	402194	8576113	Plus	70917-71191
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	402538	9801137	Minus	96314-96539
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	402762	9230904	Minus	123298-124036
	402862	2956660	Minus	18518-18656
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	402951	9408717	Plus	73252-73329,73718-73877,76217-76299,78195-78401
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	403186	9838287	Minus	117513-117856
	403211	7630841	Minus	159211-159369
40	403247	7656833	Mirais	76626-77140
45	403251	7677983	Plus	100391-100652
	403327	8440025	Minus	174311-174451,174587-174705,175523-175592
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	403665	7249278	Plus	69027-69375
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	403942	7711825	Minus	99606-99757
	403997	7708819	Plus	134427-134593
60	404139	9838113	Plus	76707-76891
	404247	7406725	Minus	83949-84214,84312-84415,84499-84677,84878-85114
	404282	2276311	Plus	61503-62205
	404348 404668	7630858 9797204	Minus Minus	28895-29062 11332-11546,12584-12718
65	404682	9797231	Minus	40977-41150
-	404795	4826439	Plus	147501-147780
	404825	6478944	Plus	210382-210494
	404938	7381808	Minus	165838-165950
70	405075	7770506	Minus	124680-125321
70	405147	9438278	Minus	158996-159557
	405161	9968260	Plus	157607-157785 161171-161299
	405163 405187	9966267 7229826	Minus Pius	117025-117170,118567-118736
	405217	7239551	Plus	32646-33138
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	405243	7249201	Minus	22312-23197
	405327	6094661	Minus	120550-120750
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	406059	9103984	Minus	13856-14004

	406101	9124019	Plus	125325-125831
	406118	9143818	Plus	53997-54629
	406150	9886026	Minus	59331-59701
_	406158	7144874	Plus	62393-63016,65012-65578
5	406343	9255974	Plus	17284-17440,18489-18646,18917-19004,19384-19638
	406357	9256093	Minus	77181-77415
	406563	7711604	Plus	34401-34538

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TABLE 29A: 2286 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO NORMAL BODY

Table 29A lists about 2286 genes that are up regulated in kilopathic pulmonary fibrosis samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" (diopathic pulmonary fibrosis expression level to "average" normal adult tissues sample expression was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90° percentite amongst idiopathic pulmonary fibrosis camples. The "average" normal adult tissue level was set to the 95° percentile amongst non-malgnant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15° percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eas probeset Identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelO: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of IPF to normal body tissue

0.5			-		
25	Pkey	ExAcon	Unigene ID	Unigene Title	R1
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	211.8
	442275	AW449467	Hs.54795	ESTs	189.7
	431433	X65018	Hs,253495	surfactant, pulmonary-associated protein	134.1
30	441835	AB036432	Hs.184	advanced glycosylation end product-spect	130.4
	417204	N31037	Hs.1074	surfactant, pulmonary-associated protein	116.8
	421798	N74880	Hs.264930	N-acylsphingosine amidohydrolase (acid c	92,1
	406964	M21305		gb:Human alpha satellite and satellite 3	80,7
25	443709	AI082592	Hs.134662	ESTs	67.1
35	431164	AA493650	Hs.94367	Homo seplens cDNA: FLJ23494 fis, clone L	61.4
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	57.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitiat	54.6
	457200	U33749	Hs.197764	thyroid franscription factor 1	44.9
40	432519 443324	A)221311 R44013	Hs.130704 Hs.164225	ESTs, Weakly similar to BCHUIA S-100 pro ESTs	42.7 39.8
TU	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 ffs, clone HE	27.3
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	27.3 27.1
	444527	NM_005408	Hs.113B3	small Inducible cytokine subfamily A (Cy	27.1
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	26.9
45	424084	A1940675	Hs.20914	hypothetical protein FLJ23056	22.2
	421659	NM_014459	Hs.106511	protocedherin 17	21.0
	450478	AW451709	Hs.271200	ESTs	20.2
	444342	NM_01439B	Hs.10887	similar to lysosome-associated membrane	19.7
	447033	A)357412	Hs.157601	ESTs	19.4
50	445885	A1734009	Hs.127699	KIAA1603 protein	18.9
	41188D	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo saplens	17.9
	432437	VV07088	Hs.293685	ESTs	17.8
	424105	A1142336	Hs.43977	Human DNA sequence from clone RP11-196N1	17.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, cione CO	17.2
55	440807	AJW269421	Hs.128093	ESTs	16.7
	424917	A1636208	Hs.96901	hypothetical protein FLJ23049	16.4
	433365	AF026944	Hs.293797	ESTs	16.4
	445279	R41900	Hs.22245	ESTs	16,4
60	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	16.4
OU	405654	44000 400	** ****	FOT	16.1
	449328	A1982493	Hs.197647	ESTs	16.1
	449494	AW237014	Hs.315369	Homo sapians cDNA: FLJ23075 fis, clone L	15.7
	408826 417728	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	15.5
65	440452	AW138437 A1925136	'Hs,24790 Hs,55150	KIAA1573 protein ESTs, Weakly similar to CAYP_HUMAN CALCY	15.0 14.8
03	452039		Hs.172510	ESTs	14.4
	40B771	AW732573	Hs.47584	potassium vollage-gated channel, delayed	14.3
•	421464		Hs.190086	ESTs	14.1
	421554		Hs.97775	ESTs	13.8
70	431869		Hs.124945	ESTs, Weakly similar to A46010 X-linked	13.2
	434424		Hs,325335	Homo sapiens cDNA: FLJ23523 fis, close L	13.2
	431924		Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	12.9
	459702				12.7
	421110	AJ250717	Hs.1355	cathepsin E	12.6
75	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	12.6
	423575		Hs.163443	Homo sapiens cONA FLJ11576 fis, clone HE	12.5
1	423244		Hs.209602		12.2
	427585		Hs.179729		12.1
90	436982		Hs.5378	spondin 1, (f-spondin) extracellular mat	12.1
80	451561		Hs.177403		12.0
	424086		Hs.102267		120
	435299		Hs.122614		12.0
	429496	AA453800	Hs.192793	ESTs	11.9

	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
	436061	AI248584	Hs.190745	Homo saplens cDNA: FLJ21326 fis, clone C	11.2 10.9
5	431385 421470	BE178536 R27496	Hs.11090 Hs.1378	membrane-spanning 4-domains, subfamily A annexin A3	10.8
-	440209	H05049	Hs.22269	neurexin 3	10.8
	428927	AA441837	Hs.90250	ESTs	10.7
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	10.5
10	424717	H03754	Hs.152213	wingless-type MMTV Integration site fami	10.4
10	416402 446998	NM_000715 N99013	Hs.1012 Hs.16762	complement component 4-binding protein, Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.4 10.4
	442176	AA983764	Hs.128910	ESTs	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
1.5	452883	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	10.3
15	417015	M83772	Hs.80876	flavin containing monooxygenase 3	10.3 10.3
	422022 447724	AA302420 AW298375	Hs.200442 Нв.24477	ESTs ESTs	10.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	10.0
-00	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	9.9
20	446232	A1281848	Hs.194691	retinoic add induced 3	9.9
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	9.9 9.8
	453382 412372	AA709285 R65998	Hs.5997 Hs.285243	hypothetical protein FLJ13078 hypothetical protein FLJ22029	9.6 9.8
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 (H	9.8
25	407568	AA740964	Hs.62699	ESTs	9.8
	414259	W44633	Hs.301296	Homo saplens cDNA: FLJ23131 fis, clone L	9.6
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin ESTs	9.5 9.5
	441484 422425	AA935481 W79117	Hs.58972 Hs,58559	ESTs	9.5 9.4
30	406747	AJ925153	Hs.217493	annexis A2	9.4
	450050	Al681268	Hs.257883	ESTs	9.4
	431337	N48107	Hs.292593	ESTs	9.3
	408427 447048	AW194270 AW393080	Hs.177236 Hs.228320	ESTS	9.3 9.3
35	453636	R67837	Hs.169872	hypothetical protein FLI23537 ESTs	9,3
	443450	N66045	Hs.133529	ESTs	9.2
	418735	N48769	Hs.44609	ESTs	9.2
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0923 (f	9.1
40	449802 441233	AW901804 AA972965	Hs.23984 Hs.135568	hypothetical protein FLJ20147 ESTs	9.1 9.1
	459587	AA031956	113.100000	gbzk15e04.s1 Soares_pregnant_uterus_NbH	9.0
	436245	AW450963	Hs.119991	ESTs	9,0
	445189	A1936450	Hs.147462	ESTs	8.9
45	410781	Al375672	Hs.165028	ESTs	8.9
45	446868 415817		Hs.135100 Hs.78867	ESTs protein tyrosine phosphatase, receptor-t	8.8 8,8
	425664		Hs.159003	transient receptor polential channel 6	8.8
	414958	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	8.8
50	410334		Hs.291993	ESTs	8.8
20	442510 409238		Hs.249B90 Hs.51515	ESTs Homo sapiens mRNA; cDNA DKFZp564Gt12 (fr	8.6 8.7
	431089		Hs.283676	ESTs, Weakly similar to unknown protein	8.7
	444929	A1685841	Hs.161354	ESTs	8.7
55	413802		Hs.32241	ESTs. Weakly similar to S65657 alpha-1C-	8.6
55	444218 412719		Hs.10684 Hs.129911	Homo sapiens clone 24421 mRNA sequence ESTs	9,6 8,6
	453445		Hs.91453	EST3	8.5
	419261		Hs.89791	wingless-type MMTV Integration site famil	8.5
60	451110		Hs.265398	ESTs, Weakly similar to transformation-r	8.5
60	433815 432203		Hs.112757	ESTs	8.3 8.3
	451103		Hs.49 Hs.25956	macrophage scavenger receptor 1 DKFZP564D206 protein	8.3
	425921		Hs.162211	solute carrier family 6 (neurotransmitte	8.3
~=	424989	AA985520	Hs.23576	ESTs	8,3
65	433231		Hs.143552	KIAA1493 protein	8.2
	40B217 431808		Hs.279860 Hs.270737	tumor protein, translationally-controlle tumor necrosis factor (ligand) superfami	8.1 8.1
	436751		Hs.294054	ESTs	8.0
	452891		Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	8.0
70	413048		Hs.75182	mannose receptor, C type 1	8.0
	426803		Hs.179747	ecotropic viral integration site 5	7,9
	409718 423424		Hs.56045 Hs.128433	sre homology three (SH3) and cysteine of prostaglandin D2 synthese, hematopoletic	7.8 7.8
	429597		Hs.2442	a disintegrin and metalloproteinase doma	7.7
75	421013	M62397	Hs.1345	mutated in colorectal cancers	7.7
	437479		Hs.101277		7.6
	416778 421478		Hs.79876 Hs.97258	steroid sulfatase (microsomal), arylsulf ESTs. Moderately similar to \$20530 ribos	7.6 7.6
	444396		Hs.4257	ESTs, Moderately similar to \$29539 ribos ESTs	7.6
80	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	7.6
	450718		Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.6
	44549: 446466		Hs.38489 Hs.308	ESTs, Weakly similar to 138022 hypotheti arrastin 3, retinal (X-arrestin)	7.6 7.6
	-1919401	, ,,,,,,,,,,,	1101000	or common formations.	7.0

	449108	Al1406B3	Hs.98328	hypothetical protein MGC13040	7.5
	422798 416030	R92347 H15261	Hs.34574 Hs.21948	ESTs, Wealdy similar to ALU1_HUMAN ALU S ESTs	7.5
_	426486	BE178285	Hs.170056	Homo saplens mRNA; cDNA DKFZp586B0220 (f	7.5 7.4
5	424906	A1566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	7.4
	448206	BE622585	Hs.3731	ESTs, Moderately similar to 138022 hypot	7.3
	432133 447112	AB033088 H17800	Hs.272567 Hs.7154	KIAA1262 protein ESTs	7.3 7.3
	446917	Al347863	Hs.156672	ESTs ESTs	7.3 7.3
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.3
	431761	AW002846	Hs.105468	hypothetical protein FLJ22690	7.3
	428743 413499	AL080060 BE144884	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr gb:CM0-HT0182-041099-065-e11 HT0182 Homo	7.2 7,2
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	7.2
15	438122	A1620270	Hs.129837	ESTs, Wealdy similar to Z263_HUMAN ZINC	7.2
	449611	AI970394	Hs.197075	ESTS	7.2
	453616 410060	NM_003462 NM_001448	Hs.33846 Hs.58367	dynein, axonemai, light intermediate pot glypican 4	7,2 7.2
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
20	452571	W3151B	Hs.34665	ESTs	7.2
	453736	AL118674	Hs.34871	zinc finger fromeobox 1B	7.2
	409203 405494	AA780473	Hs.687	cytochrome P450, subfemily IVB, polypept	7.2 7.2
~~	442832	AW206560	Hs.253569	ESTs	7.1
25	420193	AI460080	Hs.202869	ESTs	7.1
	434217 427356	AW014795 AW023482	Hs.23349 Hs.97849	ESTs ESTs	7.0
	436396	A1683487	Hs.152213	wingless-type MMTV Integration site famil	7.0 6.9
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6,9
30	442377	AA993807	Hs.167367	ESTs	6.9
	441143 445122	A1027604 AW241632	Hs.159650 Hs.147377	ESTS	6.9
	431353	AA828032	Hs.189076	hypothetical protein FLJ23598 ESTs	6.9 6.9
25	407510	U96191		gb;Human trophoblast hypoxia-regulated f	6.8
35	426753	T89832	Hs.17027B	ESTs	6.8
	445186 451963	AW614544 Al825440	Hs.123641 Hs.224952	protein tyrosine phosphatase, receptor t ESTs	6,8 6.8 .
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.B
40	433426	H69125	Hs.133525	ESTs	6.8
40	434377 415236	AW137148	Hs.306593	Homo sapiens cDNA FLI11382 fis, clone HE	6.8
	409031	R41400 AA376836	Hs.76728	gb:yt94b12.s1 Soares infant brain 1NIB H ESTs	6.8 6.7
	427558	D49493	Hs.2171	growth differentiation factor 10	6.7
45	437259	A1377755	Hs.120695	ESTs	6.7
43	421952 447081	AA300900 Y13896	Hs.98849 Hs.17287	ESTs, Moderately similar to AF161511 1 H	6.7
	430099	AW194988	Hs.20537	potassium inwardiy-rectifying channel, s hypothetical protein FLI 13942	6.7 6.7
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	6.7
50	413472	BE242870	Hs.75379	solute carrier family & (glial high affi	6.7
50	424750 403574	D29956	Hs.152818	appdagu specific biojesse 8	6.6 6.6
	439759	AL359055	Hs.67709	Homo saplens mRNA full length insert cDN	6.6
	415025	AW207091	Hs.72307	ESTa	6.5
55	448104 444271	AJ674818 AW452569	Hs.316433	Homo sapiens cDNA FLI11375 fis, clone HE	6.5
	437157		Hs.149804 Hs.120655	ESTS ESTS	6.5 6.5
	444050	AW138295	Hs.135024	ESTs	6.5
	414569		Hs.118258	prostate cancer associated protein 1	6.5
60	447505 424433	AL049268 H04607	Hs.18724 Hs.9218	Homo sapiens mRNA; cDNA DKFZp564F093 (fr ESTs	6.5 6.4
-	40737B	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	6.4
	445424		Hs.12695	cortactin SH3 domain-binding protein.	6.4
	422544 449765		Hs.118140 Hs.206832	KIAA0716 gene product	6.4
65	413930		Hs.75818	ESTs, Moderately similar to ALUS_HUMAN A RAB11A, member RAS oncogene family	6.3 6.3
	417246		Hs.21411	ESTs	6.3
	453652		Hs.2836B	ESTs, Moderately similar to \$65657 alpha	6.3
	411514 438909			gb:IL3-CT0219-271099-022-H12 CT0219 Homo	6.3
70	446002		Hs.145789	gb:Homo sepiena full length insert cDNA ESTs	6.3 6.3
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
	419150		Hs.89640	TEK tyrosine kinase, endothelial (venous	6.3
	424202 431723		Hs.15032 Hs.16762	RAN binding protein 17 Homo sepiens mRNA; cDNA DKFZp564B2062 (f	6.3 6.2
75	415511		Hs.182362	ESTs	6.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.2
	416879 432803		Hs.42599	ESTS chysication of NCI CCAD CC2 Home serious	6.2
	432803 442862		Hs.15738	gb:sk41f01.s1 NCI_CGAP_GC2 Homo sapiens ESTs	6.2 6.2
80	435974	U29690	Hs.37744	Homo sapiens beta-1 edrenergic receptor	6.2
	441082		Hs.202665	ESTs	6.2
	404599 453931		Hs.25144	ESTs	6.1 6.1
		,			0.1

	420252	AW270404	Hs.193161	ESTs	6,1
	431622	AW979271	Hs.293184	ESTs	6.1
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.1
_	415457	AW081710	Hs.7369	ESTs, Weakly skrillar to ALU1_HUMAN ALU S	6.0
5	424693	BE169810	Hs.47557	ESTs	6.0
	419172	AW338625	Hs.22120	ESTs	6.0
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.0
	453037	AA045175	Hs.177552	aTES	6.0
10	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.0
10	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	6.0
	422352	AA766296	Hs.99200	ESTs	5.9
	433527	AW235613	Hs.133020	ESTs	5.9
	420077	AW512260	Hs.87767	ESTs	5.9
	429703	T93154	Hs.28705	ESTs	5.9
15	433098	AW190593	Hs.151143	ESTs	5.9
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	5.9
	449416	Al651016	Hs.246311	ESTs	5.9
	459023	AW968226	Hs.60798	ESTs	5.9
	450584	AAB40403	Hs.60371	ESTs	5.9
20	427660	AI741320	Hs,114121	Homo saptens cONA: FLJ23228 fis, clone C	5.9
~~	429125	AA446854	Hs.271004	ESTs, Weakly similar to 138022 hypotheti	5.9
	450025	AK001875	Hs.24321	Homo sepiens cDNA FLJ12028 fis, clone HE	5.9
	433479	AW511459	Hs.249972	ESTs	5.8
	443113		Hs.132908	ESTs	5.8
25		AI040685	Hs.120368	ESTs	
23	430414	AW365665			5.8
	419752	AA249573	Hs.15261B	ESTs, Moderately similar to ZN91_HUMAN Z	5.B
	435420	A]928513	Hs.59203	ESTs	5.B
	404916	A A000040	tt. pana	testes development related them come	5.8
20	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.8
30	448253	H25899	Hs.201591	ESTs ·	3.0
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5. B
		Al699629	Hs.156781	ESTs	5.8
	435082	AA664273	Hs.186104	Homo saplens cDNA FLJ13803 fis, clone TH	5.7
2.5	436842	AA827176	Hs.124316	ESTs	5.7
35	437260	AA747807	Hs.149500	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-e04 ST0131 Homo	5.7
	428043	T92248	Hs.2240	uteraglobin	5.7
	408045	AW138959	Hs.245123	ESTs	5.7
40	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	5.7
40	428508	BE252383	Hs.184668	SBBI31 protein	5.7
	453393	AW956392	Hs.110376	ESTs	5.6
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	5.6
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.6
	429784	M89796	Hs,30	membrane-spanning 4-domains, subfamily A	5.6
45	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	404043				5.5
	415094	D59513	Hs.330778	ESTs	5.5
	453049	BE537217	Hs.30343	ESTs	5.5
50	430153	AW968128	Hs.336679	ESTs	5.5
	410811	AW805687	Hs.300648	EST8	5.5
	443903		Hs.135223	ESTs	5.5
	429420		Hs.202289	hypothetical protein DXFZp434P1735	5.5
	444471	AB020684	Hs.11217	KIAA0877 protein	5,5
55	452542			gb:RCO-ST0174-191099-031-a07 ST0174 Homo	5.5
	434088		Hs.249270	hypothetical protein PRO1966	5.5 5,5
	432113		Hs.152385	ESTs	5.5
	446608		Hs.257846	ESTS	5.5 5.5
	419945		Hs.118923	ESTs	5.5 5.5
60	454024	AA993627	Hs.293907	hypothetical protein FLJ23403	5.4 5.4
~~	420209		Hs.126485	hypothetical protein FLJ12604; KIAA1692	5.4 5.4
	439382		Hs.103070	ESTs	5.4 5.4
	428895		Hs.187247	ESTs	5.4
	446577		Hs.15420	KIAA1500 protein	5.4
65	419247		Hs.89784		
05				fragile X mental retardation 1	5.4
	427778		Hs.105323	ESTs	5.4
	437138 431322		Hs.271245	ESTS	5.4
			11. 400040	gb:EST382704 MAGE resequences, MAGK Homo	5.4
70	430437		Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.4
70	435202		Hs.170204	KIAAD551 protein	5.4
	415076		Hs.77890	guanylate cyclase 1, soluble, beta 3	5.3
	434992		Hs.283358	ESTs	5.3
	454039		Hs.245540		5.3
75	456408		Hs.23450	mitochondrial ribosomal protein S25	5.3
75	406554				5.3
	426269		Hs.168950		5.3
	416769		Hs.115436		5.3
	414299		Hs.71730	ESTs	5.3
00	420362		Hs.97206	huntingtin interacting protein 1	5.3
80	459564			· · · · · · -	5.3
	425509		Hs.15B213	sperm associated antigen 6	5.3
	401497			W II	5.3
	440727	Al073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	5.2

	428434	AW363590	Hs.65551	Homo sepiens, Similar to DNA segment, Ch	5.2
	408776	AA057365	Hs.63356	ESTs, Weakly similar to 138022 hypotheti	5,2
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	5.2
5	451050	AW937420	Hs.69662	ESTs	5.2 5.2 ·
3	400297 404957	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	5.2 5.2
	452771	T05477	Hs.333265	ESTs	5.2
	438885	A1886558	Hş.184987	ESTs	5.2
10	428244	Al564123	Hs.42500	ADP-ribosylation factor-like 5	5.2 5,2
10	420481 455047	U50525 AW852530	Hs.98201	Human BRCA2 region, mRNA sequence CG029 gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2 5.2
	408729	AA195764	Hs.72639	ESTs	5.1
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALUB_HUMAN A	5.1
15	425342 417154	AF093419 A1874701	Hs,16937B Hs.21388	multiple PDZ domain protein ESTs	5.1 5.1
1.5	411869	W20027	Hs.23439	ESTs	5.1
	427043	AA397679	Hs.3991	ESTs	5.1
	445635	A)769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
20	442973 422083	BE567665 BE156476	Hs.286550	Home sapiens cDNA: FLJ23156 ffs, clone t. gb:QV0-HT0368-040100-082-c05 HT0368 Home	5.1 5.1
20	448299	AA497044	Hs.20887	hypothetical protein FL.110392	5.1
	408677	AI279892	Hs.46801	sorting nextin 14	5.0
	404097		11 004014	rad.	5.0
25	437636 452822	AA764781 X85689	Hs.291844 Hs.288617	ESTs hypothetical protein FLJ22621	5.0 5.0
25	410733	D84284	Hs.66052	CD38 antigen (p45)	5.0
	439140	W85737	Hs.290830	ESTs	5.0
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	5.0 5.0
30	405547 423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp686H0718	5.0
20	449168	NM_016206	Hs.23142	colon carcinoma related protein	5.0
	455431	AW938484		gb:CM0-DT0057-290200-253-d06 DT0057 Homo	5.0
	452281	T93500	Hs.28792 Hs.269128	Homo saplens cDNA FLJ11041 fis, clone PL ESTs	5.0 5.0
35	411149 432441	N68715 AW292425	Hs.163484	ESTs	5.0
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	5.0
	440615	A1733055	Hs,130806	ESTs	5.0
	450109 449895	AI539295 AA164569	Hs.115740 Hs.34550	KIAA0210 gene product ESTs	5.0 5.0
40	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.9
	404593				4.9
	423607	AA328329	Hs.6591	ESTS	4.9
	432009 419235	AL137424 AW470411	Hs.306458 Hs.288433	Homo saplens mRNA; cDNA DKFZp761G2123 (f neurotrimin	4.9 4.9
45	436304	AA339622	Hs.108887	ESTS	4.9
	434613	Al021826		gbms92b10.x5 NCL_CGAP_Pr3 Homo sapiens	4.9
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	4.9 4.9
	415245 428780	N59650 A1478578	Hs.27252 Hs.50636	ESTs .	4.9
50	406333	147,0010	· ibiococo		4.9
	445034	AW293376	Нв.143659	ESTs	4.8
	440202 424638	AW516211 AI472106	Hs.125300 Hs.49303	ring finger protein 21, interferon-respo Homo saptens cDNA FLJ11663 fis, clone HE	4.8 4.8
	451497	H83294	Hs.284122		4.8
55	427652	AI673025	Hs.43874	ESTs, Moderately similar to 154374 gens	4.8
	458722		Hs.282832		4.8
	407327 411018		Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.B 4.8
	415261	T40928	Hs.8346	ESTs	4.8
60	453543		Hs.48919	Homo sapiens cDNA FLJ11508 fls, clone HE	4.8
	438014 407829		Hs.121806 Hs.29725	Homo sapiens cDNA FLJ 11971 fils, clone HE hypothetical protein FLJ 13197	4.8 4.8
	441006		Hs.7627	CGI-60 protein	4.8
c=	412222	AA528283	Hs.292737	ESTs	4.B
65	424115		Hs.293965		4.8
	453197 439398		Hs.109057 Hs.221504		4.8 4.8
	436397		Hs.169B35		4.0
7 0	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	4.8
70	410901		Lin 400700	gb:MR4-ST0124-270300-005-b11 ST0124 Hamo wolensin 2	4.8 4.8
	425916 447020		Hs,162200 Hs.16986	hypothetical protein FLJ11046	4.8
	427457	AW779105	Hs.164682	L ESTs	4.7
75	451620	AW4498BB	Hs.257224		4.7
75	408936 420036		Hs,22607 Hs,52792	ESTs Homo saplens mRNA; cDNA DKF2p586H823 (f	4.7 4.7
	424508		Hs.149770		4.7
	430345	AK000282	Hs,239681	hypothetical protein FLJ20275	4.7
80	427669		Hs.255938		4.7
30	417181 435347		Hs.1071 Hs.116963	susfactant protein A binding protein 3 ESTs	4,7 4.7
	425458		Hs.182889		4.7
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	4.7

		11440000	11 450400	con	4~
	436594	Al419982		ESTs Human glucocorticold receptor alpha mRNA	4.7 4.7
	421237 432731	U25029 R31178		fibronecia 1	4.7
		AL079741		Homo sapiens cDNA FLJ14236 fls, clone NT	4.7
5	426320	W47595	Hs.169300	transforming growth factor, bela 2	4.7
	419751	AW195581	Hs.93121	KIAA0761 protein	4.6
	433515	AA595800	Hs.190246	ESTs	4.6
	4513B1	BE241831	Hs.172330	hypothetical protein MGC2705	4.6
10	452784 438297	BE463857 AW515196	Hs.15125B Hs.258238	hypothetical protein FLJ21062 ESTs, Moderately similar to ALU1_HUMAN A	4. 6 4.6
10	406992	882472	15.20200	gb:beta-pol=DNA polymerase beta (exon a	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	435933	AA805520	Hs.192075	ESTS	4.6
10	447997	H00656	Hs.29792	ESTs, Weakly similar to 138022 hypotheti	4.6
15	445657	AW612141	Hs.279575	Homo sagiens G-protein coupled receptor	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6 4.6
	447700 423735	AJ420183 AA330259	Hs.171077	ESTs, Weakly similar to T21259 hypotheti gb:EST33963 Embryo, 12 week li Homo sapi	4.6
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4,6
20	416258	N45661	Hs.90011	adenylosuccinate synthese	4.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	4.6
	454359	N71277		gb:za36e03.s1 Soares fetal liver splean	4.5
	422977	AA631498	ll anina	gb:np83h04.s1 NCI_CGAP_Thy1 Homo saplens	4.5
25	433485	AM93076	Hs.201967	aldo-keto reduciase family 1, member C2	4.5 4.5
23	450192 432015	AA263143 AL157504	Hs.24596 Hs.159115	RAD51-interacting protein Homo sapiens mRNA; cDNA DKFZp586O0724 (f	4.5 4.5
	407266	AJ235664	18.135113	gb:Homo sapiens mRNA for Immunoglobulin	4.5
	409041	AB033025	Hs.50081	KIAA1199 protein	4.5
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone 1.	4.5
30	452526	W38537	Hs.280740	hypothetical protein MGC3040	4.5
	403271				4.5
	450656	AA010539	Ha.18912	ESTS	4.5
	446096	A1276454	He useco	gb;q171a12x1 Soeres_NhHMPv_S1 Homo sapi Homo sepiens mRNA for KIAA1771 protein,	4.5 4.5
35	454036 437960	AA374756 A1669586	Hs.93560 Hs.222194	ESTs	4.5
23	440562	H39048	Hs.127432	ESTs	4.5
	410615	AW/72721		gb:hl95c01.x1 NCL_CGAP_Thy8 Homo sapiens	4.5
	413583		Hs.5888	ESTs	4.5
40	419449	H18417	Hs.57483	Homo saplens cDNA FLI14294 fis, clone PL	4.5
40	442324	R63578	Hs.28426	ESTs	4.4
	453080		Hs.23921	hypothetical protein DKFZp547A023	4.4 4.4
	43574 7 446509		Hs.134398 Hs.132892	ESTs protocadhedin 20	4.4
	448030		Hs.325960	membrane-spanning 4-domains, subfamily A	4.4
45	414998		Hs.77729	oxidised low density lipoprotein (tectin	4.4
	446089		Hs.173696	ESTs	4.4
	434367		Hs.3830	KIAA0893 prolein	4.4
	434757		Hs.132921	ESTs	4.4
50	413453 454438		Hs.128065	ESTs cell division cycle 27	4.4 4.4
50	458154		Hs.172405 Hs.335018	ESTs .	4.4
	430417		Hs.50701	ESTs	4.4
	434819		Hs.291541	ESTs, Weakly similar to ALUB_HUMAN IIII	4.4
c	438796		Hs.109590	genethonin 1	4.4
55	415451		Hs,268720	ESTs, Moderately similar to ALU1_HUMAN A	4.4
	420931		Hs.100431	small inducible cylokine B subfamily (Cy	4.4 4.4
	414812 451895		Hs.77367 Hs.16970	monokine induced by gamma interferon ESTs	44
	435434		Hs.187850	ESTa	4.4
60	449623		Hs.120440	EST	4.4
	433563	AI732637	Hs.277901	ESTs	4.3
	444649		Hs.197628	ESTs	4.3
	441594		Hs.208765	ESTs, Moderately similar to ALU7_HUMAN A	4.3
65	443314 400292		Hs.54646 Hs.72472	ESTs ESTs	4.3 4.3
V.	427972		Hs.181304	putative gene product	4.3
	446932		Hs.125644	ESTs	4.3
	445640		Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sapi	4.3
70	452393		Hs.99858	ribosomal protein L7a	4.3
70	44320		Hs.29843	Homo sapiens cDNA FLJ13103 fis, clone NT	4.3
	400608		the ormane	ERT	4,3 4.3
	411158		Hs.273629 Hs.132992		4.3
	435772 439831		Hs.151489		4.3
75	45551		, N.101703	gb;CMO-HT0180-041099-065-b04 HT0180 Homo	4.3
	44325		Hs.11614	HSPC065 protein	4.3
	43603	3 H75391	Hs.255748	ESTs	4.3
	42021		Hs.286073		4.3
80	410519		Hs.131705	ESTs	4.3 4.3
00	40118 41885		Hs.273294	hypothetical protein FLJ20069	4.3
	42573		Hs.159388		4.3
	44786		Hs,288885		4.3

	409435	A1810721	Hs.95424	ESTs	2.8
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.B
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_8r5 Homo sapiens	2.8
_	444381	BE387335	Hs.283713	ESTs, Weakly similar to \$64054 hypotheti	2.8
5	412189	R60982	Hs.22581	ESTs	2.8
	420976	A1924940	Hs.108082	ESTs, Wealdy similar to T31636 hypotheti	2.8
	448330	AL036449	Hs.207163	ESTs	2.8
	418912	NM_000685	Hs.89472	angiolensin receptor 1	2.8
10	422505	AL120862	Hs.124165	EST ₆	2.8
10	427752	AA470687	Hs.104772	ESTs	28
	433513	A1566356	Hs.171437	ESTs	28
	433703	AA210863	Hs.3532	nemo-like klnase	2.B
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
15	405621				2.8
15	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.8
	450400	A1694722	Hs.279744	ESTs	2.8
	456844	AI264155	Hs.152981	COP-diacylglycerol synthese (phosphatida	2.8
	418342	BE002723	Hs.226627	leptin receptor	2.8
20	420756	AA411800	Hs.189900	ESTs	2.8
20	423532	BE090503		gb:RC8-BT0717-110400-011-F11 BT0717 Homo	28
	440320	AA879294		gb:rw86e09.s1 NCI_CGAP_Pr12 Homo septens	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	439831	AW136488	Hs.25545	ESTs	2.8
25	425661	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	2.8
25	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	28
	418658	AW874263	Hs.32468	ESTs	28
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.6
	421340	F07783	Hs.1369	decay accelerating factor for complement	2.6
20	449071	NM_005872	Hs.22980	breast carcinoma amplified sequence 2	2.8
30	409241	AF070602	Hs.51649	Homo sepiens clone 24504 mRNA sequence	2.8
	448219	AA228092	Hs.42656	KJAA1681 protein	2.8
	408936	AL138043	Hs.293549	ESTs	2.B
	410784	AW803201		gb:1L2-UM0077-070500-080-E06 UM0077 Homo	2.8
25	426471	M22440	Hs.170009	transforming growth factor, alpha	2.8
35	454456	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	2,8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	401335				2.7
	436577	W84774	Hs.17643	ESTs	2.7
40	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
40	421003	T720B0	Hs.95667	F-box protein 30	27
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	27
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.7
	436007	Al247716	Hs.232168	ESTs	2.7
4.5	408874	AW818091	Hs.252730	ESTs	2.7
45	418036	Z37976	Hs.83337	latent transforming growth factor beta b	2.7
	435625	H50654	Hs.113999	ESTs	2.7
	435766	R11673	Hs.186498	ESTs	2.7
	410327	T33130	Hs.301746	RAP2A, member of RAS encogene family	2.7
~~	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
50	417177	NM_00445B	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
	429710	Al337113	Hs.146025	hypothetical protein FLJ23594	2.7
55	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltranster	2.7
	441928	AJ370188	Hs.211454	ESTs	2.7
	409721	AW887732	Hs.257861	ESTs .	2.7
C 0	427112	Z32887	Hs.290951	ESTs	27
60	403776				2.7
	420159	A1572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427B39	AA608823	Hs.98244	EST8	27
	432B37	AA310693	Hs.87329	HSPC072 protein	2.7
	438782	AA828380	Hs.126733	ESTs	2.7
65	449396	BE169100	Hs.195029	ESTa	2.7
	458043	AW979009	Hs.32610B	ESTs	27
	438171	AW976507	Hs.293515	ESTs	2.7
	452959	A1933416	Hs.189874	ESTs	27
	439556	Al623752	Hs.163603	ESTs .	2.7
70	446152	AI292036	Hs.15002B	ESTs	2.7
	434803	AW974640	Hs.303413	ESTs	2.7
	407771	AL138272	Hs.52713	ESTs	27
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434l0428	2.7
~-	417543	AA203620	Hs.110153	ESTs	2.7
75	401517				27
	403677				27
	416337	H48713		gbryg78d02.r1 Soeres fetal liver spleen	2.7
	423401	NM_001992	Hs.128087	coagulation factor it (thrombin) recepto	27
00	446800	AI341635	Hs.156486	ESTs	2.7
80	457906	AW975939	Hs.153290	Homo saplens cDNA FLI14318 fis, clone PL	2.7
	452277	AL049013	Hs.28783	KIAA1223 protein	2.7
	416913	AW934714		gicRC1-DT0001-031299-011-e11 DT0001 Homo	2.7
	416370	N90470	Ha.203697	ESTs, Weakly similar to 138022 hypotheti	2.7

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	,4.0
	451353	N21043	Hs.42932	ESTs	4.0
	437075	AA743748	Hs.4075B	ESTs	3.9
5	410505	AW752139	Hs.314323	ESTs	3.9
2	449746	AI688594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.9
	426116	AA868729	Hs. 144694	ESTs	3.9
	415716	N59294	Hs. 179662	nucleosome assembly protein 1-like f	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
10	417718	T86540	Hs.193981	ESTs	3.9
10	436772	AW975688	Hs.74170	metallothionein 1E (functional)	3.9
	401045			·	3.9
	408767	AA057279	Hs.211928	ESTs	3.9
	407303	AA016296	Hs.165200	ESTs, Weakly similar to A56194 thromboxa	3.9
1.5	432583	AW023624	Hs.162282	polassium channel TASK-4; polassium chan	3.9
15	451623	H77818	Hs.268991	ESTs	3.9
	450063	A1681509	Hs.277133	ESTs	3.9
	416734	H81213	Hs.14825	ESTs, Wealtly similar to KIAA1503 protein	3.9
	419276	BE165909	Hs.306881	MSTP043 protein	3.9
•	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
20	436149	A1754308	Hs.159452	ESTs	3.9
	422667	H25642	Hs.133471	EST ₆	3.9
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.9
	458219	H22195	Hs.31874	ESTs	3.9
~ ~	443613	Al079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.9
25	439810	AL109710	Hs.85568	EST	3.9
	436578	A1091435	Hs.134859	ESTs	3.9
	415598	A1433165	Hs.9856	ESTs	3.9
	425087	R62424	Hs.126059	ESTs	3.9
	454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	3.9
30	409719	Al769160	Hs.108681	Homo sapiens brain tumor associated prot	3.9
	452466	N84635	Hs.29664	hypothetical protein DKFZo564B052	3.9
	424962	NM_012288	Hs.153954	TRAM-like protein	3.9
	435823	R07856	Hs.16355	ESTs	
	440533	A)140686	Hs.263320	ESTs	3.9
35	429334	D63078	Hs.188180	Homo sapiena cDNA: FLJ23038 fis, clone L	3.9 3.9
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphata linked moi	
	430039	BE253012	Hs.153400	ESTs. Weekly similar to ALU1_HUMAN ALU S	3.9
	417461	R38403	Hs.13305	ESTs	3.9
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cONA DKFZp586J1922 (f	3.9
40	419140	A1982647	Hs.215725	ESTs	3.8
	415652	T79213	Hs.272073	ESTs	3.8
	430140	AW296771	Hs.221999	ESTs	3.8
	446898	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.8
	422165	AL041199	Hs.14B1	histidine decarboxylase	3.8
45	417706	T90797	Hs.268623	ESTs	3.B
	424296	Al631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.B
	450522	A1698839	7401100110	gb:wd31f02.xt Soares_NFL_T_GBC_S1 Home s	3.8
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.8
	449729	R72032	Hs.29235	ESTs	3.8
50	414700	H63202	Hs.38163	ESTs	3.8
	440999	AW449445	Hs.120021	DKFZP4341092 protein	3.8
	439335	AA742697	Hs.62492		3.8
	408625	AW243323	Hs.266785	ESTs, Wealthy similar to B39068 proline-r ESTs	3.8
	421987	Al139161	Hs.286131	CGI-101 protein	3.8
55	418915	AJ474778	Hs.118977	ESTs	3,8
	410224	M55513	Hs.150208	potassium voitage-gated channel, shaker-	3.8
	429846	AB023021	Hs.225945	from denomination Of the 44 2) 4 4	3.8
	442849	R10099	Hs.269805	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	427191	BE221825	Hs.97691	ESTs ESTs	3.B
60	407942	AA378608	Hs.5894		3,0
	437030	AA742577	Hs.303781	hypothetical protein FLJ10305 EST	3.8
	427940	AA417812	Hs.38775	ESTS	3.8
	443054	Al745185	Hs.8939	yes-associated protein 65 kDa	3.7
	449679	AI823951	Hs.129700	lolloki-like 1	3.7
65	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3,7
	458563	AV658444	Hs.280776		3.7
	456443	AW967500	Hs.133543	tankyrase, TRF1-Interacting ankyrin-rela ESTs	3.7
	439957	Al453184	Hs.66357	ESTs .	3.7
	446999	AA151520	Hs.334822		3.7
70	428414	AL049980	Hs.184216	hypothelical protein MGC4485	3.7
. •	455170	AWB60972	119° 104V10	DKFZP564C152 protein	3.7
	418379	AA218940	No 127516	gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.7
	419720	AA249131	Hs.137516	fidgetin-like 1	3.7
	443584	A1807036	Hs.337778	hypothetical protein FLJ11068	3.7
75	416185		Hs.267245	hypothetical protein FLJ14803	3.7
	417235	AW975861	Hs.47357	KIAA1785 protein	3.7
	441720	AA810278	Hs.24250	ESTS	3.7
	451421	Al346487	Hs.28739	ESTS	3.7
	417355	W16522	Hs.237689	Homo sepiens cDNA FLJ13539 ffs, clone PL	3.7
80	449321	D13168	Hs.82002	endothelin receptor type B	3.7
50	424808	AA001150	Hs.132937	ESTs	3.7
	452338	AA382523	Hs.105689	MSTP031 protein	3.7
	409248	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	3.7
	400246	AB033035	Hs.51965	KIAA1209 protein	3.7

	104007	41004000	Hs.197653 1	ESTs	3.7
	421037 427088	AI684808 AA398085		ESTs	3.7
	420637	AW976153	1 2011 12000	gb:EST388262 MAGE resequences, MAGN Homo	3.7
	420026	AI831190		ESTs	3.7
5	429419	AB023225		KIAA1009 protein	3.7 3.7
	447410	A1470235	Hs.172698	EST	3.7
	404274	1117007	Hs.34024	ESTs	3.7
	416320 412642	H47867 BE244598		hepalocyte growth factor (hapapoletin A;	3.7
10	431716	D89053	Hs.268012	fally-acid-Coenzyme A ligase, long-chain	3.7
. •	446025	AW305075		KIAA0729 protein	3.7
	450458	AA009926		gb:zi07e05.rt Soares_fetal_liver_spleen_	3.7 3.6
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	3.6
1.5	438257	AW474419	Hs.224794	ESTS	3.6
15	440887	A1799488	Hs.135905	EST8 gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.6
	454693 432189	AW81342B AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.6
	407726	AA435679	Hs.88594	ESTs	3.6
20	436026	A1349764	Hs.217081	ESTs	3.6 3.6
	448776	BE302464	Hs.30057	MRS2 (S. carevisiae)-like, magnesium hom	3.6
	452293	A)871833	Hs.304609	ESTs matrix metalloproteinase 7 (matrilysin,	3.6
	428330	L72524	Hs.2256 Hs.129445	hypothetical protein FLJ12496	3.6
25	443268 429208	AIB00271 AA447990	Hs.190478	ESTs	3.6
20	458429	AV646559	Hs.12346	Homo saplens cDNA: FL121399 fis, clone C	3.6
	404476			•	3.6
	405848				3.6 3.6
20	438209		Hs.6111	anyl-hydrocarbon receptor nuclear transl	3.6
30	403937		U- 411610	ESTs	3.6
	437918		Hs.121629 Hs.332557	ESTs, Weakly similar to A46010 X-linked	3.6
	432408 4376 4 1		Hs.291911	ESTs	3.6
	439635		Hs.94891	hypothetical protein FLJ22729	3.6
35	446102		Hs.252956	ESTs	3.6
	41B384		Hs.25130	Homo saplens cDNA FLJ14923 fis, clone PL	3.6 3.6
	425403		Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	432030		Hs.143789 Hs.188546	ESTs ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
40	446453 452055		Hs.141693	hypothetical protein MGC10858	3.5
40	440801		Hs.190535	ESTs	3.6
	432779		7,0	gb:EST391351 MAGE resequences, MAGP Homo	3.6
	440B86		Hs.190516		3,6 3.6
4.5	401049			COT-	3.6
45	44942		Hs.197030	ESTs ESTs	3.6
	41807		Hs.8724 Hs.156739	make a k month of h	3.6
	42303 43546		115.100103	gb:zj1Bf08.s1 Soares_fetal_liver_spleen_	3.6
	43801		Hs.336846	EST	3.6
50	45520			gb;PM1-MT0010-200300-001-g08 MT0010 Homo	3.6
	43329	3 AF007835	Hs.32417	hypothetical protain MGC4309	3.5 3.5
	45653	6 AW135986	Hs.257859	ESTS	3.5
	42867		11a PO7	gb:zw80c03.s1 Soares_betls_NHT Homo sap Fc fragment of IgE, high affinity I, rec	3.5
5 5	41440 43534		Hs.897 Hs.190599		3.5
55	44505		Hs.12259	KIAA0630 protein	3.5
	4494		Ha.23590	solute carrier family 16 (monocarboxylic	3.5
	44265		Hs.201378	ESTs, Weakly similar to T12545 hypotheli	3.5 3.5
C D	42312			gb:PM2-SN0018-290300-003-c09 SN0018 Homo gbzh86e08.s1 Soares_fetal_liver_spleen_	3.5
60	4495		Hs.15939		3,5
	4284	34 AF056209 09 AW117207	Hs,98523	ESTs	3.5
	4310		Hs.29079		3.5
	4269		Hs.13212		3.5
65	4276		Hs.1570	histamine receptor H1	3.5 3.5
	4375		Hs.24462		3.5
	4215		Hs.97293	ESTs gb:ny57g81.s1 NCL_CGAP_P:18 Homo septens	3.5
	4336		Hs,10897		3.5
70	4218 4304				3.5
70	4518		Hs.11476		3.5
	4576		Hs.33678	SI EST	3.5
	4108	58 AW105231			3.5 3.5
7,5	4278		Hs.12604		3.5 3.5
75	453		Hs.28483		3.5
		983 W55956 600 AW819001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
		718 AI798680		3 ESTs	3.5
_	416	548 H62953		gb;yr47f05.c1 Soares fetal liver spleen	3.5
80	420	381 D50640	Hs.3376		3.5 3.5
	410	908 AA121686			3.5 3.5
		080 AW44476	1 Hs.4456	5 ESTs gb:Human nonspecific crossreacting antig	3.5
	4100	685 M18728		Ant imitted transference avanagement a	

	404200				3,5
		BE565892	Hs.83077	interleukin 18 (interleron-gemma-inducin	3.5
	433285	AW975944		ESTS	3.5
5		AW974093	Hs.292775	ESTs gb;MR0-HT0241-200100-006-g02 HT0241 Homo	3.5 3.5
5	433492 410252	AW605849 AW821182	Hs.61418	microfibrillar-associated protein 1	3.4
	428804	AK000713	Hs. 193736	hypothetical protein FLJ20706	3.4
		AA434579	Hs.143591	ESTs	3.4
10	410004	AJ29B027	Hs.5057	carboxypeptidase O	3.4 3.4
10	422093 441736	AF151852 AW292779	Hs.111449 Hs.169799	CGI-94 protein ESTs	3.4
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase Inhibito	3.4
	405970			• • • • • • • • • • • • • • • • • • • •	3.4
15	431954	AK001974	Hs.272242	hypothetical protein FUJ11112	3.4 3.4
15	459482 410361	AA625339 BE391804	Hs.237052 Hs.62661	EST, Weakly similar to 138022 hypothetic guanylate binding protein 1, Interferon-	3.4
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.4
	402230				3.4
20	436120	AI248193	Hs.119860	ESTs	3.4 3.4
20	405336 434374	AA631439		gb:np85d02.s1 NCI_CGAP_Thy1 Homo captens	3.4
	42B911	Z43846	Hs.194478	Homo septens mRNA; cDNA DKFZp434O1572 (F	3.4
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.4
25	416057	Al927382	Hs.29857	ESTS	3.4 3.4
25	435496 436088	AW840171 AA704687	Hs.265398 Hs.191294	ESTs, Weekly similar to transformation-r ESTs	3.4
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.4
	454076	AW204712	Hs.61957	ESTs	3.4
20	431733	AW298410	Hs.21475	ESTs	3.4 3.4
30	432974 412576	BE348793 AA447718	Hs.233331 Hs.107057	ESTs ESTs	3.4
	446142	AJ754693	Hs.145968	ESTs	3.4
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol	3.4
25	433384	A1021992	Hs.124244	ESTs	3.4
35	413621	A)808648	Hs.184156	ESTs gb;nc06c05.s1 NCL_CGAP_Pr1 Homo saptens	3.4 3.4
	419646 435111	AA244199 A1803082	Hs.157212	ESTs	3,4
	421236	AJ287622	Hs.151956	ESTs	3.4
40	433917	A1809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	3.4
40	403515	D49E9C	Ue 2466	MAARRA gene product putalive Corretai	3.4 3.4
	429657 453375	D13626 A1990114	Hs.2465 Hs.240091	KIAA0001 gene product; putative G-protei ESTs	3.4
	448185	AA262105	Hs.4094	Homo sapiens cONA FLJ14208 fis, clone NT	3.4
4 00	412209			8b:RCO-NN1012-270300-031-c07 NN1012 Homo	3.4
45	421065		11- 057947	gb:E8T33382 Embryo, 12 week li Homo sapi	3.4 3.4
	409642 420092		Hs.257347 Hs.88045	ESTs ESTs	3.4
	453365		Hs.17404	ESTs	3.3
50	437007		Hs.202599	EBTs, Weakly similar to 138022 hypotheli	3.3
50	408031		Hs.42173	Homo sepiens cDNA FLJ10366 fis, clone NT	3.3 3.3
	439024 418432		Hs.35598 Hs.85112	ESTs insulin-like growth factor 1 (somatomedi	3.3
	417991		Hs.190008	ESTs	3.3
	403356				3.3
55	433650		Hs.26456 Hs.269259	ESTs ESTs, Weekly similar to \$23650 retroviru	3.3 3.3
	41031E 427019		Hs.173233		3.3
	413714		Hs.7142B	ESTs	3.3
60	430887		Hs.260287		3.3
60	413618 420908		Hs.100261	gb:PMO-HT0339-200400-010-F04 HT0339 Homo Homo saplens mRNA; cDNA DXFZp5648222 (fr	9.3 3.3
	43616		Hs.301645		3.3
	40569				3.3
<i>C</i> =	43280		Hs.131703		3.3 3.3
65	43380 43619		Hs.112742 Hs.24139	ESTs Homo sagiens cDNA: FLJ23137 fis, clone L	3.3
1	43545		Hs.303008		3.3
	41184		Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
70	44840			gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.3
70	41043 41642		Hs.63668 Hs.79306	toll-like receptor 2 eukaryotic translation initiation factor	3.3 3.3
	43839		Hs.27693		3.3
	44430	1 AK000136	Hs.10760	asporin (LRR class 1)	3.3
75	42879	5 R45503	Hs.97469		3.3
75	45892		Hs.24427		3.3 3.3
	43593 40026		Hs.11786	9 ESTs	3.3 3.3
	41055		Hs.64311	a disintegrin and metalloproteinase doma	3.3
00	41290	3 BE007967	Hs.15579		3.3
80	40088		LL- 40700	3 ESTs	3.3 3.3
	44950 40880		Hs.19769 Hs.28900		3.3
	4185		Hs.24664		3.3

	150004	D40700	U= 404000	FOT-	3.3
	453204 450696	R10799 A1654223	Hs.191990 Hs.16026	ESTs hypothetical protein FLJ23191	3.3
	427374	A)150033	Hs.143686	ESTs	33
	443367	AW071349	Hs,215937	ESTs	3.3
5	446645	Al336596	Hs.156294	ESTs	3.3
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.3
	428457	AK002121	Hs.184465	hypothetical protein FLJ11259	3.3
	408761	AA057264	Fs.238936	ESTs, Wealdy similar to (defline not ava	3.3
10	403895	41110777700	11- 00000	EM-	3.2 3.2
IV	414899 409044	AW975433 AI129586	Hs.36288 Hs.33033	ESTs hypothetical protein FLJ14623	3.2 3.2
	447233	AW246333	Hs.17901	Homo saplens, clone IMAGE:3937015, mRNA,	3.2
	422219	AW978073	Hs.1010	regulator of mitolic spindle assembly 1	3.2
	427119	AW8B0562	Hs.114574	ESTs	3.2
15	437073	AI885608	Hs.94122	ESTs	3.2
	443B30	Al142095	Hs,143273	ESTs	3.2
	454962	AW847645		gb:IL3-CT0213-280100-656-A04 CT0213 Homo	3.2
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_Ut2 Homo saplens	3.2
20	417561	AW974345	11- 454070	gb:EST386449 MAGE resequences, MAGM Harno	3.2 3.2
20	446063 423609	A1720140 AA328348	Hs.151079 Hs.218289	ESTs ESTs	3.2
	428004	AA/49563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	453370	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.2
	435808	AA702866	Hs.113150	ESTs	3.2
25	424001	W67883	Hs.137476	paternally expressed 10	3.2
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	3.2
	418946	A)798841	Hs.164526	ESTs	3.2
	431750	AA514986	Hs.283705	ESTs	3.2
30	425188	AK002052	Hs.155071	hypothatical protein FLJ11190 ESTs	3.2 3.2
50	428268 418878	AA424957 W20090	Hs.294132 Hs.6616	ESTs	3.2
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.2
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b (H.sap	3.2
	44642B	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.2
35	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	Al201849	11 460070	gbqs76g04.x1 NCt_CGAP_Pr28 Homo saplens	3.2
	407339		Hs.132670	ESTs	3.2
40	414093 438458		Hs.283077	centrosomal P4.1-associated protein; unc gb:EST387294 MAGE resequences, MAGN Homo	3.2 3.2
-70	419340		Hs.87530	ESTs	3.2
	423448		Hs.128753	Homo saplens cDNA FLJ20769 fis, clone CO	3.2
	45703D		Hs.173381	dhydropydmidinase-lika 2	3.2
	421187		Hs.102471	KIAA0660 gene product	3.2
45	419929		Hs.93810	cerebral cevernous malformations 1	3.2
	429276		Hs.198612	G protein-coupled receptor 51	3.2
	423841		11- 400 400	gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.2
	438839 410085		Hs.128490 Hs.58589	ESTs .	3.2 3.2
50	427961		Hs.143134	glycogenin 2 ESTs	3.2
50	429228		Hs.337139	EST8	3.2
	431548		Hs.9711	novel protein	3.1
	441839		Hs.29160	ESTS	3.1
	410389		Hs.8177	ESTs, Weakly similar to PIHUB6 sallvary	3.1
5 5	441274		Hs.131357	ESTs	3.1
	452401		Hs.29352 Hs.119898	tumor necrosis factor, alpha-induced pro ESTs -	3.1 3.1
	436154 406752		U8.119030	gb:qu49f06.x1 NCI_CGAP_Lym6 Homo sepiens	9.1
	450689		Hs.243010	Homo saplens cDNA FLJ14445 fis, clone HE	3.1
60	434164		Hs.148135	serine/threcoline kinase 33	3.1
	436739	BE208022	Hs.127685	KIAA1627 protein	3.1
	451674	AA019104	Hs.175483	Homo sapiens cDNA: FLJ22016 fis, clone H	3.1
	421166		Hs.10230B	polassium inwardly-rectifying channel, a	3.1
65	437872		Hs.5887	RNA binding motif protein 7	3.1
U.S	440046		Hs.6877	hypothetical protein FLJ10483 splicing factor, arginine/serine-rich 2	3.1 3.1
	452B24 426457		Не.73965 Нв.169965		3.1
	4247B0		Hs.153058		3.1
	456551		Hs.293156		3.1
70	410763		Hs.8966	hypothetical protein FLJ21776	3.1
	431814		Hs.270847		3.1
	440099		Hs.6909	DKFZP564G202 protein	3.1
	43640		Hs.29088	ESTS	3.1
75	43743		Hs,269622	ESTS	3.1 3.1
, ,	40327 40864		Hs.57837	ESTs	3.1
	42413		Hs.199669		3.1
	43322		Hs.238415		3.1
00	43463	6 AA083764	Hs.6101	hypothetical protein MGC3178	3.1
80	45051	9 AA010066	Hs,224849		3.1
	41508		Hs.27179	Homo sepiens cDNA FLJ12933 fis, clone NT	3.1
	40790		Hs.252908 Hs.252744		3.1 3.1
	45231	1 AW304029	(13.23214	LOIG	3.1

	101010	********************\	II- north	FOT-	3.1
	434849 446770	AW292765 AV660309		ESTs ESTs, Wealdy similar to PLLP_HUMAN PLASM	3.1
	424238	AA337401	Hs.137635	ESTs	3.1
_	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.1
5	447829	A1433029	Hs.164104	ESTs	3.1 3.1
	406506 428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	3.1
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.1
10	451229	AW967707	Hs.48473	ESTs	3.1 3.1
10	401103 433589	AA886530	Hs.188912	ESTs	3.1
	459370	AA889982	Hs.271826	ESTs, Weakly similar to 138022 hypotheti	3.1
	438533	A1440266	Hs.170673	ESTs, Wealdy similar to T24832 hypotheti	3.1
1 5	404288				3.1
15	406195	AW169287	Hs.22588	ESTs	3.1 3.1
	438202 425516	BE000707	Hs.29567	ESTS	3.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.1
20	422692	AA332376	Hs.24135	transmembrane protein vezatin; hypotheti	3.1
20	435414	AW270550 T78517	Hs.116957 Hs.13941	ESTs ESTs	3.1 3.1
	418950 426890	AA393167	Hs.41294	ESTS	3.1
	457447	X7B261	Hs.272177	Hisapiens mRNA for TRE17 5 extremity an	3.1
O.F.	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.1
25	459371	R20991	Hs.28625	gb:yg06h01.r1 Soares infant brain 1NIB H ESTs	3.1 3,1
	421823 447247	N40850 AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.1
	452896	AAB31508	Hs.32553	ESTs	3.1
20	425895	Al269484	Hs.161427	zinc finger protein 215	3.1
30	451403	AA885569	Hs,40919	Homo saplens cDNA FLJ14511 fis, clone NT	3.1 3.1
	407340 401862	AAB10168	Hs.284289	vitiligo-essociated protein VIT-1	3.1
	444325	AW152618	Hs.16757	ESTs	3.1
25	408171	AA301228	Hs.43299	hypothetical protein FLJ 12890	3,1
35	423949		Hs.130912 Hs.176376	ESTs ESTs	3.1 3.0
	419519 434683		Hs,202639	ESTs	3.0
	418454		Hs.195870	hypothetical protein FLJ14991	3.0
40	415086		Hs.118726	ESTs	30
40	419220		Hs,291759 Hs.53565	ESTs Homo sapiens PIG-M mRNA for mannosyltran	3.0 3.0
	418549 443634		Hs.134460	ESTs	3.0
	429682		Hs.211602	SMC1 (structural maintenance of chromoso	3.0
AE	405090		11 Am 100m	11 * . NAIA CI (40040 E 3)[C	3.0
45	432267		Hs.274227 Hs.132117	Homo sapieus cDNA FLJ10010 fis, clone HE ESTs	3.0 3.0
	443253 444974		Hs.151612	ESTS	3.0
	445717		Hs.149332	ESTs	3.0
50	449347		Hs.295901	KIAA0493 protein	3.0 3.0
50	452778 414888		Hs.5921 Hs.77558	Homo sapiens cDNA: FLJ21592 fis, close C thyroid homons receptor interactor 7	3.0
	424408		Hs.146409		3.0
	410371	AA084482	Hs.1 15850	ESTs	3.0
55	426384		Hs,303662		3.0 3.0
22	418200 427050		Hs.205654 Hs.161803		3.0
	449579		Hs.134014		3.0
	411004	AW813242		gh:MR3-ST0191-020200-207-g10 ST0191 Home	3.0
60	454031 45560		Hs.194293 Hs.816	ESTs, Weakly similar to 154374 gene NF2 SRY (sex determining region Y)-box 2	3.0 3.0
OO	44748		Hs.18705	KIAA1233 protein	3.0
	43941		Hs.56254	ESTs	3.0
	43663		Hs.272093		3.0
65	41908 4125 6		Hs.89591	Kalimann syndrome 1 sequence gb:EST374647 MAGE resequences, MAGG Homo	3.0 3.0
U.	41545		Hs.12839	ESTs	3.0
	42787		Hs.98198	ESTs	3.0
	44704		Hs.17170	G protein-coupled receptor 4	3.0
70	45419 45467			gb:MRO-H70071-191199-001-b04 HT0071 Hamo gb:RC3-ST0186-248400-111-b05 ST0186 Hamo	3.0 3.0
,0	41512		Hs.22245	ESTS	3.0
	44466		Hs.47783	B aggressive lymphoma gene	3.0
	40022			absolute 2000 E4 MILL NO. 7 Name analysis and	3.0 3.0
75	41190 41950		Hs.13742	gb;601193893F1 NIH_MGC_7 Homo saplens cD 2 ESTs	3.0
1.	44656		Hs.14145		3.0
	45728	5 Al038858	Hs.13052	2 Kv channel-interacting protein 1	3.0
	43499		Hs.26037		3.0 3.0
80	43620 42453		Hs.5076 Hs.15040	Horno saplens cDNA: FLJ22128 fis, clone H 2 activin A receptor, type I	3.0
20	4498		Hs.18200	ESTS	3.0
	4276	9B AW972594	Hs.29414	Q ESTs	3.0
	45149	94 A1799444	Hs.24709	5 ESTs, Moderately similar to ALU7_HUMAN A	3.0

					3.0
	442994	AI026718	Hs.16954	ESTs	3.0 3.0
	408165	AL137573		Homo saplens mRNA; cDNA DKFZp564A2463 (f ESTs	3.0
	421072 456273	AI215069 AF154846		zinc finger protein	3.0
5	404548	7,7 (4-10-10			3.0
	428201	AA424158		ESTs	3.0
	441519	AA972740		ESTs	3.0 3.0
	445413	AA151342		CGI-147 protein ESTs	3.0
10	418717 428839	A1334430 A1767756		Homo sepiens cONA FLJ14814 fis, clone NT	3.0
10	407758	D50915		KIAA0125 gene product	3.0
	431906	AW326038		ESTs	3.0
	424968	AA349086	Hs.259746	ESTs, Weakly similar to A46010 X-linked	3.0 3.0
15	431023	A)283133	Hs.297420	ESTs matrium 3	3.0
15	432596 452412	AJ224741 AA029608	Hs.278461 Hs.61373	ESTs	3.0
	421309	A1222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	438128	AA904430	Hs.122049	ESTs, Wealdy similar to T2D4_HUMAN TRANS	2.9
00	408321	AW405882	Hs.44205	codistation	2.9 2.9
20	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN!	2.5
	400880 417014	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!!	29
	422278	AFU72873	Hs.114218	frizzled (Drosophila) homolog 6	2.9
	406603				2.9
25	425573	AB006423	Hs.158308	serine (or cysteine) proteínase inhibito	2.9 2.9
	427878	C05766	Hs.181022 Hs.29553	CGI-07 protein ESTs	2.9
	451700 451797	A1470262 AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.9
	423025	AA831267	Hs.12244	hypothetical protein FLJ 20097	2.9
30	422634	NM_016010	Hs.118821	CGI-62 protein	2.9
	448966	AW372914	Hs.86149	phospholnosttol 3-phosphate-binding prot	2.9 2.9
	408690	AW864542 AW206972	Hs.253595	gb:PM4-SN0016-120500-003-h02 SN0016 Homo ESTs	2.9
	408525 412248		13,233350	gb;RC3-HT0585-160300-022-c02 HT0585 Homo	2.9
35	432507		Hs.324667	ESTs	2,9
	447290	A1476732	Hs.263912	ESTS	2.9
	424188		Hs.142634	zinc finger protein	2.9 2.9
	431448 400325		Hs.334473 Hs.247924	hypothetical protein DKFZp56401278 Homo saplens endogenous HiV-1 related se	29
40	408408		Hs.44690	Homo sepiens done 24739 mRNA sequence	2.9
	423119		Hs.131976	ESTs	2.9
	423717		Hs.152003	ESTS	2,9 2,9
	424152		Hs.141489	Horno sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
45	431980 434980		Hs.324507 Hs.14553	hypothetical protein FLJ20986 sterol O-acyltransferese (acyl-Coenzyme	2.9
-1-3	444339		Hs.31562	ESTs	2.9
	446745		Hs.156400	ESTs	2.9
	459201		11. 400035	gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9 2.9
50	430573 451073		Hs.136345 Hs.206063	ESTs ESTs	2.9
20	440575		Hs.126006		29
	402046				2.9
	426883		Hs.97365	ESTs	2.9 2.9
55	435731 420651		Hs.269543 Hs.187636		2.9
33	43B32		Hs.123369		2.9
	45312		Hs.221849		29
	41834		Hs.159501		2,9 2.9
60	43159		Hs.297221	gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sepiens Homo sepiens cDNA FLJ10136 fis, clone HE	2.9
UU	43618 45944		18.231221	gb:tz46c03.y1 NCI_CGAP_Bm52 Homo sapien	2.9
	45195		Hs.10299	Homo seplens cDNA FLI13545 ffs, clone PL	29
	40843		Hs.107716	hypothetical protein FLJ22344	29
65	45603		11-000046	gb:U-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.9 2.9
05	44211 42072		Hs.202242 Hs.99886	2 ESTs complement component 4-binding protein,	2.9
	43384		Hs.280728		2.9
	42423		Hs.143507		2.9
70	429B2		Hs.40747		2.9 2.9
70	43791		Hs.12162		2.9 2.9
	44133 4434!		Hs.129354 Hs.14350		2.9
	43887		Hs.12429	2 Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	44450	31 NM_004469	Hs.11392	c-fos Induced growth factor (vascular en	2.9
75	4446	31 AW995395	Hs.84520		2.9 2.9
	4581		Hs.15320 Hs.16883		2.3
	4360- 4157		Hs.18781		2.9
~~	4492	99 AA299919	Hs.84561	ESTs	2.9
80	4570	03 578234	Hs.17240		2.9 2.9
	4088				2.9
	4246 4261		Hs.15104 Hs.11583		29

	440040	**************************************	Hs.78531	Homo saplens, Similar to RIKEN cDNA 5730	29
		AW236021 AW081608		ESTs	2.9
		AA984472		KIAADU80 protein	2.9
_		AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (i	2.9
5	442655	AW027457		ESTs, Weakly similar to B34087 hypotheti	2.9
		AA278300	Hs.124292	Homo saplens cDNA: FLJ23123 fis, done L	29 29
	430447	W17064	Hs.332848	SWI/SNF related, matrix associated, acti gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	2.9
	416871 439737	H98716	Hs.41271	goryx 13005.5 1 503res menanocyte 2ND ner 10 Homo saplens mRNA full length insert cON	29
10	406815	A1751438 AA833930	Hs.286036	IRNA Isopanianyipyrophosphate transferas	2.9
10	401094	70700000	113,200000	a data to a barren d'Adres de la companya del companya de la companya de la companya del companya de la company	2.9
	401526				2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9 2. 9
15	41B2B2	AA215535	Hs.9B133	ESTs .	29
	442927	A1024347	Hs.131519	ESTs	2.9
	450006	A1241555	Hs.60171	ESTs, Weakly similar to T17227 hypotheti	2.8
	419231 416623	AL046294 N74925	Hs.136245 Hs.38761	Homo sapiens cDNA; FLJ21564 fls, clone C	2.8
20	403329	141-4020	110,00101	TOTAL DEPOSIT OF A C. T. T. S.	2.8
20	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.8
	419038	AW134924	Hs.190325	ESTs	2.8
	440106	AA864988	Hs.127699	KIAA1603 protein	2.8 2.8
0.5	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	2.8
25	431745	AW972448	Hs.163425	ESTs Homo sapiens, clone IMAGE:3939163, mRNA,	2.8
	421426 433014	AA291101 NM_014711	Hs.33020 Hs.279912	KIAA0419 gene product	2.8
	455100	BE160198	16,210012	gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.8
	441790	AW294909	Hs.132208	ESTs	2.6
30	404443				2.8
	428129	AI244311	Hs.26912	ESTs	2.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.8 2.8
	42394B	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	2.8
35	449327	A1638743	Hs.224672	ESTs	2.8
23	400983 415786	AW419196	Hs.257924	hypothetical protein FLJ13782	2.8
	411213		Hs.69285	neuropilin 1	2.8
	420896		Hs.24444	Homo sapiens cONA: FLJ22165 fis, clone H	2.8
	409994		Hs.57735	acetyl LDL receptor; SREC	28
40	430388	AA356923	Hs.240770	mudear cap binding protein subunit 2, 2	2.8
	419530		Hs.90821	ryanodine receptor 2 (cardiac)	2.8 2.8
	455092		11- 70077	gb:CM0-HT0323-151299-126-b04 HT0323 Homo	28
	458118 440192		Hs.78277 Hs.190596	_DKFZP434F2021 prolein ESTs	2.B
45	448466		Hs.171066	ESTS	28
75	414869		Hs.21479	ubinucleia 1	2.8
	440351		Hs.7179	RAD1 (S. pombe) homolog	2.6
	407594	AW057584	Hs.160681	ESTs	. 28
£Ω	439235		Hs.46608	EST8	2.8 2.8
50	417061		Hs.188691		2.8
	434812 409731		Hs.189496 Hs.56145	thymosin, beta, identified in neuroblast	2.8
	455512		10.00	gb:RC3-HN0001-240400-012-c01 HN0001 Homo	2.8
	4083B0		Hs.44532	ជារប្រជុំប្រជុំ ប្រជុំ ប្រជា ប្រជុំ ប	2.8
55	435998		Hs.131793	ESTs	2.8
	410672			gb:RC8-UM0014-170300-022-C05 UM0014 Homo	2.8 2.8
	432791		Hs.194015	i ESTs gb:ypt/rc06.s1 Soares breast 3NbHBst Homo	2.8
	416288 43888		Hs.128705		2.8
60	45155			ATP-binding cassette, sub-family A (ABC1	28
	41694		Hs.43157	ESTs	2.8
	42175		Hs.107872	2 hypothetical protein FL)20761	2.8
	43839	8 AA805526	Hs.13027		2.8 2.8
<i>(</i> =	43531		Hs.18972	ESTS	2.8
65	41460		11- 40449	gb:601283601F1 NIH_MGC_44 Homo saplens c 1 ESTs, Weekly similar to S00755 pleckstri	28
	43650 41319		Hs.12112 Hs.22404		2.8
	41382				2.8
	40132			,,,,,	2.8
70	40829	6 AL117452	Hs.44155	DKFZP586G1517 protein	2.8
	42853		Hs.18478	6 TBP-Interacting protein	28
	42345		Hs.469	succinate dehydrogenese complex, subtinit	2.8 2.8
	43602		Hs.39972	ESTs, Weakly similar to 136566 reverse t gb:Human alpha-1 spectrin gene, exon 12.	2.0 2.8
75	40597 42617		Hs.12505		2.8
15	4521		Hs. 8236	ESTs	2.8
	4397		Hs.57664		2.8
	4231	30 AW897586	Hs.21213	B ESTs	28
00	4306		Hs.10083		2.8 2.8
80	4341		U_ ores	gbzu86h0t.st Soares_testis_NHT Homo sap	28 28
	4274 4298		Hs.26934 Hs.19224		2.8
	4290		Hs.7033		28
			. 101. 200		

		AJ810721	Hs.95424	ESTs	2.8 2.8
	442191	W95186	Hs.8136	endothellal PAS domain protein 1 gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	2.B 2.B
	407305 4443B1	AA715284 BE387335	Hs.283713	EST's, Weakly similar to \$64054 hypotheti	2.8
5	412189	R60982	Hs.22581	ESTs	2.8
•	420976	A1924940	Hs.108082	ESTs, Wealdy similar to T31636 hypotheti	2.8
	448330	AL036449	Hs.207163	ESTs	2.B
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
10	422505	AL120862	Hs.124165	ESTs	2.8
10	427752	AA470687	Hs.104772	EST3	2.8
	433513	A1566355	Hs.171437	ESTs	2.B
	433703 448912	AA210863	Hs.3532 Hs.22559	nemo-like kinase	2.B 2.8
	405621	D83781	NS.22008	KIAA0197 protein	2.8
15	430687	BE274217	Hs,249247	heterogeneous nuclear protein similar to	28
	450400	Al694722	Hs.279744	ESTs	2.8
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthese (phosphalida	2.8
	418342	BE002723	Hs.225627	leptin receptor	2.8
~~	420756	AA411800	Hs.189900	ESTs	2.8
20	423532	BE090503		gb:RC8-BT0717-110400-011-F11 BT0717 Homo	2.8
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo septens	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	439831 425661	AW136488	Hs.25545	ESTS	2.8 2.8
25	407949	AL133627 W21874	Hs.158923 Hs.247057	Homo sapiess mRNA; cDNA DKFZp434K0722 (f ESTs, Weakly similar to 2109260A B cell	2.0 2.8
ب	418658	AW874263	Hs.32468	ESTs	28
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	421340	F07783	Hs.1369	decay accelerating factor for complement	2.B
	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.8
30	409241	AF070602	Hs.51649	Homo sepiens clone 24504 mRNA sequence	2.8
	448219	AA228092	Hs.42656	KIAA1681 protein	2.8
	408936	AL138043	_ Hs.293549	ESTS	2.B
	410784	AW803201	11- 47anon	gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
35	426471	M22440	Hs.170009	transforming growth factor, alpha gb:ft.3-CT0219-281099-024-A03 CT0219 Homo	2.8 2.8
33	454456 455310	AW752710 AW893961		gb:RC4-NN0027-050400-011-d11 NN0027 Homo	2.8
	401335	A11030501		Section Minors and State Minors Links	2.7
	436577	W84774	Hs.17643	ESTs	2.7
4.0	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
40	421003	T72080	Hs.95667	F-box protein 30	27
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ 14991	2.7
	436007	AJ247716	Hs.232168	ESTs	2.7 2.7
45	408874 418036		Hs.252730 Hs.83337	ESTs latent transforming growth factor beta b	2.7
75	435625		Hs.113999	ESTs	27
	435766		Hs.186498	ESTs	27
	410327		Hs.301746	RAP2A, member of RAS oncogene family	2.7
	416805		Hs.79981	Human clone 23560 mRNA sequence	2.7
50	417177		Hs.81452	fatty-ackd-Coenzyme A ligase, long-chain	2.7
	423020		Hs.1608	replication protein A3 (14kD)	2.7
	427134		Hs.173561	EST	2.7
	428137		Hs.170999	ESTs hypothetical protein FLJ23594	2.7 2.7
55	429710 430844		Hs.146025	gbcye38d07.r1 Stratagene lung (937210) H	27
75	417576		Hs.82285	phosphoribosylglycinamide formyltranster	2.7
	441928		Hs.211454	ESTs	2.7
	409721		Hs.257861	ESTs	2.7
C 0	427112		Hs.290951	ESTs	2.7
60	403776				2.7
	420159		Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839		Hs.98244	ESTS	2.7 2.7
	432B37 438782		Hs.87329 Hs.128733	HSPC072 protein ESTs	2.7
65	449396		Hs.195029	ESTs	2.7
-	458043		Hs.32510B	ESTs	2.7
	438171		Hs.293515	ESTs	2.7
	452959		Hs.189874	ESTs	2.7
70	439556		Hs.163603	EST8	2.7
70	446152		Hs.150028	ESTs	2.7
	434803		Hs.303413	ESTs COTA	27
	407771		Hs.62713 Hs.68055	ESTs hypothetical protein DKFZp43410428	2.7 2.7
	411069 417543		Hs.110153		2.7
75	401517		1 15.1 10 133	2010	27
	403677				27
	416337			gb:yq78d02.r1 Soeres fetal liver spleen	2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
ρΛ	446800		Hs.156486		2.7
80	457906		Hs.153290		2.7
	452277		Hs.28783	KIAA1223 protein	2.7
	416913 416370		Hs.203697	gb:RC1-DT0001-031299-011-a11 DT0001 Homo ESTs, Weakly similar to 138022 hypotheli	2.7 2.7
	710011	- 100714	, M. EMUUJI	Co.of second onlines to tooote (ilbonion	Li

	400045	A A 700 00 00 00	11- 440000	1	0.7
	408715 410743	AA768873 AA089474	Hs.112250 Hs.272153	hypothetical protein FLJ23518 ESTs	2.7 2.7
	427138	N77624	Hs.173717	phosphalidic acid phosphalase type 2B	27
_	435260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.7
5	427565	AJ287280	Hs.97933	ESTs, Weakly similar to T46370 hypotheti	2.7
	406092	* * 4770555		-t	2.7
	410008 438504	AA079552 AW665281	Hs,224625	gbzm20h12.st Stratagena pancreas (93720 ESTs	2.7 2.7
	414783	AW069569	Hs.278270	unactive progesterone receptor, 23 kD	2.7
10	411479	AW848047		gb:lL3-CT0214-291299-052-A12 CT0214 Homo	27
	418686	Z36830	Hs.872681	8А ліхепле	2.7
	413795	AL040178	Hs.142003	ESTs	2.7
	457528 444230	AW973791 H95537	Hs.292784 Hs.146067	ESTs ESTs	2.7 2.7
15	403760	Haddai	115.140001	C318	27
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.7
	428904	AJ312526	Hs.46640	ESTs	2.7
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	2.7
20	458638	N78553 AJ003631	Hs.282204	nucleosomel binding protein 1	2.7 2.7
20	459267 424834	AK001432	Hs.153408	gb:AJ003631 Selected chromosome 21 cDNA Homo sapiens cDNA FL110570 fis, clone NT	2.7
	433906	Al 167816	Hs.43355	ESTs	2.7
	428956	AF059214	Hs.1946B7	cholestero) 25-hydroxylase	2.7
25	446554	AA151730	Hs.301789	nuclix (nucleoside diphosphale linked moi	2.7
23	446035 421585	NM_006558 U95626	Hs.13565 Hs.302043	Sam68-like phosphotyrosine protein, T-ST chemokine (C-C molif) receptor-like 2	2.7 2.7
	445158	A)992108	Hs.127206	ESTs	2.7
	421175	Al879099	Hs.102397	GIOT-3 for genedotrophi inducible transc	2,7
20	401793				2.7
30	410181	At468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	427038 451343	NM_014633 AVV975057	Hs.173268 Hs.293353	KIAA0155 gene product ESTs	2,7 2,7
	455992	BE179015	1 10.230000	gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
~ ~	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wit	2.7
35	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	2.7
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypothes	2.7
	407930 453891	AA045847 AB037751	Hs.188361 Hs.36353	Homo sapiens cDNA FLJ 12807 fis, clone NT Homo sapiens mRNA full length Insert cDN	2.7 2.7
	451487	AAD18072	113.00000	gb:ze51g02.r1 Soares retina N2b4HR Homo	2,7
40	418269	AA806113	Hs.189025	ESTs	2.7
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	2.7
	459160 441963	Al904723	Hs.126002	gb:CM-BT068-120299-092 BT056 Homo saplen ESTs	2.7
	440273	A1733307 A1805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fls, clone L	2.7 2.7
45	426902	Al125334	Hs.97408	ESTs	27
	414271	AK000275	Hs.75871	protein kinase C bloding protein 1	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	445265 422988	A1218295 AW673B47	Hs.144942 Hs.97321	ESTS	2.7 2.7
50	428613	AB037749	Hs.186928	KIAA1328 protein	2.7
	444619	BE538062	Hs.8172	ESTs, Moderately similar to A46010 X-lin	2.7
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	2.7
	402800 425071	NM_013989	Hs.154424	delodinase, lodothyronine, type !!	2.7 2.7
55	414729		Hs.281901	ESTs	2.7
	453716		Hs.152675	ESTs	2.7
	452693		Hs.48589	zinc linger protein 228	2.7
	439818 443305		Hs.19934 Hs.133318	Homo saplens mRNA full length insert cDN ESTs	2.7 2.7
60	416709		Hs.283108	hemoglobin, gamma G	2.7
	419077	AA233885	Hs.164526	ESTs	2.7
	453878		Hs. 19025	DC32	2.7
	445560 446817		Hs.201955 Hs.134166	ESTs ESTs	27 27
65	442137		Hs,128830		2.6
	410406		Hs.1466	glycerol kinase	2.6
	442242		Hs.90424	Homo saplens cDNA: FLJ23285 fis, clone H	2.6
	407830		Hs.587	arylacetamide deacetylase (esterase)	2,6
70	415138 407055		Ha.295944	tissue factor pathway inhibitor 2 gb:H.sapiens DNA for endogenous retrovir	2.6 2.6
	408812		Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	440310		Hs.125405	ESTs	2.6
	425659		Hs, 158836		26
75	418217 428667		Hs.13442 Hs.74407	ESTs nucleolar protein p40; homolog of yeast	2.6 2.6
, 0	414573		Hs.71999	ESTs	2.6
	420000		Hs.94262	p53-inducible ribonucleotide reductase s	2.6
	452821		Hs.160874		2.6
80	440138 428483		Hs.318127 Hs.321444		2.6 2.6
	441350		Hs.7782	paraneoplastic antigen MA2	2.0 2.6
	405059				26
	425178	H16097	Hs.161027	ESTs	2.6

	442952	A1743261	Hs.131860	ESTs	2.6
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	2.6
	456179	H75490	Hs.271930	ESTS	2.6
_		AA812434	Hs.119023	SMC2 (structural meintenance of chromoso	26
5	459456 425527	AA486036 AL162032	Hs.190124 Hs.158258	ESTs Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.6 2.6
	424711	NM_005795	Hs.152175	calcitorin recentor-like	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
10	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo septens	2.6
10	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6 2.6
	438295 445550	Al394151 Al242754	Hs,37932 Hs.137306	ESTs ESTs	26
	450469	Al955049	Hs.281326	ESTs	26
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: harny2)	2.6
15	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.6
	429250	H56585	Hs.198308	typtophan dch basic protein	2.6 2.6
	437906 426775	AA771704 AA384564	Hs.194626 Hs.106829	ESTS .	2.6
	443372	AI792557	Hs,133107	ESTs	2.6
20	453785	Al368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	425465	L18964	Hs.1904	protein kinase C, lota	2.6
	422746	NM_004484	Hs.119651	glypican 3	2.6 2.6
	413450 424527	Z99716 AW138558	Hs.75372 Hs.267158	N-acetylgalactosaminidase, alpha- ESTs, Weakly similar to 154374 gene NF2	2.6
25	414180	AI863304	Hs.120905	Homo seplens cDNA FLJ11448 fis, clone HE	2.6
	411402	BE297855	Hs.69855	NRAS-related gene	2.6
	445264	AJ218263	Hs.323472	EST	2.6 2.6
	458861 415227	Al630223 AW821113	Hs.72402	gb;ed06g08.r1 Proliferating Erythroid Ce ESTs	26
30	435429	AW592035	Hs.254414	ESTs, Weakly similar to 1805195B RNA-bin	2.6
-	434445	Al349306	Hs.11782	ESTs	2.6
	448570	AI923944	Hs.30913	ESTs	26
	452381	H23329	Hs.290880	ESTs, Wealdy similar to ALU1_HUMAN ALU S	2.6 2.6
35	422879 409026	A1241409 Al.137554	Hs.188092 Hs.49927	ESTs protein kinase NYO-SP15	2.6
25	425717	X07282	Hs.171495	ratinoic acid receptor, beta	2.6
	429127	AA749382	Hs.118797	ublquitta-conjugating enzyme E2D 3 (homo	2.6
	438298	H23542	Hs.181788	ESTS	2.6 2.5
40	442717 443555	R68362 N71710	Hs.180591 Hs.21398	ESTs, Weakly similar to T23976 hypotheti ESTs, Moderately similar to A Chain A, H	2.6
-10	444517	AI939339	Hs.1468B3	ESTs	26
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	26
	452453		t (= 049009	gb:QV-BT009-101198-051 BT009 Homo sapten	26 26
45	455870 437939		Hs.313803 Hs.141840	ESTs, Highly similar to AF157833 1 noncl ESTs, Wealdy similar to S59501 interfero	2.6
	430719		Hs.293796	ESTs	26
	452864		Hs.287629	hypothetical protein FLJ 14260	26
	432095		Hs.105769	ESTs	2.6 2.6
50	431086 407783		Hs.211561 Hs.172028	ESTs a disintegrin and metalloproteinase doma	26
50	423952		Hs.136102	KIAA0853 protein	2.6
	453403		Hs.61779	Homo sepiens cDNA FLJ13591 fis, clone PL	2.6
	408172		Hs.46039	phosphoglycerate mulase 2 (muscle)	2.6 2.6
55	430933 420691		Hs.275343	gb:MR3-SN0010-270300-103-h02 SN0010 Homo ESTs	2.0 2.6
JJ	429761		Hs.135173		2.6
	437958		Hs.121668	ESTs, Moderately similar to PC4259 fami	2.6
	407494			gb:Human forkhead family (AFX1) mRNA, pa	26
60	436464 407137		Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S obcye53h05.s1 Soares fetal liver spleen.	2.6 2.6
00	446223		Hs.119699		26
	438647		Hs.163230	ESTs	2.6
	438192		Hs.337620		2.6
65	417218		Hs.285754		2.6 2.6
05	440460 41 4 612		Hs.234478 Hs.76578	projein inhibitor of activated STAT3	2.6
	42817		Hs,12565	ESTs	2.6
	45734	3 NM_013938	Нв.247862		2.6
70	424020		Hs.39738	ESTS	26 28
/V	45522 41196		Hs.280115	gb:QVO-NN1922-120500-220-c07 NN1022 Homo ESTs	2.6 2.6
	43265		Hs.3076	MHC class II transactivator	26
	4554B	B AA102322		gb:zi90f03.r1 Stratagene colon (937204)	2.6
75	43434		Hs.12868	5 ESTs. Weakly similar to T17228 hypotheti	26 26
13	40428 41874		Hs.196379	ESTs, Weakly similar to putative p150 [H	26
	45471			gb:QV4-ST0212-091199-023-110 ST0212 Homo	26
	42982	B AB019494	Hs.225767		2.6
80	43638 44858		Hs.240079 Hs.28338	5 Homo sapiens cDNA FLJ13234 fis, clone OV KJAA1546 protein	2.6 2.6
50	43286		Hs.15248		2.6
	44047	9 AA886461	Hs.20816	1 ESTs	2.6
	44318	O A1467915	Hs.36053	ESTs	2.6

	400070	6 4 44 27 0 4	11- 175/45	ESTs	2.5
	428978 4 4467 0	AA442784 H58373		hypothetical protein MGC5370	2.5
	453459	BE047032	Hs.2577B9	ESTs	2.5
_	418122	R42778		Homo sapiens done IMAGE:32106, mRNA seq	2.5 2.5
5	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequipproline-rich protein with nuclear target	2.5
	414373 458760	AW162907 AW98631	Hs.75969 Hs.111334	femilin, light polypeptide	2.5
	434131	Al858275	Hs.143659	ESTs	2.5
1.0	441805	AA2B5136	Hs.301914	neuronal specific transcription factor D	2.5 2.5
10	457292	A)921270	Hs.334882	hypothetical protein FL/14251	2.5
	417351 409695	190278 AA296961	Hs.15049	ESTs gb:EST112514 Adrenal gland tumor Homo sa	2.5
	432824	AK001783	Hs.279012	hypothetical protein FLI10921	2.5
	438038	AJ732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.5
15	454836	AW833711	11- 7076	gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5 2.5
	453919 422487	AW959912 AJ010901	He.7076 Hs.198267	KIAA1705 protein mucin 4, trachaobronchial	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
	427491	R43279	Hs.22574	ESTs, Weakly similar to 138022 hypotheti	25
20	435102	AW899053	Hs.76917	F-box only protein 8	2.5 2.5
	409617	BE003760	Hs.55209	Homo septens mRNA; cDNA DKFZp434K0514 (F gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.5 2.5
	455866 432887	BE149024 AI926047	Hs.162859	EST8	2.5
	407756		Hs.36260	ubiquitin specific protease 18	2.5
25	401078			1	2.5 2.5
	410365		Hs.62669	Homo sapiens mRNA; cONA DKFZp586D0923 (f gb:EST60061 Activated T-cells XX Homo sa	2.5
	425201 457112		Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	455252		110.20022	gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
30	444542	AR161293	Hs.280380	aminopepidase	2.5
	419249		Hs.8976B	gamma-aminobulyric acid (GABA) A recepto	2.5 2.5
	428497 457336		Hs.98584 Hs.291029	ESTS ESTS	2.5
	427621		Hs.179882	hypothetical protein FLJ12443	2.5
35	423782	AJ472209	Hs.323117	ESTs	25
	430403		Hs.241382	tumor necrosis factor (figand) superfami	2.5 2.5
	429927 408562		Hs.2522 Hs.31141	adenylate cyclase B (brein) Homo sapiens mRNA for KIAA1568 protein,	2.5
	417137		Hs.81281	mitochandrial ribosomal protein S21	2.5
40	436787	AA908554	Hs.192756	ESTs	2.5
	440331		Hs.202151	ESTs	2.5 2.5
	429718 417169		Hs.211933 Hs.246773	collagen, type XIII, alpha 1 ESTs	2.5
	453020		Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	2.5
45	455286		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2,5
	45065		Hs.25275	Kruppel-type zinc finger protein	2.5 2.5
	400433 41574		Hs.287767	Sequence 8 from Patent WO9950285 gb:EST94257 Activated T-cells I Homo sap	25
	44634		Hs.309940	EST's	2.5
50	45020		Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	25
	45320		Hs.26270	hypothetical protein FLI11588	2.5 2.5
	42552 43312		Hs.158244 Hs.13775	KIAA0479 protein hypothetical protein SMAP31	2.5 2.5
	40874		Hs.646	carboxypeptidase A3 (mast cell)	2.5
55	42565		Hs.119471	ESTS	2,5
	40125		N. 004.14		25 25
	42660 44953		Hs.97141 Hs.23672	ESTs, Weakly similar to hypothetical pro low denally lipoprotein receptor-related	2.5
	43313		Hs.59729	semaphorin sem2	2.5
60	42580		Hs.258189		2.5
	42951		Hs.204370		2.5 2.5
	43726 45430		Hs.258110 Hs.28338	ESTs KIAA1546 protein	2.5
	45563		120,2000	gb:MR0-BT0265-231199-002-e09 BT0265 Homo	2.5
65 ·	40187	78			25
	45038		Hs,174880		2.5 2.5
	4385 4574		Hs.12920	gb:nv54h12r1 NCl_CGAP_Ew1 Homo sepiens casein lúnase 1, gamma 3	2.5
	4273		Hs.16385		2.5
70	4197	21 NM_001650	Hs.28865	3 aquaposin 4	2.5 2.5
	4316				2.5 2.5
	4462 4212		Hs.15000 Hs.7086	9 ESTs hypothetical protein MGC12435	2.5
	4342		Hs.26303		2.5
75	4560	88 BE177320	Hs.15614	B hypothetical protein FLJ13231	2.5
	4343		Hs.13137		2.5 2.5
	4361 4522		Hs,30092 Hs.15842		2.5
	4337		Hs.39982		2.5
80	4120	150 H96503	Hs.10908	7 Homo sapiens cDNA: FLJ22845 fls, clone K	2.5
	4223		ti- 47004	gb:EST180209 Liver, hepatocellular carci	2.5 2.5
	4275 4283		Hs.17931 Hs.18375		2.5
	-72.00				

	400042	A1580090	Hs.48295	DNA Nationna familia	26
	408813 414109	BE250744	FIS.49255	RNA halicase family gb:600943376F1 NiH_MGC_17 Homo sapiens c	2.5 2.5
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.5
5	419985	H86373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.sa	2.5
5	417859 434334	T26453 AA912476	Hs.116750	gb:AB214F6R Infant brain, LLNL array of	2.5 2.5
	448015	Al458065	Hs.23196	Homo sapiens cDNA FLJ13221 fis, clone NT ESTs	2.5
	454190	AW177821	(10.20100	gb:lL3-HT0059-180899-007-C05 HT0059 Home	2.5
10	445865	A12625B4	Hs.145575	ESTs .	25
10	451800	AW977435	Hs.323867	ESTs	2.5
	456987 403568	A1557290	Hs.173536	ESTs	2.5 2.5
	435209	AW027809	Hs.187698	Homo saplens cytomegalovirus partial fus	2.5
1.7	430371	DB7466	Hs.240112	KIAA0276 protein	25
15	418033	W68180	Hs.259855	elongation factor-2 kinase	25
	412095 453619	A1624707 H8764B	Hs.5921 Hs.33922	Homo sapiens cDNA: FLJ21592 fis, clone C Homo sapiens, clone MGC:9084, mRNA, comp	2.5 2,5
	431071	AA491379	110.00322	gbraa65105.rt NCI_CGAP_GCB1 Homo saplens	2.5
	407939	W05608	Hs.312679	ESTs, Weekly similar to A49019 dynein he	2.5
20	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	2.5
	444575	A1264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	25
	408420 417318	NM_006915 AW953937	Hs.44766 Hs.12891	reiinitis pigmentosa 2 (X-linked recessi ESTs	24 24
	413382	BE090689	710112001	gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.4
25	406748	AW339106	Hs,217493	annexin A2	2.4
	445898	AF070623	Hs.13423 Hs.293332	Homo saplens clone 24468 mRNA sequence	24
	441817 450551	AW969706 AJ010046	Hs.25155	ESTs neuroepithelial cell transforming gene 1	24 24
	457940	AL360159	Hs.306517	Homo sapiens TRipartite motif protein ps	2.4
30	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	2.4
	436907	AA737171	Hs.131809	ESTs	2.4
	429399 448782	AA452244 AL050295	Hs.16727 Hs.22039	ESTs KIAA0768 protein	2.4 2.4
	434404	AW445034	Hs.256578	EST8	2.4
35	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kldney disease,	2.4
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	2.4
	442295 450705	A1827248 U90304	Hs.224398 Hs.25351	Homo saplens cDNA FLJ11469 fis, clone HE	2.4 2.4
	425508	NM_003666	Hs.16B205	iroquois homeobox protein 5 basic laucine zipper nuclear factor 1 (J	2.4
40	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	2.4
	458986	AI802772	Hs.208655	ESTs	2.4
	443861	AW449462 BE092219	Hs.134743	ESTS	2.4 2.4
	412879 415250	F02614	Hs.27319	gb:1L2-8T0734-240400-071-804 BT0734 Homo ESTs	2.4
45	434627	Al221894	Hs.39311	ESTs	2.4
	443919	Al091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	2.4
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.4 2.4
	400385 411322	NM_020389 AVV887330	Hs.283104 Hs.172405	putative capacitative calcium channet cell division cycle 27	2.4
50	434638	H50758	11011121100	gb:yp86e06.r1 Soeres fetal liver spieen	2.4
	435559	AF209198	Hs.42636	zinc finger protein 277	2.4
	447849 448005		Hs.164277	ESTs ESTs	2.4 2.4
	454201	AB023191	Hs.170378 Hs.44131	KIAA0974 protein	2.4
55	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.4
	449486	AI652715	Hs.270811	ESTa	2.4
	421516		Hs.105379	FT005 protein	24
	412167 426910		Hs.190089	gb:CM0-NN0057-150400-335-e11 NN0057 Homo ESTs, Moderately similar to ALU1_HUMAN A	2.4 2.4
60	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	2.4
	400641				2.4
	430576 434423		Hs.293574 Hs.3844	ESTs LiM domain only 4	2.4 2.4
	412104		Hs.240951	Homo saplens, Similar to RIKEN cDNA 2210	2.4
65	441499		Hs.101689	ESTs	2.4
	418113		Hs.B3484	SRY (sex determining region Y)-box 4	2.4
	417819		Hs.133540	ESTs	24
	431728 425025		Hs.268107 Hs.12407	muitmerin ESTs	2.4 2.4
70	421168		Hs.330780	cylochrome P450, subfamily IIB (phenobar	2.4
	409432		Hs.54460	small Inducible cylokine subfamily A (Cy	24
	408867		Hs.656	cell division cycle 25C	2.4
	439446 445038		Hs.57873 Hs.143917	ESTs dJ467N11.1 protein	2.4 2.4
75	4506B2		Hs.25320	Homo sapiens clone 25142 mRNA sequence	24
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624		Hs.278639	KIAA1684 protein; likely homolog of mous	2'4
	449523 428784		Hs.54443	chemokine (C-C molif) receptor 5	24
80	453864		Hs.193470 Hs.21068	purinergic receptor P2X, ligand-gated to hypothetical protein	2.4 2.4
	426497		11021000	gb:EST92807 Skin turnor I Homo sepiens cD	24
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.4
	426603	AA382291		gb:EST95683 Testis I Homo saplens cDNA 5	2.4

	447357	Al375922	Hs.159367	ESTs	2.4
	452631	AI 188658		ESTs	2.4 2.4
	405041 405472				2.4
5	409744	AVV675258		Homo saplens mRNA; cDNA DKFZp586P2321 (f	2.4
		AA612960 Al379921		ESTs ESTs	2.4 2.4
		AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.4
10		AA018515		Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.4 2.4
10		A1285970 BE218603		ESTs ESTs	2.4
	444106	A1123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.4
		T61572		Human clone 23574 mRNA sequence serine carboxypepildase 1 precursor prot	2.4 2.4
15		W28673 A1335361	Hs.226376	ESTs	2.4
		AW749856		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	2,4 2.4
		AW974995 BE151746		gb:EST387100 MAGE resequences, MAGN Homo gb:PM1-HT0305-061299-003-e06 HT0305 Homo	2.4
		AA431791	Rs.113823	ClpX (caseinolytic protease X, E. coli)	2.4
20		AA448460	Hs.112017 Hs.128352	GE36 gene ESTs	2.4 2.4
		AW276240 AB014544	Hs. 21572	KIAA0644 gene product	2.4
	432949	AA570749	Hs.298866	ESTS	2.4 2.4
25	444314 417420	A1140497 T85150	Hs.258814	gb:ow76b09.s1 Soares_fetal_liver_spleen_ ESTs	2.4
	427551	T96203		gb:ye48b07.r1 Soares tetal liver spicen	2.4
	420057 434950	AA806899 AW974892	Hs.184387	ESTs gb;EST386997 MAGE resequences, MAGN Homo	2.4 2.4
- 2	425497	AA524596		gtxnh34b02.s1 NCI_CGAP_Pr3 Homo sapiens	24
30	438214	H08076	Hs.26320	TRABIO protein	2.4 2.4
	416100 419637	H18700 W27493	Hs.268799	ESTs gb:31k10 Human relina cDNA randomly prlm	2.4
	449432	AW451361	Hs.196529	E8Ts	2.4 2.4
35	454403 419179	BE065985 AW275291	Hs.113009	gb:RC3-BT0319-120200-014-a09 BT0319 Homo hypothetical protein FLJ22527	24
55	436391	AJ227892	Hs.146274	ESTS	2,4
	449511 447499	Al436187 AW262580	Hs.296261 Hs.147674	guanine nucleolide binding protein (G pr protocadhatin beta 16	2.4 2.4
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.4
40	412877 435985	BE011168 AA703154	Hs.191934	gb:PM3-BN0218-100500-003-d08 BN0218 Homo ESTs	2.4 2.4
	440674	BE561546	162-101004	gb:601347208F1 NIH_MGC_8 Homo sepiens cD	2.4
	448476	AW294072	Hs.141376	ESTs CDC14 (cell division cycle 14, S. cerevi	2.4 2.4
45	444100 435731	AA383343 AA699581	Hs.22116 Hs.186811	ESTs	2.4
	437105	AA744554	Hs.222127	ESTs	2.4 2.4
	406091 457024	AA397546	Hs.119151	ESTs	2.4
50	404249			2 Mr	2.4 2.4
50	419556 424943	U29615 AU077260	Ks.91093 Hs.153924	chitinase 1 (chitobiosidase) death-associated protein kinase 1	2.4
	444229	AV648613	Hs.282397	ESTs	· 2.4 2.4
	404860 432223	AA333283	Hs.121001	Homo saplens, clone IMAGE:3460280, mRNA	2.4
55	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.4
	420843 434927		Hs.42321 Hs.293815	ESTs Homo saplens HSPC2BS mRNA, perilal cds	2.4 2.4
	413642		113.20015	gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
60	436998 441235		Hs.291414 Hs.135570		2.4 2.4
00	445748		Hs.13252	Human EST clone 22453 mariner transposon	2.4
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein \$14	2.4 2.3
	409073 418782		Hs.14665	gb:zt71a07.s1 Soares_pineal_gland_N3HPG ESTs	2.3
65	447870	BE139479	Hs.161492	ESTs	2.3
	437370 424765		Hs.161962 Hs.284256		2.3 2.3
	407385		Hs.272072	PESTs, Weakly similar to 138022 hypotheti	23
70	424049		Hs.138380		2.3 2.3
70	425396 430702		Hs.156369 Hs.250651		2.3
	409620		Hs.13277	hypothetical protein FLJ22054	2.3 2.3
	441675 430884		Hs.5461 Hs.248114	ESTs 4 gital cell derived neurotrophic factor	2.3
75	445523	3 Z30118	Hs.29378	B ESTs, Moderately similar to unnamed prot	23 23
	416972 443547		Hs.23767	gb:bb28c01.x1 NH_MGC_5 Homo sapiens cDN hypothetical protein FLJ12666	2.3 2.3
	417583	3 AA668782	Hs.19128	4 ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
80	422183 404513		Hs.18058	2 Homo sapiens cDNA: FLJ21836 fis, clone H	23 23
	41099	9 AWB13004		gb:RC3-ST0186-230300-019-h02 8T0186 Harno	23 23
	44850 43481		Hs.38170 Hs.11428		2.3 2.3
	10101			251	

	45700C 4147C040	11- 4 D2400	FOX-	2.3
	457065 A\476318 407945 X69208		ESTs ATPasa, Cu↔ transporting, alpha polypep	2.3
	419865 NM_007020		U1-snRNP binding protein homolog (70kD)	23
_	423596 AA328195		ESTs, Weakly similar to CTL1 protein (H.	23
5	455B07 BE141140		gb:MRO-HT0075-021299-006-d07 HT0075 Homo	23 23
	435867 AA954229 440196 N72847		ESTs	2.3
	401213	113.150751	Luis	2.3
	407291 AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo	2.3
10	442490 AW965078		thyroid receptor interacting protein 15	2.3 2.3
	452943 BE247449		hypothetical protein FLJ10525	2.3 2.3
	438138 R98299 440283 AI732892	Hs.177502 Hs.190489	ESTs ESTs	2.3
	447039 AV661798	Hs.2B2915	ESTs	2.3
15	412777 Al335773	Hs.270123	ESTs	2.3
	421424 AW452690	Hs.258775	ESTs	2.3
	406673 M34996	Hs.19B253	major histocompatibility complex, class	2.3 2.3
	440555 D31292 451516 A1800515	Hs.6853 Hs.12024	hypothetical protein FLJ22167 ESTs	23
20	424690 BE538356	Hs.151777	eukaryotic translation initiation factor	2.3
	421046 AA810B54	Hs.89081	ESTs	2.3
	423604 AA486585	Hs.258901	ESTs	23
	409029 BE087807	11-446400	gb:QV1-BT0681-290400-181-g02 BT0681 Homo	2.3 2.3
25	444206 AW301017 451836 T63673	Hs.146492 Hs.173220	ESTs ,	23
20	454784 AW820626	113.110220	gb:RC0-ST0299-180100-012-e10 ST0299 Homo	`2.3
	423673 BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.3
	436671 AW137159	Hs.146151	ESTs	2.3
20	434988 Al418055	Hs.161160	ESTs	2.3 2.3
30	452862 AW378065 439480 AL038511	Hs.B687 Hs.125316	ESTs ESTs, Weakly similar to \$33990 finger pr	23
	410606 AW418779	Hs.114889	ESTs	2.3
	426535 AU077012	Hs.288582	ESTs, Weakly similar to ublquitous TPR m	2,3
	432239 X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	23
35	430217 N47863	Hs.336901	ribosomal protein S24	2.3 2.3
	417479 Al057052 421253 Al188102	Hs.133554 Hs.31028	ESTs, Weakly similar to Z195_HUMAN ZINC ESTs	2.3
	438180 AA808189	Hs.272151	ESTs	2.3
	439715 AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	23
40	44139B AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3 2.3
	443055 AV653742	Hs.15536	hypothetical protein DKFZp761J139	2.3 2.3
	413585 A1133452 448831 AL080123	Hs.75431 Hs.22182	fibringen, gamma polypeptide zinc finger protein 23 (KOX 16)	2,3
	412953 Z45794	Hs.236809	ESTs	2.3
45	430789 AA632577	Hs.310235	ESTs, Wealdy similar to 178885 serine/th	2.3
	422757 Al909935	Hs.65551	Homo saplens, Similar to DNA segment, Ch	2.3 2.3
	423003 AL120077	Hs.122967 Hs.186547	kelch (Drosophila)-like 2 (Mayven) KIAA1374 protein	2,3
	428595 AB037795 437887 AA811524	Hs.29263	hypothetical protein FLJ11896	2.3
50	447720 AL038765	Hs.161304	ESTs	23
	452355 N54926	Hs.29202	G protein-coupled receptor 34	¹ 2.3 2.3
	40B374 AW025430	Hs.155591	forkhead box F1 ESTs	2.3
	440381 AA917808 425478 AB007953	Hs.190495 Hs.268840	ESTS	2.3
55	432231 AA339977	Hs.274127	CLST 11240 protein	23
	431757 AA196930	Hs.268526		2.3
	417517 AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.3 2.3
	452837 AL121053 417425 NM_00229	Hs.5534 Hs.82124	Homo sapiens cDNA FLJ 12961 fis, clone NT taminin, beta 1	2.3
60	423739 AA398155	Hs.97600	ESTs	2.3
	416847 L43821	Hs.60261	entrancer of filamentation 1 (cas-like do	2.3
	425876 AW005867	Hs.234058		2.3 2.3
	457411 AW085961 413136 BE066941	Hs.130093	ESTs gb:PM0-BT0340-091299-002-a:11 BT0340 Homo	23
65	420313 AB023230	Hs.96427	KIAA1013 protein	2.3
-	421751 AWB13731		ESTs, Moderately similar to S65657 alpha	23
	424827 AJ057094	Hs.95867	Homo sapiens cONA: FLJ23155 fis, clone L	2.3 2.3
	436331 Al239495	Hs.120189		23
70	439275 AF086093 449272 AW137656	Hs.141566 Hs.197645		2.3
, 0	454352 AW389668		gb:RC2-SY0168-071299-013-f06 ST0168 Homo	2.3
	428758 AA433988		hypothetical protein FLJ14303	2.3
	407242 M18728		gb:Human nonspecific crossreacting antig	2.3 2.3
75	445326 A1220072	Hs.165890		23 23
75	423778 Y09267 452607 A1160029	Hs.13282 Hs.61438		2.3
	423161 AL049227	Hs.12477		23
	418851 Al417828	Hs,19243	5 ESTs	23
٥٨	458332 A1000341	Hs.22049		2.3 2.3
80	432565 AA553477 437511 AI807500	Hs.15242 Hs.12524		2.3
	430957 A)937072	Hs.55043		2.3
	425B98 AA365649			2.3

	448225	Al476429	Hs.19238	ESTs	23
	408955	BE315170	Hs.8087	NAG-5 protein	2.3
	416509	N57713	Hs_260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
5	419699	AA248998	Hs.173044	ESTs, Weakly similar to 138022 hypotheti	23 23
5	428976 458925	AL037824 R15891	Hs.194695 Hs.281587	ras homolog gene family, member l Human (clone CTG-A4) mRNA sequence	2.3
	440348	AW015802	Hs.47023	ESTs	2.3
	436340	R42246	Hs.21606	ESTs	2.3
10	444190	Al878918	Hs.10526	cysteine and glycine-rich protein 2	2.3
10	438462	A1624122	Hs.B9578	general transcription factor IIH, polype	23
	411124 442138	AW196937 AA445973	Hs.53929 Hs.13303	ESTs, Weakly similar to ALUB_HUMAN IIII Homo segiens cDNA: FLI21784 fis, clone H	2.3 2.3
	412505	AA974491	Hs.21734	ESTs	2.3
	418236	AW994005	Hs.337534	ESTs	2.3
15	423582	BE000831	Hs.23837	Homo saplens cDNA FLJ11812 fis, clone HE	2.3
	453901	BE065902	11 #5145	gb:RC2-BT031B-150200-011-b09 BT031B Homo	2.3
	418565 433404	AK001529	Hs.86149 Hs.102720	phosphoinositel 3-phosphate-blading prot ESTs	2.3 2.3
	409517	T32982 X90780	Hs.120036	troponin I, cardiac	23
20	439871	R88518	Hs.46736	hypothetical protein FLI23476	2.3
	445641	A1245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTS	2.3
	436547 437770	AJ297351 AA767881	Hs.30824 Hs.122897	leucine zipper transcription fector-like ESTs	2.3 2.3
25	409064	AA062954	Hs.141883	ESTs	23
	442607	AA507576	Hs.288361	Homo sepiens cDNA: FLJ22698 ffs, done H	2.3
	449869	W57990	Hs.60059	Homo septens cDNA FLJ11478 fis, clone HE	23
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	2.3
30	418251 432005	AA832123 AA524190	Hs.177723 Hs.120777	ESTs ESTs, Weakly shriller to ELL2, HUMAN RNA P	2.3 2.3
50	413638	H71252	110.12011)	gb:ys12h12.s1 Soares fetal liver spleen	2.3
	415980	R52414		gb:yg80b05.rt Soares infant brain 1N/B H	2.3
	449232	AW192780	Hs.196080	ESTS	23
35	430882	BE174240	Hs.79024	heterogeneous nuclear abonucleoprotein	2.3 2.3
33	454389 436089	AW752571 W06391	Hs.83623	gb:lL3-CT0213-170100-055-F02 CT0213 Homo nuclear receptor subfamily 1, group I, m	2.3 2.3
	400238	1100301	110,00010	indicat terchini acotetui i filosopu, in	2.3
	404488				23
40	407809	AW082279	Hs.244106	ESTS	2.3
40	412303 420478	AW936336 AA521259	Hs.193796	gb:QV4-DT9021-281299-070-g11 DT0021 Homo ESTs	2.3 2.3
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586i1518 (f	23
	424073		Hs.138959	gap junction protein, alpha 7, 45kD (con	23
4 ~	426567		Hs.182962	ESTs	23
45	435708		Hs.75169	ESTs	2.3 2.3
	441417 445117		Hs.144474 Hs.147369	ESTs ESTs	2.3
	447197		10.14.000	gb;yh88b01.s1 Soares placenta Nb2HP Homo	2.3
	434220		Hs.283978	Homo saplens PRO2751 mRNA, complete cds	2.2
50	445527		Hs.83286	ESTs, Waskly similar to \$14747 sphingorny	2.2
	445280 420653		Hs.306088 Hs.88550	y-crk avian sarcoma virus CT10 oncogene ESTs	2.2 2.2
	419926		Hs.93796	DKFZP5B6D2223 protein	2.2
	447541		Hs.18800	hypothetical protein FLI 20281	2.2
55	424408		Hs.146428	collagen, type V, alpha 1	2.2
	411893 428192		Hs.273789 Hs.304742	ESTs ESTs	2.2 2.2
	435634		110.00-174	gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	437637		Hs.65792	syntrophin, gamma 2	2.2
60	438018		Hs.5999	hypothelical protein FL110298	2.2
	446164		Hs.288750	hypothetical protein PLJ23577 ESTs	2.2 2.2
	450232 439699		Hs.201326 Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	402745				2.2
65	434006		Hs.112982		2.2
	439492		Hs.103159		2.2 2.2
	436853 417648		Hs.148661	ESTs gb:yf09a12.rt Soares fetal liver spleen	2.2
	427690		Hs.283410		2,2
70	414217		Hs.279898		2.2
	45022		Hs.6929	hypothetical protein FLJ11352	2.2
	40075		Un arnon	Home agricus aCNA CL 144927 Sp. along Cl	2.2 2.2
	40844 40338		Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.2
75	43364		Hs.179586	ESTS	2,2
	44207	8 AW268583	Hs.262629	ESTs	2.2
	45568		11. 400	gb:PMO-BT0340-211299-003-c12 BT0340 Homò	2.2 2.2
	43224 43992		Hs.162160 Hs.288433		2.2 2.2
80	43243		Hs.181693		2.2
	42949	3 AL134708	Hs.145998	B EST8	2.2
	42555		Hs.130767		2.2 2.2
	45010	1 AV649989	Hs.24385	Human hbc647 mRNA sequence	44

	442757	Al739528	Hs.28345	ESTs	2.2
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	2.2 2.2
	437146 432101	AA730977	Hs.123642	gb:mv55f05,s1 NCL_CGAP_Ew1 Homo sapiens EphA3	2.2
5	459644	A1918950	ns. (20042	Chius	2,2
	453887	BE564037	Hs.36237	hypothetical protein	22
	431170	AW971246	Hs.291022	ESTs hypothetical protein FLJ14103	22 22
	428062 443682	AA420683 Al383061	Hs.9B321 Hs.47248	ESTs, Highly similar to similar to Cdc14	2.2
10	400441	M15630	Hs.99879	B-cell growth factor 1 (12kD)	2.2
	453874	AW5917B3	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.2
	425810	AI923527	Hs.31903 Hs.279938	ESTs HSPC067 protein	2.2 2.2
	433037 407162	NM_D14158 N63855	Hs.142634	zinc finger protein	2.2
15	441826	AW503603	Hs.125915	phosphotriesterase related	2.2
	446901	Al347274		gb:tc05d02x1 NCI_CGAP_Co16 Homo sapiens	2.2 2.2
	454766 414221	AW866497 AW450979		gb:UV4-SN0024-170400-178-e07 SN0024 Homo gb:UI-H-BI3-afa-a-12-0-UI.s1 NCI_CGAP_Su	2.2
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: harry2)	2.2
20	400639				22
	405149	A181227E7E	No onsens	ECTA	2.2 2.2
	424027 427531	AW337575 AA405097	Hs.201591 Hs.97957	ESTS ESTS	22
	448353	BE407125	Hs.231510	ESTs	2.2
25	417669	T99858	II ances	gb:ye58g01.r1 Soares fetal liver spleen	2.2 2.2
	449650 452335	AF055575 AW188944	Hs.23838 Hs.61272	calcium channel, voltage-dependent, L ty ESTs	22
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
20	447748	Al422023	Hs.161338	ESTa	2.2
30	403534	A181770770	Hs,281238	ESTs	2.2 2.2
	410594 438550	AW770778 AW976002	Hs.258402	ESTs	22
	439626	N22415	· Hs.189080	ESTs	2.2
25	444540	A1693927	Hs.265165	ESTS	2.2 2.2
35	450024 450221	AA005129 AA328102	Hs.24641	gb:zh90h08.r1 Soares_fatal_liver_spleen_ cytaskeleton associated protein 2	2.2
	439443	AF086261	Hs.127892	ESTS	2.2
	418824		Hs.53542	choreoacanthocylosis gene; KIAA0986 prot	2.2 2.2
40	451273 430607		Hs.26163 Hs.247324	KTAA0649 gene product mitochondrial ribesomal protein S14	2.2
70	432702		Hs.293744	ESTs	2.2
	414195	BE253293	Hs.89605	cholinergic receptor, nicotinic, alpha p	22
	425570			gb:EST68590 Fetal lung II Homo sapians c	2.2 2.2
45	414935 453153		Hs.24360	gb:C15671 Claritech human zorta polyA+mR ESTs	22
	430832		Hs.100686	ESTs, Weekly similar to JE0350 Anterior	2.2
	439867		Hs.161292	ESTS	2.2 2.2
	419780 433420		Hs.87752 Hs.293961	ESTs ESTs, Moderately similar to putative DNA	2.2
50	434690		Hs.148410	ESTs	2.2
	436572		Hs.279596	ESTS	2.2 2.2
	447044 431688		Hs.17165	regulator of G-protein signalling 13 gb:ng67c08.s1 NCL_CGAP_Lip2 Homo sapiens	2.2
	403133			Bornson on the Communication of the control	2.2
5 5	414885		Hs.269276		2.2 2.2
	432111 410073		Hs.58488	gtr:E8T384871 MAGE resequences, MAGL Homo catentin (cadhetin-associated protein), a	22
	448869		Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU 6	2.2
60	429525	5 N92540	Hs.205353		2.2
60	446565 4223B6		Hs.311 Hs.115830	phosphoribosyl pyrophosphate amidotransf haparan sulfate (glycosamine) 3-0-sulfot	2.2 2.2
	40668		Hs.272620		2.2
	40337	3			2.2
65	43136		Hs.251754 Hs.299202		2.2 2.2
05	43858 40919		Hs.175613		2.2
	41228			gb:QV1-HT0413-010200-059-g05 HT0413 Homo	2.2
	41196		Hs.118609		2.2 2.2
70	44391 42778		Hs.135292 Hs.180828		2.2
7.0	44609		Hs.13801	KJAA1685 protein	22
	43648	6 AA742221	Hs.120633		2.2
	41113 40907		Hs.22456	gb:RC5-\$T0293-061299-031-C03 \$T0293 Homo) ESTs	2.2 2.2
75	43271		Hs.29494		22
	41938	4 AA490866	Hs.39429	ESTs	2.2
	41885				2.2 2.2
	40844 43212		Hs.25320 Hs.11703		2.2
80	41802	27 AB037807	Hs.83293	hypothetical protein	2,2
	44606		Hs.27004		2.2 2.2
	43619 41198		Hs.33349 Hs.18338		22
	71120		1,0,10,00	254	

	443401	A1394067	Hs.160159 I	ESTs	2.2
		4W368576	Hs.139851 (caveolin 2	22
	416143	A1955650		plutaminyl-peptide cyclotransferase (glu	2.2 2.2
5		AVV242243		peroxisomal famesylated protein ESTs, Weakly similar to 138022 hypotheti	2.2
J		AA 164803 NM_D17413		epolin; peptide ligand for APJ receptor	2.2
		AA911342		KAA1559 protein	2.2
	420111	AA255652		gb:zs21h11.r1 NCL_CGAP_GCB1 Homo saplens	2.2 2.2
10		AF032922		syntaxin blnding protein 3 chloride channel, caldum activated, fam	2.2
10		BE062109 AL137957		gb:DKFZp761D2315_r1 761 (synonym: harry2)	2.2
		AA525248	Hs.149723	ESTs	2.2
	431848	A1378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	2.2
1.5		D61594		tyrosylprotein sulfotransferase 1	2.2 2.2
15		AW885757 AF019612		ESTs membrane-bound transcription factor prof	2.2
		BE217923	Hs.149595	ESTs	2,2
	449369	AA001256	Hs.27260	ESTs	2.2
00	425514	AF112345	Hs.158237	inlegrin, alpha 10	22 22
20	455821	BE143341	LL- 401027	gb:MRO-HT0162-191099-002-d04 HT0162 Homo sine oculis homeobox (Drosophila) homolo	2.2
	427224 432284	AL135554 AA532807	Hs.101937 Hs.105B22	EST's	2.2
	403467	POWOZOBI	113.10002	2010	2.2
0.5	436032	AA150797	Hs.109276	latexin protein	2.2
25	404356	4 E4 4 G G G A	13- 000000	hanting archite DD/19046	22 22
	434205 405257	AF119861	Hs.283032	hypothetical protein PRO2015	2.2
	402103				22
• •	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.2
30	432985	T92363	Hs.178703	ESTs	2.2 2.2
	417649 431 2 77	AW239285 AA501806	Hs.82359 Hs.249965	tumor necrosis factor receptor superfami ESTs	22
	454056	A1368836	Hs.24808	ESTs, Weakly similar to 138022 hypotheti	2.2
	401694				2.2
35	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2 2.2
	431364 44590B	AW971382 R13580	Hs.294016 Hs.13436	ESTs, Moderately similar to B34087 hypot Homo saplens clone 24425 mRNA sequence	2.2
	448390	AL035414	Hs.21058	hypothetical protein	2.2
	449939	TB6420	Hs.272139	ESTs	2.2
40	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.2 2.2
	404555 418186	BE541042	Hs.23240	Homo sapiens cONA; FLJ21848 fis, clone H	2.2
	419981	AA897581	Hs.128773	ESTs	2,2
	449581	Al989517	Hs.181605	ESTs	2.2
45	419229	A1827237	Hs.282884	ESTe	2.2 2.2
	403891 423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	22
	443479	AF027219	Hs.9443	zinc finger prolein 202	2.2
	425329		Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	2.2
50	453345	AA302862	Hs.90063	neurocalcin delta	2.2 2.2
	424335 451072		Hs.28170 Hs.117929	ESTs ESTs	2.2
	451072		Hs.82719	Homo sepiens mRNA; cDNA DKFZp586F1822 (f	2.2
	411571		Hs.70811	hypothetical protein FLJ20516	2.2
55	438035		Hs.146123	poly(A) polymerase gamma	2.2 2.2
	432374 400241		Hs.301885	Horno saptens cDNA FLJ11346 fis, clone PL	2.2
	408908		Hs.250822	serine/threonice kinase 15	2.2
-	409564		Hs.54943	fracture callus 1 (ret) homolog	22
60	411151		11- 004000	gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2 2.2
	446009 456855		Hs.231926 Hs.153863		21
	416441		113.100000	nb:601301552F1 NIH_MGC_21 Homo sapiens c	2.1
	414891	R27124	Hs.268754		2.1 2.1
65	430172		Hs.1618B9		2.1 2.1
	422109 422989		Hs.1473 Hs.1602	gestrin-relessing peptide dihydropyrimidine dehydrogenese	2.1
	448552		Hs.20104	hypothetical protein FLI00052	2.1
	42237		Hs.115700		2.1
70	45072		Hs.250505		2.1 2.1
	438379 41260		Hs.171391 Hs.44898		2.1
	45127		Hs.235795		2.1 2.1
	41214	0 AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.1
75	41599		Hs.145807		2.1 2.1
	41553 43713		Hs.26873 Hs.29726		2.1
•	41530		Hs.12799		2.1
	45015	2 Al138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA 68	21
80	42114		Hs.29329		2.1 2.1
	42141 45175		Hs.57637 Hs.22693		21
	41792		Hs.82932		2.1

	40004E 16	01383	Hs.173451 r	netallothlonein 1A (functional)	2.1
		W088658		ESTs	21
		57130		ESTs	21
-		86737	Hs.193536	ESTs	2.1 2.1
5		1338247		Homo sapiens mRNA; cDNA DKFZp586L0120 (f	2.1
		J634578		ESTs ESTs, Moderately similar to ALU1_HUMAN A	2.1
		A767373 A428240		ESTs	2.1
		F115402		E74-like factor 5 (ets domain transcript	2.1
10		VA972742		ESTs	2.1
		J02687	Hs.385	ims-related tyrosine kinase 3	21 21
	406018	1.077240	Hs.43047	Homo seplens cDNA FLJ13585 fis, clone Pl.	21
		VA373210 VW876523		hypothetical protein FLJ12910	21
15		AA496479		ESTe	2.1
		U918049	Hs.124961	ESTs	2.1
		A1445255		ESTs	21 21
		AA166655		ESTs ESTs	2.1
20		A(538880 AF035119	Hs.94812 Hs.8700	deleted in liver cancer 1	2.1
20		AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	2.1
		AW963137	Hs.194233	ESTs, Moderately similar to ALU1_HUMAN A	2.1
		AJ133123	Hs,20196	adenylate cyclase 9	2.1 2.1
25		AJ091458	Hs.134559 Hs.2633	ESTs desmoglain 1	2.1
23		NM_001942 AW967109	Hs.13804	hypothetical protein dJ462O23.2	21
		AW157431	Hs.248941	ESTs	2.1
		AA664192		gb;ac05b03.s1 Stratagene lung (937210) H	2.1
20		BE047698	Hs.188785	ESTs	2,1 2.1
30		AA311301	Hs.276627 Hs.840	ESTs Indoleamine-pyrrole 2,3 dioxygenase	2.1
		M34455 AW963897	Hs.44743	KiAA1435 protein	21
		AA863360	Hs.26040	EST's, Wealdy similar to fatty acid omega	2.1
25	427434	BE538374	Hs.301732	hypothetical protein MGC5306	21
35		W28418	Hs.30715	potassium voltage-gated channel, lsk-rel ESTs	2.1 2.1
	459325 416996	AW088369 W91892	Hs.282184 Hs.59609	ESTS	21
	425638	NM_012337	Hs.158450	nasopharyngeel epithelium specific prote	2.1
	408000	L11690	Hs.620	bullous pemphigold antigen 1 (230/240kD)	2.1
40	416894	W73921	Hs.50743	ESTs	2.1 2.3
	424687	J05070	Hs.151738 Hs.160473	matrix metalloproteinase 9 (getalinase B ESTs	2.1
	437378 454100	Al198823 Al693231	Hs.126043	chromosome 21 open reading frame 51	21
	452786	R61362	Hs.106542	ESTs, Wealdy similar to T09052 hypotheti	2.1
45	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	21 21
	400631	AF173937	Hs.109494 Hs.125843	secreted protein of unknown function ESTs, Wealdy similar to T17227 hypotheti	21
	440028 426490	AW473675 NM_001621	Hs.170087	aryl hydrocarbon receptor	21
	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.1
50	407995	Al094748	Hs.100134	hypothetical protein FLJ12787	2.1 2.1
	449911	Al262105	Hs.12653	ESTs	2.1
	449509 452762	AA001615 AW501435	Hs.84561 Hs.278582	ESTs v-akt murine thyrnoma viral oncogene homo	2.1
	422839	Al674784	Hs.296908		21
55	435040	A1932350	Hs.152825	ESTs	21
	401200			3. 1. 3.5.1 (1	2.1 2.1
	41624B	H99169 BE170551	Hs.23450 Hs.8700	mitochondrial ribosomal protein 825 delated in liver cancer 1	21
	442262 449754	H00820	Hs.30977	ESTs, Weakly similar to B340B7 hypotheti	2.1
60	453908	AW613920	Hs.282178	ESTs	2.1
	446965	BE242873	Hs.16677	WD repeat domain 15	2.1 2.1
	412798	AW998657	Hs.119120 Hs.92576	E3 ubiquitin ligase SMURF1 ESTs	2.1
	416085 418378	H18072 AW962081	URBESTU	gb;EST374154 MAGE resequences, MAGG Homo	2.1
65	455995			gh:lL3-HT0618-060500-125-B07 HT0818 Homo	2.1
	422411	AW749443	Hs.22511	ESTS	21
	410888		11-7840	gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.1 2.1
	446893 442992		Hs.7110 Hs.13297	ESTs ESTs	2.1
70	407021		113.132.37	gb:Human mariner1 transposase gene, comp	2.1
, 0	43693B		Hs.161393	B ESTs	2.1
	433194	AB040B83	Hs.83243		2.1 2.1
	454790		Ne 9740	gb:RC2-ST0301-120200-011-112 ST0301 Homo epklidymis-specific, whey-ecidic protein	2.1
75	431130 434739		Hs.2719 Hs.14413		2.1
,,,	406468				2.1
	457023	AA001732	Hs.17323		21
	416226		Hs.34372		2.1 2.1
80	422306 432810		Hs.22728 Hs.23054		21
UV	412894		Hs.18651		2.1
	430602	2 D13752	Hs.18492	7 cytochrome P450, subfamily XIB (steroid	2.1
	436981	AA740891	Hs.29331	6 ESTs	2.1

	452501 A	B037791	Hs.29716	hypothetical protein FLJ10980	2.1
		B020653		KIAA0846 protein	21
		A330310	Hs.241B1	ESTs	2.1
5		34524		gb:yy56d10.st Soares_multiple_sclerosis_ ESTs	2.1 2.1
5		A866199 29138		coenzyme Q, 7 (rat, yeast) hornolog	2.1
		A719813	Hs.117662	ESTs	2.1
		A743331	Hs.272572	hemoglobin, alpha 2	2.1 2.1
10		(14614 (B023197	Hs.191254 Hs.227743	ESTs KIAA0980 protein	2.1
10		VL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.1
		3E074910		gb:RC5-8T0580-170300-021-F12 BT0580 Homo	2.1
		W972853	Hs.112237	ESTS abit 18 2004 blumon fold from aDMA filmon.	2.1 2.1
15	444610 / 400451	1174783		gb:HA2501 Human letal liver cDNA library	2.1
13		N87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	21
		N702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1 2.1
		NM_003081 AJD21989	Hs.84389 Hs.131903	synaptosomal-associated protein, 25kD ESTs	2.1
20	400196	NU21303	16.131303	LUIA	2,1
		NM_014747	Hs.78748	KIAA0237 gene product	2.1
		L34657	Hs.78146	platelet/endothellal cell adhesion molec	21 21
		AF075045 AA425234	Hs.271609 Hs.79886	ESTs ribose 5-phosphate isomerase A (ribose 5	2.1
25		H68441	Hs.13528	hypothetical protein FLI14064	2.1
		AA085803	Hs. 192997	ESTs, Moderately similar to 178885 serin	2.1 2.1
		BE379584 BE144017	Hs.34789	dollchyl-diphosphooligoseccharide-protei gb:MRO-HT0165-191199-004-d09 HT0165 Homo	2.1
		A1538323	Hs.52620	integrin, beta 6	2.1
30	447373	AJ381922	Hs_158781	ESTs	2.1
		AW301344	Hs.122908	DNA replication factor ESTs	2.1 2.1
	413918 402820	AW015898	Hs.71245	ωis	2.1
		AA347923		gb:EST54302 Fetal heart II Homo sapiens	21
35	428552	AW274560	Hs.129520	ESTS FFTs Medicartoly similar to MAA0061 pro	2,1 2.1
		BE548300 AW578003	Hs,192999 Hs.22826	ESTs, Moderately similar to KIAA0961 pro tropomodulin 3 (ubiquitous)	21
	420838	AW118210	Hs.5244	ESTs	21
40	428231	U17989	Hs.183105	nuclear autoantigen	2.1 2.1
40	434933 444870	R91095 AJ200621	Hs.4276 Hs.148504	KIAA1701 protein ESTs	2.1
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	429183	AB014604	Hs.197955	KIAA0704 protein	21
45	439155	HB1076	Hs.269001 Hs.250723	ESTs hypothetical protein MGC2747	2.1 2.1
43	442787 429864	W93048 AA460039	Hs.286	ribosomal protein L4	21
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.1
	437140	AA312799	Hs.283689	activator of CREM in testis KIAA0990 protein	2.1 2.1
50	421991 446534	NM_014918 A)307356	Hs.110468 Hs.175225	ESTs	2.1
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	44483B	AV651680	Hs.208558	ESTs	2.1 2.1
	402318 410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU 8	21
55	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	421306	AA806207	Hs,125889		2.1 2.1
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	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.1
60	428060	AA420616	Hs.249483		2.1 2.1
	419953 443718	BE267154 A(083580	Hs.125752 Hs.221373		2.1
	4441B7	AW138466	Hs.151274	ESTs	2.1
C.E.	428048	AA705745) . nanta	gb:zf41b11.s1 Soares_fetal_heart_NbHH19W	2.1 2.1
65	420195 417404	N44348 NM_007350	Hs.26243 Hs.82101	Homo sapians cDNA FLJ11177 fis, clone PL pleckstrin homology-like domain, family	21
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.1
	430335	D80007	Hs.239499		2.1 2.1
70	414618	A1204600 AA621763	Hs.9697B Hs.17043		2.1
70	434029 410945		(13.170-10-	gb:QV2-ST0145-071299-017-h10 ST0145 Homo	2.1
	421247	BE391727	Hs.10291		2.1
	433374		Hs.33278		2.1 2.1
75	445644 450271		Hs.27159 Hs.20092		21
	448084		Hs.27100	0 ESTs, Weekly similar to 138022 hypotheti	2.1
	407864		Hs.40539		2.1 2.1
	430998 435542		Hs.20403 Hs.26953		2.1
80	443544		Hs.16359	ESTs	2.1
	421103	AJ625835	Hs.27104	Homo sepiens mRNA; cDNA DKFZp667D226 (fr	2.1 2.1
	405759 446242		Hs.7360	ESTs	2.1
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	457938	A)373638	Hs.133900	ESTs	21
	433017		Hs.279914	zine finger protein 232	2.1
	436729		Hs.3337	transmembrane 4 superfamily member 1	2.1
5	432839		Hs.45207	hypothetical protein KIAA1335	2.1
,	439224		Hs.145950	ESTs, Highly similar to T08692 hypotheti	2,1
	410976		Hs.25092	hypothetical protein MGC10744	2.1
	454574			gb:MR4-ST0117-070100-027-a04 ST0117 Homo	2.1
	411020		Hs.67726	mecrophage receptor with collagenous str	2.1
10	452279		Hs.61260	hypothetical protein FLJ13184	2.1
10	446891		Hs.282878	ESTs	2.1
	434294		Ps.76194	ribosomal protain S5	21
	449057	AB037784	Hs.22941	KIAA1363 protein	21
	432769	AA620814	Hs.144959	ESTs	21
15	441224		Hs.7753	calumenin	2.1
15	407891	AA486620	Hs.41135	endomucin-2	21
	429017		Hs.66295	ការៅពី-PDZ-domain-containing protein	21
	406817	A1936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
	430566		Hs.190149	ESTs	2.1
20	449208	AW263635	Hs.48643	ESTs	21
20	451397		Hs.84529	ESTs, Wealdy similar to Z2D2_HUMAN ZINC	2.1
		H3B857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.1
	444779	Al192105	Hs.147170	ESTs	20
	433672		Hs.28B038	TLS-associated serine-arginine protein 1	2.0
25	415954		Hs.42251	ESTs	2.0
25	420273	Al652864	Hs.197257	ESTs	2.0
	411354	AW992424	Hs.288141	hypothelicai protein MGC3156	2.0
	422389	AF240635	Hs.115897	protocedherin 12	2.0
	446994		Hs.16755	MBIP protein	2.0
20	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypopt	2.0
30	422654	AA314316	Hs. 163725	ESTS	20
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	20
	405634				20
		H04150	Hs.107708	ESTs	2.0
25	431958		Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.0
35	422095	Al868872	Hs.282804	hypothetical protein FLJ22704	2.0
	442010	A1032680	Hs.132213	ESTs	2.0
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	425312	AA354940	Hs.145958	ESTs	2.0
40	415191	AA190381	Hs.120810	ESTs	2.0
40	416406	DB6961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.0
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1	2.0
	413753		Hs.75517	taminin, beta 3 (nicein (125kD), kalinin	20
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	
	433571	AA765256	Hs.135191	ESTs, Weekly similar to unnamed protein	20
45	417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.0 2.0
	409190	AU076536	Hs.50984	sarooma amplified sequence	20
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:E8T35757 Embryo, 8 week I Homo saplen	
~~	429418	Al381028	Hs.118769	ESTs	2.0
50	445B29	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.0
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	2.0
	400462			13 Paris 2000 Promite EDECOCT	2.0
55	422003	AA381760	Hs.296326	ESTs	2.0
	444585	AW170015	Hs.6594	ESTs	2.0
	44489B	A1201548	Hs.308338	ESTs	2.0
	403525			20.0	2.0
10	443031	AW134696	Hs.49418	ESTs	2.0
60	430818	Al311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo saplens	2.0
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	2.0
	440941	BE268362	Hs.7535	COBW-like protein	20
	409627	AW997628	Hs.313637	ESTs	2.0
~ =	433258	Al806626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN [I]]	2.0
65	412863	AA121673	Hs.59757	zinc finger protein 281	2.0
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.0
		BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog	2.0
	417280	AW173116	Hs_262206	ESTs	2.0
		AB011137	Hs.300938	KIAA0565 gene product	2.0
70	424800	AL035588	Hs.153203	MyoD family inhibitor	2.0
	446019		Hs.279789	histone deacetylase 3	2.0
	435472		Hs.283022	triggering receptor expressed on myeloid	20
	424882	Al379461	Hs.153636	far upstream element (FUSE) binding prot	2.0
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	400859		. 10		2.0
	405829				2.0
~ ~		AW752247	Hs.293853	ESTs	2.0
80	420314	HB1671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	437733	A1792574	Hs.122876	ESTS VIBBIDLY SITHLAND 122000 RYPOINED	2.0
	452019	Al.157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
					2.0

					4.0
	430706	NM_003540	Hs.247816	H4 histone family, member C	2.0
	420558	F09247	Hs.247735	protocadherin alpha 10	20
	452759	AW590773	Hs.258996	ESTs	2.0
_	408496	A1683802	Hs.136182	ESTs	2.0
5	420674	NM_000055	Hs.1327	butyrylcholinesterase	20
	410358	AW97516B	Hs.13337	ESTs. Weakly similar to unnamed protein	2.0 2.0
	450086	AW016343	Hs.233301	ESTS	2.0
	410853	H04588	Hs.30469	ESTs	2.0 2.0
10	438607	AW080237	Hs.252884	ESTs	2.0
10	422232	D43945	Hs.113274	transcription factor EC	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
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	438315	R58795	Hs.82419	ESTs	2.0
15	445261	T79759	Hs.282939	ESTs, Weakly similar to 138022 hypotheti	2.0
10	401986	172702	110,202,000	Lors, Fromis a rodect in police	2.0
	420335	AA258771	Hs.43616	Homo sepiens mRNA for FLJ00029 protein,	2,0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
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	458433	AL135352	Hs.255883	ESTs, Weakly similar to 138022 hypotheti	2.0
	417494	Al369494	Hs.222137	ESTs	2.0
	416045	H15990	Hs.31403	ESTs	2.0
	424181	AL039482	Hs.142517	Homo saplens mRNA; cDNA DKFZp434P0810 (f	2.0
25	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.0
	41157B	AW238524		gb:xp27c05.x1 NCI_CGAP_HN10 Homo sapiens	20
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	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	20
20	43560B	AW183971	Hs.250896	ESTs	20
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	458308	Al828155	Hs.211055	ESTs	2.0
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35	427244	AA402400	Hs.178045	ESTs	2.0
22	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	2.0
	438979	AW976218	Hs.32565	ESTs	2.0
	400285 405966				2.0
	407407	AF050198		gb:Homo sagiens putative mitochondrial s	2.0
40	427739	AW196755	Hs.98105	NYD-SP14 protein	2.0
••	433584	AW295399	. 10100100	gb:UI-H-BI2-ahr-h-03-0-UI.s1 NCL_CGAP_Su	2.0
	448956	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.0
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	418836	AJ655499	Hs.161712	ESTs :	2.0
	45310B	Al311457	Hs.99472	ESTs	2.0
	447101	N72185	Hs.44189	ESTs	20
50	408873		Hs.182278	calmodulin 2 (phosphorylase kinase, delt	2.0
50	426226	AA769045		gb;paB0h07,s1 NCI_CGAP_GCB1 Homo saplens	2.0
	401157	1440-0-	la annia	And an implementation of the state of	20
	407721		Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.0 2.0
	425646		Hs.158512	cyclin-dependent kinase-like 2 (CDC2-rel	2.0
55	408964 419839		Hs.49349	beta-site APP-cleaving enzyme phospholipase A2, group VII (platelet-ac	2.0
55	402855		Hs.93304	hitoshitoshase vs. gioth an therease	20
	443644		Hs.93270	EBTs, Moderately similar to \$65657 alpha	2.0
	445672		Hs.282862		20
	432343		Hs.2961	S100 calclum-binding protein A3	2.0
60	411941		Hs.25201	ESTs, Weakly similar to FAT DROME CADHER	2.0
	430664		Hs.303303		20
	402812			·	2.0
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	2.0
	448133		Hs.73769	foliate receptor 1 (adult)	2.0
65	402048				2.0
	423347		Hs.234557		20
	423957		Hs.136235		2.0
	433347		**	gb:Homo saptens Ras-GRF2 mRNA, partial c	2.0
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70	439217		Hs.42975	ESTs	2.0 2.0
	44660	9 BE395090	Hs.15535	Homo saplens clone 24582 mRNA sequence	2.0

TABLE 3B: Ust of accession numbers for primekeys lacking unique elio's for Table 3A. Forsuch such probeset is listed a gene cluster number from which the o'igonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Cakland Callifornia). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

80 Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

Pkey CAT number Accession

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AW970622 AA503009 AA502998 AA502989 AA502805 T92188
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AW972777 AA526796 AA558305
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AA721522 AW975443 T93070
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                                  421802 1
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AF085839 R69137 AW188788 R69254
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AA828995 AA834879 Al926361
AA879294 N67538 Al474541
BE561546 Z25124 Al307139 Z28800
Al079356 W23287
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                                                          AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220 AW178206 AW178209 AW178209 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108
    75
                                                          AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156
                                                          AW178104 AW178163 AW178093 AW178208 AW178137 AW176140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
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N71277 AW390764
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                   454389
                                     1156B2 1
                                                          BE065985 BE065944 BE066008 BE066083 BE066093
                   454403
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40	455631 455678 455685 455807	1347545_1 1349716_1 1350393_1 1370914_1	BE06600 BE06697 BE14114	1 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072 7 8E066017 BE066074 6 BE066928 BE066927 0 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108 1 BE143344 BE143378 BE143358
45	455821 455866 455992 455995	1372714_1 1377119_1 1398552_1 1398903_1	BE14902 BE17901	1 BE149354 BE149356 BE149025 BE149057 BE152819 BE149030 BE149052 BE149023 BE149055 5 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997 8 BE179798 BE179980 79 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368
50	456034 458804	142696_1 75803_1 798085_1	BE01136 AL15762	73 AA136653 AA136656 AW419361 AA364556 AA432073 BE 166345 AA663654 AV226665 BE 17272 BED 11363 BE 17636 BE 1763
20	458861 459160 459201 459267	920051_1 925883_1 966605_1	A)904723 AW3911	7 AGS04725 AI904729 AI904722 AI904758 AI904736 77 W45021 11 AJ003650 AJ003651
55	TABLE 600	•		
	TABLE 290 Pkey:	Unione annual	ber correspon	ding to an Eos probeset
60	Ref: Strand: Nt_position	human chroi Indicates Dâ	nosome 22." IA strend fron	unit to an Exercitise to column are Genbank identifier (Gi) numbers. "Dunham I, et al." refers to the publication entitled "The DNA sequence of Dunham I, at al., Nature (1999) 402:489-495. The product of the exensivere prodicted. The product of the exens were prodicted. The product of the exens were producted.
65	Pkay	Ref	Strand	Nt_position
70	400451 400462 400608 400839	8113550 9929659 9887666 9887597	Minus Minus Minus Plus	82189-82320 197610-197785 98756-97558 23150-23580
,,	400641 400756 400869	8117693 8119084 9757499	Plus Minus Minus	4788-4992 38734-38857 91888-92018,98131-98294,99474-89570
75	400880 400889 400983 401045 401049	9931121 9958234 8081198 8117619 7232177	Phis Minus Plus Phis Plus	29235-29336,36363-36580 169782-170036 107903-108832 90044-90184,91111-91345 149157-150692
80	401078 401094 401103 401157	3687273 9965511 8568122 9438289	Plus Plus Minus Minus	105052-105171 137130-137302,139283-139506 98330-98449 114133-114247,114567-114645
	401189	9690246	Minus	90815-80929

	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116445,116847-116907,122853-123067,124982-125407
	401213	985B40B	Plus	98243-98380,98489-98619
	401254	9796309	Plus	152209-152383
_	401323	9212516	Plus	213509-214450
5	401335	9884881	Plus	15736-16352
	401497	7381770 7877912	Plus Plus	92507-92813 29278-29770
	401517 401526	7770561	Plus	91570-93177
	401575	7229604	Minus	76253-76364
10	401694	3540172	Minus	64056-64168
	4D1793	726388B	Minus	102945-103083
	401862	7770606	Minus	55839-56993,59145-59293 462368 462474 462000 462106
	401878 401986	8099802 4406829	Minus Minus	162268-162474,163089-163195 - 31137-31293 -
15	402048	8072415	Phis	166394-188556,168167-168395
	402048	8072512	Plos	43936-44078
	402102	8117771	Minus	174566-174740
	402103	7249203	Plus	14453-15414
20	402230 402318	9966312 7582559	Minus Minus	29782-29932 12843-13403
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	402745	9212200	Minus	76516-76690
	402800	6010175	Plus	43921-44049,46181-46273
25	402812	6010110	Plus	25026-25091,25844-25920
25	402820 402855	6456853 9662953	Minus Minus	82274-82443 59763-59909
	403133	7331427	Plus	3B314-3B634
	403271	7230852	Plus	134283-134485
	403277	8072597	Minus	27494-27642
30	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403356 403378	8569930 9438244	Plus Minus	92839-93036 44264-4443
	403388	9438331	Plus	112733-113001,114599-114735 ' .
35	403467	9929556	Maus	73431-73602
	403515	7656757	Minus	173358-179553
	403525	7960440	Plus	152431-153243 46652-47332
	403534 403568	8076917 B101145	Minus Minus	85509-8565B
40	403574	8101156	Plus	5542-5176
	403637	8671936	Minus	<u>142647-142771,145531-145762</u>
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
45	403760 403776	7712202 7770611	Minus Minus	45910-46260,47563-47824 1414-1513,1624-1756
45	403895	7381715	Minus	3502-4002,4070-4308
	403937	7711761	Minus	12609-12773
	404043	9558573	Plus	29042-29136,46597-46699
50	404097	7770701	Plus	55612-55781
20	404200 404249	6010176 8655533	Minus Plus	7066-7210 . 64270-64633
	404274	9885189	Plus	104127-104918
	404285	2326514	Plus	32282-32416
c e	404288	2769644	Plus	3512-3691
55	404356	7830858	Minus	126433-126623
	404443 404476	7579073 8080699	Minus Plus	87198-87441 101841-102043
	404488	8113286	Minus	64835-64994
	404513	6151941	Minus	112837-113339
60	404548	8570305	Minus	83896-84162
	404555	7243881	Minus Minus	63953-64157 - 69039-70100
	404561 404588	9795980 6456728	Minus	40059-40210
	404593	9944086	Minus	74922-75788
65	404599	8705107	Plus	110443-110733
	404860	8979555	Plus	65852-66081
	404916 404957	7341826 7407927	Plus Plus	91057-91188 147512-148011
	405041	7547195		121230-121714
70	405059	7656683		349-822
	405090	6072525		38552-39202
	405257	7329310		73121-73273
	405336 405472	6094635 8439781		33287-33563 106297-106447,108462-108596
75	405472 405494	8050952		70284-70518
, ,	405547	1054740		124361-124520,124914-125050
	405621	5523811	Plus	59362-59607
	405634	5306288		17856-17957,18302-18412,18837-18927,22790-22989
80	405654 405692	4895156 4314424		53624-537/59 61379-62562
00	405759			18283-18399
	405829	7109593) Minus	15628-16127
	405848	7651809) Minus	28135-28244

	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
	406018	6758904	Minus	37795-38168
_	406091	9123919	Minus	197370-197935
5	406092	9123919	Plus	251370-251797,252168-252882
	406149	7144791	Minus	444 64-45164
	406195	7289992	Minus	36293-36827
	406333	9213235	Plus	64689-64798
	406468	9795553	Plus	4373-4515,8870-9046,11366-11509,11625-11880
10	406506	7711374	Minus	6843-8077
	406554	7711566	Plus	t06956-107121
	406603	8272659	Minus	39506-39694

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TABLE 30a: ABOUT 1840 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO HYPERSENSITMITY PNEUMONITIS (HP)

Table 30A lists about 1840 genes that are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with hypersensitivity pneumonitis [HP] samples. These were selected from about 59660 probesets on an Affymetrix/Eos Hu03 Gene Chilp array such that the ratio of "average" kilopathic pulmonary fibrosis sample expression was greater than or equal to about 2.0. The "average" kilopathic pulmonary fibrosis level was set to the 90° percentile amongst kilopathic pulmonary fibrosis samples. The "average" hypersensitivity pneumonitis level was set to the 90° percentile amongst hypersensitivity pneumonitis samples. 20

Pkey: Unique Eos probeset identifier number rkey: unique tos proceset identiner number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of IPF (idiopathic pulmonary fibrosis) to HP (hypersensitivity pneumonitis)

30	Pkey	ExAcon	Unigene ID	Unigene Tille	R1
30	450478	AW451709	Hs.271200	ESTs	20.2
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	405654	71001100	190,27 4712	hyposidades propert to 10274	11.B
	440209	H05049	Hs.22269	neurexin 3	10.8
35	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antegon	10.4
	439606	W79123	Hs,58561	G protein-coupled receptor 87	10.3
	425259	ALD49280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	10.2
	426230	AA367019	Hs.241395	protease, serine, 1 (typsin 1)	9.5
	416653	AA768553	Hs.74170	metallothlonein 1E (functional)	9.3
40	4204B1	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	9.2
	403574				9.1
	415817	U88967	Hs.78867	protein tyrosine phospitatase, receptor-t	B.B
	419519	Al198719	Hs.176376	ESTs	8.2
4.5	435256	AF193766	Hs.13872	cytokine-like protein C17	8.1
45	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	B.1
	429629	BE501732	Hs.30622	Homo sepiens cDNA FLJ13010 fis, clone NT	8.0
	405443				7.8
	428766	AA477989	Hs.98800	ESTS	7.7
50	441802	AA968636	Hs.127877	ESTs	7.6
50	453649	Y07494	Ha.34114	ATPase, Na+K+ transporting, alpha 2 (+)	7.5
	447410	A1470235	Hs.172698	EST	7.2
	442353	BE379594	Hs.49135	ESTs, Moderately similar to ALU7_HUMAN A	7.2
	405494				6.9
EE	442377	AA993807	Hs.167367	ESTs	6.9
55	409928		Hs.57549	hypothetical protein dJ473B4	6.B
	420407		Hs.145010	Hpopolysaccarkle-specific response 5-li	6.8
	415236			gb.yf94b12.s1 Soares infant brain 1NIB H	6.8
	451562		Hs.10770B	ESTs .	6.B
C 0	403310				6.7
60	445189		Hs.147482	EŜTS	6.7
	409632		Hs.55279	serine (or cysteine) proteinase inhibito	6.7 6.6
	439780			gis:Homo sapiens mRNA full length insert	6.6
	402076		11- 25052	FOTo	6.5
65	415025		Hs.72307	ESTs	6.5
U.S	406690		Hs.220529	carcinoembryonic antigen-related cell ad	8.5
	438557		Hs.143509	hypothetical protein FLJ21924	6.4
	426042		Hs.76391	myxovirus (influenza) resistance 1, homo matrix metalloproteinase 1 (infersitial	6.4
	418007 409545		Hs.83169 Hs.19002	hypothetical protein MGC4675	6.4
70			Hs.313	secreted phosphoprotein 1 (osteopontin,	6.4
70	446619 411968		Hs.118609	ESTs	6.4
	440274		Hs.7122	scrapie responsive protein 1	6.3
	442879		Hs.8813	syntaxin binding protein 3	6.3
	419238		Hs.135159	Homo saptens cDNA FLJ11481 fis, clone HE.	6,3
75	420185		Hs.158047	ESTs	6.3
,,,	415672		Hs.193579	ESTs	6.2
	455486		1 id. 1300/3	pb:zi90f03.r1 Stretagene colon (937204)	6.2
	420026		Hs.166676	ESTs	6.1
	44686		Hs.135100	ESTs	6.1
80	43162		Hs.293184	ESTS	6.1
	40726		LISASSIUT	gb;Horno saplens mRNA for immunoglobulin	6.1
	421300		Hs.96617	ESTs	6.0
	41604		Hs.31403	ESTs	6.0

		41000000	12 400040	Land Test Seekele PMT7-7040440	6.0
	414175 42 4 693	A1308876 BE169810	Hs.103849 Hs.47557	hypothetical protein DKFZp761D112 ESTs	6.0 6.0
	424693	AA715013	Hs.169835	ESTS	6.0
	440504	Al948966	Hs.130017	ESTs, Weakly similar to JN0908 Hr-transp	6.0
5	40971B	D86640	Hs.56045	src homology three (SH3) and cystaine ri	6.0
	403625	.1			6.0 5.9
	418986 416035	Al123555 H42314	Hs.81796	ESTs gbyy009e02,s1 Soares adult brain N2b5HB5	5.9
	400292	AA250737	Hs.72472	ESTs	5.9
10	442849	R10099	Hs.269805	ESTs	5.9
	440887	AJ799488	Hs.135905	ESTs	5.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	5.7 5.7
	410934 431374	AW811114 BE258532	Hs,251871	gb:MR2-ST0131-111199-016-a04 ST0131 Homo CTP synthese	5.7
15	444963	AI916973	Hs.213603	ESTs	5.7
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	5.6
	444992	R37658	Hs.21375	ESTs	5,6
	416575	W02414	Hs.38383	ESTS	5.5 5.5
20	431211 451830	M86849 H18433	Hs,323733 Hs.21542	gap junction protein, beta 2, 26kD (conn KJAA1035 protein	5.5
20	446466	H3B026	Hs.308	arrestin 3, retinal (X-arrestin)	5.5
	404043				5.5
	423454	AL110456	Hs.469	succinale dehydrogenese complex, subunit	5.5
25	455540 434683	8E080231 AW298724	Hs.202639	gb:RC4-BT0629-120200-012-f11 BT0629 Homo ESTs	5.5 5.5
2.5	445898	AF070523	Hs.13423	Homo sapiens close 24468 mRNA sequence	5.5
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	5.5
	428895	AA437124	Hs.187247	ESTs	5,4
30	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	5.4 5.4
30	419249 455047	X14767 AW852530	Hs.89768	gamma-aminobutydo acid (GABA) A recepto gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.4 5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	403637	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		•	5.3
25	414725	AA769791	Hs.125300	ring finger protein 21, interferon-respo	5.3
35	409073 403329	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	5.3 5,3
	434001	AW950905	Hs.3697	serine (or cystelne) proteinase inhibito	5.3
	459664	7111000000	1.0.0001	admir for distance in the same	5.3
40	401497	7			5.3
40	410797	AW857191	11- COOCC	gb:RC2-CT0304-080100-011-b12 CT0304 Home	5.2 5.2
	411402 448844	DE297855 Al581519	Hs,69855 Hs, 177164	NRAS-related gene ESTs	5.2
	435202		Hs.170204	KIAA0551 protein	5.1
	439418		Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.1
45	443584		Hs.267245	hypothetical protein FLJ 14803	5.1
	434352 43083B		Hs.86492 Hs.169395	small muscle protein, X-linked hypothetical protein FLJ12015	5,1 5,1
	430882		Hs.79024	heterogeneous nuclear ribonucleoprotein	5.1
	440129		Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.0
50	437636		Hs.291844	ESTS	5.0
	455747 455464			gb:RC5-8T0580-170300-021-F12 BT0580 Homo gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.0 5.0
	418771		Hs.25329	ESTs	5.0
	434820			gbms90f05.x5 NCL_CGAP_Pr3 Homo saptens	5.0
55	440615		Hs.130806	ESTs	. 5.0
	454482 400432		Hs.287767	gb:RC3-HT0230-160200-016-e08 HT0230 Homo Sequence 8 from Patent WO9950285	4,9 4,9
	436505		Hs.121121	ESTs, Weakly similar to \$00755 pleckatri	4.9
	423607		Hs.6591	ESTs	- 4.9
60	407415			gb:Homo saplens tetracyline transporter-	4.9
	401878 443162		Hs.9029	DKFZP434G032 protein	4.9 4.9
	45132		Hs,5978B	ESTs	4.9
	440518		Hs.7239	SEC24 (S. cerevisiae) related gene famil	4.9
65	40633				4.9
	40910		Hs.255877	ESTs	4.8 4.8
	408000 4214B3		Hs.620 Hs.104715	bullous pemphigoid antigen 1 (230/240kD) Inversin	4.8
	44275		Hs.28345	ESTs	4.8
70	45971	7			4.8
	43663		Hs.26766	ESTs	4.8 4.8
	41222 45010		Hs.292737 Hs.24385	ESTs Human hbc647 mRNA sequence	4.8 4.8
	41090		1 10.25000	gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
75	42621	7 AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	44164		Hs.144104	ESTs	4,B
	42297 42536		Hs.132221	gbmp83h04.s1 NCI_CGAP_Thy1 Homo sepiens hypothetical protein FLJ12401	4.8 4.8
	41495		113. 134221	gb:Ct5506 Cloriech human aorta polyA+mR	4.8
80	41196	5 BE467339	Hs.280115		4.7
	40334			-L-OUR OT0044 400400 4F0 140 000044 11	4.7
	41172 44327		Hs.195704	gb:CM3-CT0341-190400-152-h12 CT0341 Homo ESTs	4.7 4.7
	T1021	. 00,000	1 10. 1331 134	20.0	4.3

	417181 426097	L10123 BE327369	Hs.1071 Hs.112238	surfactant protein A blinding protein ESTs	4.7 4.7
	439199	R40373	Hs.26299	ESTs	4.7
_	440728	AW086077	Hs.153272	Homo saplens cDNA: FLJ22715 fis, clone H	4.6 4.6
5	434381 417428	AA631834 N87579		gb:np77h05.s1 NC1_CGAP_Pr2 Homo sepiens qb:LL2030F Human fetal heart, Lambda ZAP	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	431242	AA987742	Hs.251278	KIAA1201 protein	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6 4.6
10	442360 452171	AI374621 AI863302	Hs.29055 Hs.211930	ESTS EST	4.6
	440801	AA906366	Hs.190535	ESTs	4.5
	411738	AW859353	. 2.110000	9b:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
1.5	431447	AA505138	Hs.291341	ESTs	4.5 4.5
15	433485	A1493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	401365 408281	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	4.5
	411657	AW855583		gb:CM4-CT0278-221099-027-f07 CT0278 Homo	4.5
20	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	4.5
20	428528	AI004034	Hs.9863B	ESTs Homo sapiens mRNA for KIAA1771 protein,	4.5 4.5
	454036 417252	AA374756 AA195014	Hs.93560 Hs.85971	ESTs	4.5
	417135	AA422067	Hs.50547	ESTs	4.5
~-	403089				4.4
25	420691	AA829433	Hs.275343	ESTS	4.4 4.4
	412147 425578	AW895984 U65652	Hs.158313	gb:QV4-NN0039-040500-197-e08 NN0039 Homo chromosome 17 open reading frame 1A	4.4
	430403	AF039390	Hs.241362	tumor necrosis factor (ligand) superfami	4.4
	45443B	AA224053	Hs,172405	cell division cycle 27	4.4
30	435434	AA680387	Hs_187850	ESTs	4.4
	420828	AA280778	Hs.186878	ESTs	4.3 4.3
	435586	A1279137	Hs,151498	ESTs ribosomal protein L7a	4.3 4.3
	452393 416170	H87398 H42454	Hs.99858 Hs.220645	ESTs	4.3
35	408691	AW250525	1 DILLEVO IV	gb:2821626.5prime NIH_MGC_7 Homo sapiens	4.3
	428912	AW103117	Hs.98949	ESTs, Weakly similar to MEA6 [H.saplens]	4.3
	455511	BE144762	13 45004	gb:CMO-HT0180-041099-085-b04 HT0180 Homo	4.3 4.3
	413849 401189		Hs.15384	AP1 gamma sebunit binding protein 1	4.3
40	425733		Hs.159388	Homo sepiens clone 23578 mRNA sequence	4.3
	447863		Hs.288885	Homo saplens cONA FLJ14245 fis, clone OV	4.3
	422654		Hs.163725	ESTs	4.3
	435463		13- 00070	gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3 4.3
45	417919 405784		Hs.86379	ESTs	4.3
10	431B53		Hs.70834	ESTs	4.3
	409629		Hs.279724	ESTs	4.2
	403281				4.2 4.2
50	427173		Hs.97540	ESTs gb:AF063536 Homo sapiens library (Yu Y)	4.2 4.2
50	433717 406777		Hs.150580	putative translation initiation factor	4.2
	410481		Hs.321450	pregnancy specific beta-1-glycoprotein 2	4.2
	419511		Hs.75113	general transcription factor IIIA	4.2
55	452291		Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4,2 4,2
33	449762 421100		Hs.54868 Hs.172844	ESTs ESTs	4.2
	43938		Hs.103070	ESTs	4.1
	404957	7			4.1
60	43633		Hs.82302	Homo sepiens cDNA FLJ14814 fis, clone NT	4.1 4.1
60	446393 452721		Hs.301956 Hs.239708	zīnc finger protein ESTs	4.1
	45638	14010010	(18.239100	gb:47e1 Human relina cDNA randomly prime	4.1
	40625		Hs.311054	Homo saplens mRNA full length insert cDN	4.1
CF	41697			gb:bb28c91.x1 NIH_MGC_5 Home saplens cDN	4.1
65	42709		Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1 4.1
	40334 43899			gb:od77b08.s1 NCI_CGAP_Ov2 Homo saplens	4.1
	44492		Hs.144871	Homo sagiens cDNA FLJ13752 fis, clone PL	4.1
	40159		Hs.110950	Rag C protein	4.1
70	41869		Hs.87409	thrombospondia 1	4.1
	41429		Hs.71730	ESTs Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.1 4.0
	45274 45855		Hs.30504 Hs.245856	ESTs	4.D
	42106			gb:EST33362 Embryo, 12 week il Homo sapi	4.B
75	43929	4 AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	44120		Hs.128757	ESTs	4.0
	43437		Hs.306593 Hs.169071	Homo sapiens cDNA FLJ11382 fls, clone HE ESTs	4.0 4.0
	44047 41837		Hs.169071 Hs.137516		4.0
80	435B7		Hs.20152	ESTs	4.0
= -	43720	33 AA747822		gb:rx97a04.s1 NCI_CGAP_GCB1 Homo sapiens	4.0
	4440		Hs.282375	ESTs gb:MR0-SN0039-300300-001-c02 SN0039 Home	4.0 4.0
	41174	45 AW867826		go:miru-airuuss-suussuu-uu i-tuuz sivuuss nuimb	7.0

			11. 0040	NA OC. 2040CCC —TNI	40
		U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0 4.0
	405521 411597	AW852925		gb:PM0-CT0248-131099-001-110 CT0248 Homo	4.0
_		W05433	Hs.49890	ESTs	4.0
5	404822				4.0 4.0
	441107 404834	AA917075	Hs.190520	ESTs	4.0
		AW995044	Hs.26239	Human DNA sequence from clone RP11-43882	4.0
		AA968441	Hs.126866	ESTs	4.0
10		AA721252	Hs.291502	ESTs	4.0 4.0
		AW118681	Hs.126051	Homo saplens thyrnic stromal lymphopoiati	3.9
		Z25935 AW805687	Hs.86379 Hs.300648	ESTs ESTs	3.9
		H05468	Hs.164502	ESTs	3.9
15		AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs ESTs, Moderately similar to S65657 alpha	3.9 3.9
	440356 452768	AI933184 AW069459	Hs.127922 Hs.61539	ESTs	3.9
	455241	AWB76249	1 2010 7000	gb:PM4-PT0019-131299-006-B05 PT0019 Homo	3.9
20	409070	AAD63003	Hs.224560	ESTs	3.9
	409044	Al129586	Hs.33033	hypothetical protein FLJ 14623	3.9 3.9
	419091 422591	T85332 L07648	Hs.178294 Hs.118630	ESTs MAX-interacting protein 1	3.9
	403188	LUTOTO	118.170000	140 24 ureneman 2 brogon .	3.9
25	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	3.9 3.9
	413585	Al133452	Hs.75431	fibrinogen, gamma polypeptide ESTs	3.9 3.9
	436149 443682	A1754308 A1383061	Hs.159452 Hs.47248	ESTs. Highly similar to similar to Cdc14	3.9
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
30	439818	AL360137	Hs.19934	Homo saplens mRNA full length Insert cDN	3.9
	438361	AAB05656	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.9 3.9
	451221 455475	Al949701 AW948126	Hs.210589	ESTs gb:RC0-MT0013-280300-031-a12 MT0013 Homo	3.9
	433197	AB0408B9	Hs.281022	KIAA1456 protein	3.9
35	429581	T80112	Hs.192245	ESTs	3.9
	415598	A1433165	Hs.9858	ESTs	3.9 3.9
	431220 433132	N52937 AB026264	Hs.102679 Hs.284245	hypothetical protein IMPACT	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
40	404443				3.9
	407340	AA810168	Hs,284289 Hs,269259	vitiligo-associated protein VIT-1 ESTs, Weakly similar to S23650 retroviru	3.9 3.9
	41031B 412400	AA084050 AVV948066	UR'503523	gb:RC0-MT0012-290300-031-h10 MT0012 Homo	3.9
	427167	Al239607	Hs.99195	hypothelical protein MGC11324	3.9
45	438090	AA777534	Hs.191992	ESTs	3.8
	407938	AA905097	Hs.85050	phospholamban	3.8 3.8
	440454 417706	A1733037 T90797	Hs.129990 Hs.268623	ESTS ESTs	3.8
	428692		Hs.110103	RNA polymerase I transcription factor RR	3.8
50	407762		Hs.29475	ESTS	3.8
	420727		Hs.99886	complement component 4-binding protein,	3.8 3.8
	417508 413525		Hs.180877	H3 histone, family 38 (H3.3B) gb:MR0-HT0208-221299-204-610 HT0208 Homo	3.8
	425798			gb:EST74529 Pineal gland II Homo septens	3.8
55	459429	AA278779	Hs.335696	EST	3.8 3.8
	430205 437458		Hs.235168 Hs.128751	carbonic anhydrase XIV Homo sapiens cDNA FLJ12235 fis, clone MA	3.8 3.8
	437458 451073		Hs.1206063	ESTs	3.8
	452786		Hs.106642	ESTs, Weakly similar to T09052 hypotheti	3.8
60	429846		Hs.225945	fucosytransferase 9 (alpha (1,3) fucosy	3.8 3.8
	444414 402615	AW299214	Hs.8752	transmembrane protein 4	3.0 3.7
	410585		Hs.337501	ESTs	3.7
	425168	R96366		gb:yq37d04.s1 Soares fetal liver spleen	3.7
65	449729		Hs.29235	ESTS	3.7 3.7
	459359 456443		Hs.133543	gb:za40a05.r1 Soares fetal liver spleen ESTs	3.7
	439001		1 10, 1005/10	gb;Horno saplens full langth Insert cDNA	3.7
	443657	7 R14973		gb:y442f10.s1 Soares fetal liver spicen	3.7
70	404193		11_ 000000	FOT-	3.7 3.7
	416379		Hs.203933 Hs.117936		3.7
	422511 426603		113.111730	gb:EST95683 Testis i Homo sapiens cDNA 5	3.7
	41258	9 R28660	Hs.24305	ESTs	3.7
75	42103	7 AI684808	Hs.197653		3.7 3.7
	42708 42992		Hs.142390 Hs.2522	ESTs adenylate cyclese 8 (brain)	3.7
	42992 45337		Hs.240091		3.7
~~	43545	1 AF195420	Hs.303006	ESTs, Weakly similar to gamma-heregulin	3.7
80	451BB	2 A1821324	Hs.100445	S ESTs	3.7 3.7
	41998 40500		Hs.94030 Hs.296281	Homo saptens mRNA; cDNA DKFZp586E1624 (f Interleukin enhancer binding factor 1	3.7
	42218		Hs.180582		3.7
				267	

			II- FRORD		17
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.7
	432781	NM_014133	Hs.278940	PRO0618 protein	3.7
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.7
5	406964	M21305	11- 004050	gh:Human alpha satellite and satellite 3	3.7
,	430682	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.7
	449804 411505	A1535663	Hs.39379	ESTS	3.7
		AF155859	Hs.70585	molybdenum cofactor synthesis 2	3.7
	430503	AA533574	Hs.152274	ESTs	3.7
10	443305	A)050693	Hs.133318	ESTs	3.7
10	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.7
	452280	A1911410	Hs.167224	ESTS	3.6 3.6
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	
	406992 441416	562472	No. 6 40000	gir:bela-pol=DNA polymerase beta (exon a	3.6 3.6
15		Al990139	Hs.148609 Hs.30057	ESTs	3.6
13	448776	BE302464	Hs.243933	MRS2 (S. cerevisiae)-like, magneslum hom	3.6
	413998	AW103807		ESTs	3.6
	4403B5 431673	AA8842B3	Hs.192136	ESTS	3.6
		AW971302	Hs.293233	ESTs .	3.6
20	401887				3.6
20	404793	AA322506		absCCT361/6 Carabather II Users conions a	3.6
	422054 432030	ARS22500 AI908400	Un 1/2700	gb:EST25146 Cerebellum II Homo sapiens c ESTs	3.6
	449645	Al961092	Hs.143789 Hs.196155	ESTs	3.6
	404476	AUSUIUSZ	UR: 190199	C919	3.6
25	449336	AL119995	Hs, 15260	ESTs, Highly similar to AC007228 2 BC372	3.6
23	401200	LT 10000	1 30, 12200	ESTS, Taging Sittles to Accordance 2 Door 2	3.6
	403937				3.6
	437918	A)761449	Hs.121629	ESTs	3.6
	443394	Al055865	Hs.133485	ESTs	3.6
30	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.6
20	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from done 1198H6 on	3.6
	436269	AA707472	Hs.190760	ESTs	3.6
	453823	AL137967	115.150100		3.6
35	416394	H64111		gb;DKFZp761D2315_r1 761 (synonym; harny2) gb;yr57f03.r1 Soares fetat liver spleen	3.6
55	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	423035	AW449579	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435766		Hs.186498	ESTs	3.6
40	448067	R68568	Hs.183373	ste homology 3 domain-containing protein	3.6
70	441605		Hs.128801	ESTS	3.5
	414400		Hs.897	Fc fragment of IgE, high affinity i, rec	3.5
	418405		Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	437642		115.11050	gb:Homo saplens mRNA full length insert	3.5
45	450350		Hs.174880	ESTS	3.5
77	451704		Hs.205616	ESTS, Weakly similar to ALU1_HUMAN ALU S	3.5
	459037		Hs.290656	EST	3.5
	419247		Hs.89764	fragile X mental retardation 1	3.5
	423121		145,03104	gb:PM2-SN0018-290300-003-c09 SN0018 Home	3.5
50	426724		Hs.293616	ESTs	3.5
50	434273		Hs.26303	EST8	3.5
	438042		Hs.255593	ESTs	3.5
	410500		113,230000	gbtyl26c09.r1 Soares fetal liver spleen	3.5
	416154			gb:HSC0VB031 normalized Infant brain cDN	3.5
55	418432		Hs.85112	insulin-like growth factor 1 (somatomedi	3.5
	454447			gb;QV3-HTQ460-230200-101-b08 HT0460 Homo	3,5
	458067		Hs.36752	protein kinasa anchoring protein GKAP42	3.5
	44433B		Hs. 146642	ESTS	3.5
	427687		Hs.1570	histamine receptor H1	3.5
60	415929		Hs.49344	hypothetical protein FLJ11006	3.5
	416009			gb:HSC12E041 normalized infant brain cDN	3.5
	421515		Hs.105352	GaiNAc alpha-2, 6-siglytrensterase I, 1	3.5
	403515				3.5
	435793		Hs.4993	KIAA1313 protein	3.5
65	439953	AA918129	Hs.124638	ESTs	3.5
	457620		He.336753	EST	3.5
	442006	AW975183	Hs.292663	ESTs, Weekly similar to \$72482 hypotheti	3.5
	453931	AL121278	Hs.25144	ESTs	3.5
	453128		Hs.31791	acylphosphatase 2, muscle type	3.5
70	413468			gb:hz40g01.x1 NC1_CGAP_GC6 Homo saplens	3.5
	454600			gb:MR4-ST0124-270300-805-b11 ST0124 Homo	3.5
	451065		Hs.222231	ESTs, Weakly similar to granule cell man	3.5
	444493	R59410	Hs.282094	ESTs, Moderately similar to 138022 hypot	3.5
	426447	7 AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.5
75	410908		Hs.10592	ESTS	3.5
	440364	1 AA910460	Hs.128626	ESTa	3.5
	408190	3			3.5
	430762		Hs.105667	ESTs	3.5
0.0	451182	2 052562	Hs.296317	KIAA1769 protein	3.4
80	43243		Hs.293685	ESTs	3.4
	44213		Hs.128630	ESTs, Weakly similar to 2192_HUMAN ZINC	3.4
	40597				3.4
	40767	6 AW064111	Hs.279823	ESTs	3.4

		<i>L</i>			
	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	3.4
	431418	X68242	Hs.252722	Hin-1	3.4 3.4
	431954	AK001974	Hs.272242	hypothetical protein FL\$11112	3.4
5	459371 428062	R20991	11-00225	gb:yg06h01.r1 Soares Infant brain 1NIB H	3.4
	423841	AA420683 AW753967	Hs.98321	hypothesical protein FLJ14103 gb;RC2-CT0304-080180-011-h12 CT0304 Homo	3.4
	420430	A1703192		ub.wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	3.4
	443921	AI091310	Hs.134848	ESTs	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
10	443475	AI066470	Hs.134482	ESTs	3.4
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.4
	453263	R91778	Hs.99369	ESTs	3.4
	4108BB	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	3.4
1.5	456303	AA224872	Hs.115088	ESTs	3.4
15	431474	AL133990	Hs.190642	ESTs	3.4
	439702	AW085525	Hs.134182	ESTS	3.4
	458797	AW001835	Hs.13323	hypothetical protein FLJ22059	3.4 3.4
	430140	AW298771	Hs.221999	ESTs qb:EST35805 Embryo, 8 week l Homo sapian	3.4 3.4
20	423871 459278	AA331906 AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.4
20	446672	T05514	N3.34034	gb:EST03403 Fetal brain, Strategene (cat	3.4
	431548	Al834273	Hs.9711	novel protein	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
25	417863	R07483	Hs.180461	ESTs	3.3
	405455				3.3
	426235	AI631964	Hs.34447	ESTs	3.3
	439567	A1056618	Hs.134314	ESTs	3.3
	444848	AW451176	Hs.195954	ESTs	3.3
30	451426	AW205003	Hs.208063	ESTs .	. 3.3
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	3,3
	401626				3.3
	4057BO				3.3
25	417991	AA731452	Hs.190008	ESTs	3.3
35	443212	AW269515	Hs.102500	hypothetical protein FLI20481	3.3
	403356	A ID4 FOR4	11- 20407	CDS2 without destinated D beautiful and	3.3 3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	3.3
	413581	BE150618	Hs.209461	gb:RC3-HT0272-110100-013-006 HT0272 Homo Homo saptens cDNA FLJ12836 fls, clone NT	3.3
40	426701 445510	A1968103 AA946676	Hs.282824	ESTs	3.3
40	418663		Hs.41690	desmocolim 3	3.3
	447617		Hs.176675	ESTs	3.3
	448150		Hs.302739	ESTs	3.3
	410140		Hs.22269	neurexin 3	3.3
45	443283			gb:601342622F1 NiH_MGC_63 Homo saplens c	3.3
	454777			gb:QV0-ST0284-240300-173-g04 ST0294 Homo	3.3
	410767		Hs.66185	Homo Sapiens mRNA, partial cDNA sequence	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
~^	43616B	AK000883	Hs.301645	Homo saplens cONA FLI 10021 fis, clone HE	3.3
50	438456		Hs.190513	ESTs	3.3
	411186			gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.3
	411860			gb:hm30f03.x1 NCL_CGAP_Thy4 Home saplens	3.3
	433567		Hs.103132	solute carrier family 9 (sodium/hydrogen	3.3
55	433805		Hs.112742	ESTs	3.3 3.3
ככ	409434		Hs.131581	Homo saplens lestis transcript Y 7 (TTY7	3.3 3.3
	440184 456 5 55		Hs.7022	dedicator of cyto-kinesis 3 ESTs	3.3
	419189		Hs.293299 Hs.112318	6.2 kd protein	3,3
	428648		Hs. 188021	potassium voltage-gated channel, subfami	3.3
60	407995		Hs.100134	hypothetical protein FLJ12787	3,3
•	413200		Hs.222414	ESTs	3.3
	416421		Hs.79306	eukaryotic translation initiation factor	3.3
	416737	AF154335	Hs.79591	L1M domain protein	3.3
	428356	AL045991	Hs.10338	ESTs	3.3
65	429218	A369472	Hs.65407	ESTs	3.3
	432488		Hs.216640	ESTs	3.3
	433386			gb:PM1-CT0243-201099-004-d08 CT0243 Homo	3.3
	400889				3.3
70	416294		Hs.79170	KIAA0227 protein	3.3
70	446190	3 A1279299	Hs.256584	ESTs	3.3
	417801	1 AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep Homo sapiens clone IMAGE:32106, mRNA seq	3.3 3.3
	41812 41837		Hs.22217 Hs.84389	synaptosomal-associated protein, 25kD	3.3
	44335		Hs.215937	ESTs	3.3
75	44664		Hs.156294	ESTS ESTS	3.3
, ,	43429		Hs.76194	ribosomal protein S5	3.3
	45237		Hs.228474	ESTs	3.3
	41424		Hs.4007	Sarcolemmal-associated protein	3.2
	43698		Hs.5378	spondin 1, (f-spondin) extracellular met	3.2
80	43054		Hs.163203	ESTs, Weakly similar to B34087 hypotheti	3.2
	42711		Hs,114574	ESTs	3.2
	43707	3 Al885608	Hs.94122	ESTS	3.2
	43784	5 AA769578	Hs.90488	ESTs	3.2

	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	414394	A1904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.2
	417175	R44558	Hs.94002	ESTs	3.2
5	456536	AW135986	Hs.257859	EST _{\$}	3.2
,	401132	DE000012		-1. O. M. ONO.C.C. 000.000 255 LOA BUILTEA 11	3.2
	407764	BE008347	Do 451202	gb:CM0-BN0154-080400-325-h04 BN0154 Horno	3.2
	428004 4ECD47	AA449563 A1745400	Hs.151393	giutamate-cysleine ligase, catalytic sub	3.2 3.2
	450947		Hs.204662	ESTs	3.2
10	456605 452879	AJ827786	Hs.259044	ESTs	3.2
10	454754	AW905328	Hs. 180642	ribosomal protein L13 gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.2
	429479	AW819191	Ll- 00222		3.2 3.2
		AA45348B	Hs.99333	ESTs	3.2
	448090	A1608821	Hs.270289	ESTs	3.2
15	401324 404731				3.2
15		A1702700		Aprellidative NCI CCAD Vide Home engine	3.2 3.2
	419936 455571	Al792788		gb:ol91d05.y5 NCI_CGAP_Kd5 Homo septens gb:QV3-BN0096-200400-161-e01 BN0096 Homo	3.2
	433990	BE003714 AA889328	LL (1986)	ESTs	3.2
	415239		Hs.112950 Hs.139270		3.2
20	418878	R42608		ESTs	3.2
20		W20090	Hs.6616	ESTs ESTs	3.2 3.2
	438079 422183	R09564 AA431698	Hs.191223 Hs.112794		3.2
	457460	Al143312	Hs.129206	Human DNA sequence from clone 1068E13 on caseln kinase 1, gamma 3	3.2
	454145	AA046872	Hs.62798	ESTs	3.2
25	446577	AB040933	Hs.15420	KIAA1500 protein	3.2
23	430664	AW959834	Hs.303303	ESTs	3.2
	40458B	7117202004	115.500305	E019	3.2
	407834	AW084991	Hs.26100	ESTs	3.2
	413087	BE064655	DS.20100	gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
30	440790	AW593050	Hs.128580	gu.kcBib313-301235-012-603 B10313 R0110 ESTs	3.2
20	452081	AW958859	Hs.7514	Homo saplens cDNA FLJ12141 fis, clone MA	3.2
	421916	R34441	Hs.101007	Homo sapiens conv. FLJ 12141 is, done MA Homo sapiens conv. FLJ 23546 fis, clone L	3.2
	419261	X07876	Hs.89791		3.2
	419340	AA236590		wingless-type MMTV integration site fami ESTs	3.2
35	444771		Hs.87530		3.2
55	445233	AB023201	Hs.11912 Hs.297559	KIAA0984 protein ESTs	3.2
	457030	AV653034			3.2
	408334	Al301740 AW514652	Hs.173381 Hs.321637	dihydropyrimlomase-like 2 ESYs	3.2
	410085	AA428482			3.2 3.2
40	411018		Hs.58589	glycogenia 2	
70	403623	A11013420		gb:MR3-ST0192-010200-210-c05 ST0192 Homa	3.2 3.2
	432223	********	Un 101001	Dama applications of the 1986 CE-24CO200 and NA	3.2
			Hs.121001	Homo saplens, clone IMAGE:3460280, mRNA	3.2 3.2
	444050 421036	AW138295	Hs.135024	ESTs	3.2
45		AA810560	Hs.303577	ESTs	
73	401459				3.1 3.1
	404404		U- 252000	ESTs	
	45043B		Hs.253800		3.1
	414523		Hs.76353	serine (or cysteine) proteinase inhibito	3.1
50	419169		Hs.282346	ESTs, Weakly similar to S72482 hypotheti	3.1
20	441274		Hs.191357	ESTs	3.1
	450785		Hs.25459	Homo sepiens, alpha-1 (VI) collagen	3.1
	452401		Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	400816		D- cover	-hhattitit-cated at some along M	3.1
55	410307 431906		Hs.62187	phosphatidylinositol glycan, class K	3.1
3.5			Hs.37486	ESTS	3.1 3.1
	440046 450271		Hs.6877	hypothetical protein FLJ10483 ESTs	3.1
			Hs.200920		
	415811 415273		Hs.172963 Hs.22229	hypothetical protein FLJ14624 ESTs	3.1 3.1
60	450519		Hs.224849	Homo saplens cDNA FLJ12583 fis, clone NT	3.1
50	451421		Hs.237689	Homo sapiens CDNA FL3 12563 6s, Clone PL	3.1
	446364		Hs.14912	KIAA0285 protein	3.1
	436638		Hs.134984	ESTS	3.1
	418079		Hs.6911	ESTs	3.1
65	44B466		Hs.171066	ESTs	3.1
05	448835		Hs.11081	UBX domain-containing 2	3.1
	415046		Hs.56400	ESTs	3.1
	448134		Hs.34494	ESTs	3.1
	456027		Hs.13913	KIAA1577 protein	3.1
70	458023		Hs.268555	5'-3' exoribonuclease 2	3.1
, 0	417079		Hs.81134	o-o exonomociesse z interleukin 1 receptor antegonist	3.1
	421308		Hs.192843	leucine zipper protein FKSG14	3.1
	414884		Hs.183745	hypothetical protein FLJ13456	3.1
	449136		Hs.196631	ESTs	3.1
75	455756		1 120 12002		3.1
, 5	428170		Hs.12565	gb:RC1-BT0623-120200-011-g09 BT0623 Homo ESTs	3.1
	429878		Hs.127263	ESTs	3.1
	4550D0		Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	3.1
	438369		Hs.83428	nuclear factor of kappa light polypeptid	3.1
80	415840		Hs.2175B	ESTs	3.1
~~	44495		Hs.148641	ESTS	3.1
	436020		Hs.121724	ESTs	3.1
	45305		Hs.224269	ESTs	3.1

	425178	H16097	Hs.161027	ESTs	3.1
	402145 410685	AA497117	Hs.129600	CCTs. Madarataly alsofar to A1 (14, 17) (MAAN) A	3.1
	449238	AA428229	Hs.331561	ESTs, Moderately similar to ALU1_HUMAN A muscle-specific RING-finger protein 3	3.1 3.1
5	456737	BE247203	Hs.124831	CGI-67 protein	3.1
	438214	H06076	Hs.26320	TRABID protein	3.1
	436250	AY004867	Hs.85844	neurolrophic tyrosine kinase, receptor,	3.1
	411622	A1807B94	Hs.47274	Home sepiens mRNA; cDNA DKFZp564B176 (fr	3.0
10	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
10	449357	A1076363	Hs.288806	Homo sapiens cDNA FLJ11778 fis, clone HE	3.0
	418950	178517	Hs.13941	ESTs	3.0
	431508 405090	NM_012481	Hs.182979	ribosomal protein L12	3,0
	445409	A)949081	Hs.147862	ESTs	3.0 3.0
15	452778	R71338	Hs.5921	Homo sapiens cDNA; FLJ21592 fis, clone C	3.0
	455577	BE006341	INDULI	gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.0
	408235	AA053381	Hs.75969	proline-rich protein with nuclear target	3.0
	436194	AK001074	Hs.333435	Homo saplens cDNA FLJ10212 fis, clone HE	3.0
20	452073	AA625150	Hs.82098	ESTs	3.0
20	427050	AA397789	Hs.161803	ESTs	3.0
	427244	AA402400	Hs.178045	EST ₆	3.0
	448405 433767	AW207634 AA609245	Hs.170849	ESTS	3.0
	421378	AA287948	Hs.134110	gb:af13a11.s1 Soares_lestis_NHT Homo sap ESTs	3,0 3.0
25	441519	AA972740	Hs.127092	ESTs	3.0
	404367			2010	3.0
	453502	AL039786	Hs.21273	transcription factor NYD-sp10	3.0
	421948	L42583	Hs.334309	keratin BA	3.0
30	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
3 0	400608				3.0
	404042 405229	•			3,0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0 3.0
	415452	F09134	Hs.12839	ESTs	3.0
35	430371	DB7466	Hs.240112	KIAA0276 protein	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	429014	Al800518	Hs.118158	ESTs	3.0
40	405605				3.0
40	400227 439037	AF075084		abiliama contenu full localit incart albits	3.0
	439893	Al741B16	Hs.125897	gb:Homo septens full length insert cDNA ESTs	3.0 3.0
	427533	R36022	Hs.179566	hypothelical protein FLJ22624	3.0
	418355	1.42563	Hs.1165	ATPase, H+/K+ transporting, nongastric,	3.0
45	433536	A1732163	Hs.188909	ESTs, Weakly similar to alternatively sp	3.0
	448446	Al521251	Hs.171030	ESTs	3.0
	449623	C00719	Hs.120440	EST	3.0
	44556B	H00918	Hs.268744	KIAA1796 protein	9.0
50	440448 428201	AA885428 AA424158	Hs.125646 Hs.206461	ESTS	3.0
50	444148	AW003204	Hs.151167	ESTs ESTs	3.0 3.0
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	3.0
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	3.0
	440925	AW511090	Hs.130419	ESTs	3.0
55	428398	Al249368	Hs.90558	ESTs	3.0
	415913	H70302		gb:yr95f07.r1 Soares fetal liver spieen	3.0
	418145	AF121260	Hs.83577	cysteine and glycine-rich protein 3 (car	3.0
	413252 400335	8E074910 Y13187	Hs.248067	gb:RC5-BT0680-170300-021-F12 BT0580 Homo	3.0
60	426132	AA370501	1 101240001	Homo sapiens drud gena, Intron 11 gb:EST82261 Prostata gland I Homo sapien	3.0 3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	437960	R50393	Hs.278436	KIAA1474 protein	3.0
	455955	BE162394		gb:PM2-HT0451-170100-004-a08 HT0451 Homo	3.0
65	414899	AW975433	Hs.36288	ESTs	2.9
65	403786		11-400000		2.9
	430187 451700		Hs.158989	ESTs	2.9
	455866		Hs.29553	ESTs gb:CMO-HT0249-291099-084-c04 HT0249 Homo	2.9 2.9
	445900		Hs.13429	Homo saplens clone 24787 mRNA sequence	2.9
70	457041		Hs.250835	ESTs	2.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.9
	422336		Hs.115285	dhydrolipoamide S-acetyltransferase (52	2.9
	451664		Hs.153952	5' nucleolidese (CD73)	2.9
75	407244		Hs.75431	fibrinogen, gamma polypeptide	2.9
1.0	455249 428862		Hs.2316	gb:RC3-PT0028-190100-012-b06 PT0028 Homo	29
	420002 406076		Hs.2316 Hs.137011	SRY (sex determining region Y)-box 9 (ca Homo sapiens mRNA; cDNA DKFZp547P134 (fr	2.9 2.9
	405302		110110111	tome subote unand erran rate that it in fit	2.9
00	400325		Hs.247924	Homo sepiens endogenous HIV-1 related se	2.9
80	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119		Hs.131976	ESTs	2.9
	424152 431090		Hs.141480	Homo saplens mRNA; cONA DKFZp434N079 (fr	2.9
	431980	AA523695	Hs.324507	hypothetical protein FLJ20986	2.9

		4000		507	20
	425793 A 401462	VA363946	Hs.20969	ESTs	2.9 2.9
		1522129	Hs.173119	ESTs	2.9
_		VF027208	Hs.112360	prominin (mouse)-like t	29
5		VA853410	Hs.93557	proenkephalin	2.9
		VM_005323	Hs.123064	H1 histone family, member 1 (testis-spec	2.9
	425349 / 401368	NA425234	Hs,79886	rībose 5-phosphate isomerase A (rībose 5	2.9 2.9
		R96760	Hs.183758	ESTs	2.9
10		AI476732	Hs.263912	ESTs	29
		AJ027604	Hs.159650	ESTs	29
		4A370141	Hs.2281	chromogranin B (secretogranin 1)	2.9
	405783	A ICGOCO 4	Hs.148676	CET-	2.9 2.9
15		A1680624 R58624	Hs.140070 Hs.2186	ESTs eukaryotic translation etongation factor	29
		U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.9
		R09764	Hs.20416	EST ₈	2.9
		U10492	Hs.438	mesenchyme homeo box 1	2.9
20		AW845481	Un 450504	gb:MR1-CT0056-201199-008-b04 CT0056 Homo	29 29
20		AA216372 AA50B196	Hs.159501	ESTs gb:nh60f07.s1 NCL_CGAP_Pr8 Homo sapiens	2.9
		AK000998	Hs.297221	Homo septens cDNA FLJ10136 fis, clone HE	2.9
	455699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	2.9
25		BE048054		gb:tz45c03.y1 NCI_CGAP_Bm52 Homo sapien	29
25		AA578229 AF020761	Hs.324239 Hs.129583	ESTs, Moderately similar to ZN91_HUMAN Z ubiquitin-conjugating enzyme E2D 1 (homo	29 29
		NM_0031B1	Hs.143507	T brachyury (mouse) homolog	2.9
		Al140825	Hs.121623	ESTs	2.9
20		NM_006134	Hs.284142	chromosome 21 open reading frame 4	2.9
30		R05385	Hs.143509	hypothetical protein FLJ21924	29
		AA362568 AI928184	Hs.179747 Hs.122011	ecotropic viral Integration site 5 ESTs	2.9 2.9
		N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
		AW136066	Hs.19145	ESTs	2.9
35		H91010	Hs.44940	EST6	29
		R69910	Hs.29041	Home sepiens cDNA FLJ14177 fls, done NT	2.9 2.9
	435563 415628	AF210317 F13080	Hs.95497	solute carrier family 2 (facilitated glu gb:HSC3ID041 normalized infant brain cDN	2.5
	423837	AL137279	Hs.130187	Homo saplens mRNA; cDNA DKFZp43401214 (f	29
40	443246	T75157	Ha.337603	ESTs, Weekly similar to T08680 hypotheti	29
	450877	Al799608	Hs.29178	ESTs	29
	439063 401526	AF085922	Hs.113968	ESTs	2.9 2.9
	408751	N91553	Hs.258343	ESTs	29
45	417320	AA195667	Hs.86022	ESTs	29
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	Ai124682	Hs.118121	ESTS	2.9 2.9
	452148 453901	AF007143 BE065902	Hs.28205	Homo saplens clone 23736 mRNA sequence gb:RC2-BT031B-150200-011-b09 BT0318 Homo	29
50	452589	BE159915	Hs.61406	ESTs, Weakly similar to 2004389A chromos	2.8
	403011				2.B
	436154	AA764950	Hs.119898	ESTs	2.8 2.8
	408221 430345	AA912183 AK000282	Hs.47447 Hs.239681	ESTs hypothetical protein FLJ20275	2.8
55	415399	T26994	Hs.177198	ESTs	2.8
	441817	AW969706	Hs.293332	ESTs	2,8
	443556	AA256769	Hs. 949 49	methylmalonyl-CoA epimerase	2.8
	455092 439703	BE152428 AF086538	Hs.196245	gb:CM0-HT0323-151299-126-b04 HT0323 Homa ESTs	2.8 2.8
60	411024	BE062590	115, 150240	gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.6
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo saplens c	2.8
	434715	BE005346	Hs.116410	ESTs	2.8
	407594	AW057584	Hs.160881 Hs.46608	ESTs EST-	2.8 2.8
65	439235 453736	N45513 AL118674	Hs.34871	ESTs zinc finger homeobox 19	2.6
-	404967			2.1.3.1.10.1.10	2.8
	4377B3	Al6B3150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	412887	BE007420	\\ D	gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.8 2.8
70	426942 403513	AA393551	Hs.97450	ESTs	2.6 2.8
,,	419077	AA233885	Hs.164526	ESTs	2.8
	421823	N40850	Hs.28625	ESTs	2.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	2.B
75	451007 407803	H38108 AW0B16B1	Hs.32759 Hs.269064	ESTs ESTs, Wealdy similar to T42689 hypotheti	2.8 2.8
, ,	409642	AW450809	Hs.257347	ESTS	2.8
	439492	AF086310	Hs.103159	ESTs	28
	420814	AA721155	Hs.190440	ESTs	2.8
80	449508 428350		Hs.23618	hypothetical protein FLJ10704 GE36 gene	2.8 2.8
	428330 405456		Hs.112017	erro Resis	2.8
	442459	A1264628	Hs.125428		28
	415763	Z42285	Hs,5181	proliferation-associated 2G4, 38kD	2.8
				0.50	

	428532	AF157326	Hs.184786	TBP-interacting protein	28
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	449539	W80363	Hs.58446	ESTs	2.8
_	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.8
5	40B749	H65489	Hs.250659	ESTs	2.8
_	404652	1,00,00	. 1012.0000	20.0	2.8
	423130	AWB97586	Hs.21213	ESTs	
					2.8
	424960	BE245380	Hs.153952	5 nucleotidase (CD73)	2.8
10	402131				2.8
10	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	444217	AV648751	Hs.282395	ESTs	2.8
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-i01 DT0041 Homo	2.8
15	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
15					
	433513	AI566356	Hs.171437	ESTs	2.8
	448912	DB3781	Hs.22559	KIAA0197 protein	2.8
	451496	AW503407		gb:UI-HF-BN0-akw-d-11-0-UIJ1 NIH_MGC_50	2.8
~~	420273	A1652864	Hs.197257	ESTs	28
20	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	28
	420756	AA411800	Hs.189900	ESTs	28
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	425012	T77666	Hs.92414	Homo sepiens cDNA: FLJ22030 fis, clone H	2.8
	441609	AA946764			
25			Hs.133460	ESTS	2.8
ري	448870	BE181783	Hs.175358	ESTs, Wealdy similar to A47582 8-cell gr	28
	451206	H86228	Hs.271780	ESTs, Wealdy similar to 135022 hypotheti	2.8
	457314	AA479597	Hs.193669	hypothelical protein DKFZp586J1119	28
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
20	418586	AU076801	Hs.89436	cadhein 17, Li cadhein (liver-intestin	2.8
30	455310	AW893981		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	459450	AA426429	Hs.98453	EST	2.8
	424168	AW954552	Hs.142634	zinc finger protein	2.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLI11576 fis, clone HE	2.7
	427443	AA402713	Hs.97872	ESTs	
35	452092		Hs.27842		2.7
33		BE245374	118.2/Q4Z	hypothetical protein FLI11210	27
	413091	BE065063	11-0500	gb:RC1-8T0313-110500-017-e02 BT0313 Homo	2.7
	421003	172080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
40	445611	AW418497	Hs.145583	ESTs	2.7
40	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.7
	408243	Y00787	Hs.624	interleukin 8	27
	407308	H67394	Hs.331325	ESTs, Weakly similar to 138022 hypotheti	2.7
	42372B	AWB91294	Hs.132136	solute carrier family 4, sodium bicarbon	2.7
4.5	404587	M99587	Hs.104134	homeo box (H6 family) 1	2.7
45	410483	BE163567	•	gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.7
	416431	AW384459	Hs.172004	ប៊ីហែ	27
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2,7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyma A ligase, long-chain	2.7
	427134	AA39B409	Hs, 173561	EST	2.7
50	428137	AA421792	Hs.170999	ESTs	2.7
	430844	T94960		gbye38d07.r1 Stratagene lung (937210) H	27
	441218	BE327561	Hs.202945	ESTs	
	440911				2.7
		AA909536	Hs.143562	ESTs	2.7
55	411131	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo	2.7
J	438602	AI167149	Hs.123374	ESTs, Weakly similar to mariner transpos	27
	441191	A1693930	Hs.148816	ESTs	2.7
	403776				27
	420159	A1572490	Hs.99785	Homo septens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA808823	Hs.98244	ESTs	2.7
60	429905	AL080128	Hs.225998	DKFZP434C153 protein	2.7
	449396	BE169100	Hs.195029	ESTs	27
	450777	AA255646	Hs.6047B		
	458043	AW979009		ESTs, Moderately similar to S47073 finge	2.7
	405523		Hs.326108	ESTs	2.7
65					2.7
65	434849		Hs.8053	ESTs	2.7
	452755		Hs.213436	ESTs, Weakly similar to A34087 hypotheti	27
	438055		Hs.270942	ESTs	27
	42090B		Hs.100261	Homo saplens mRNA; cDNA DKFZp564B222 (fr	2.7
70	405738				2.7
70	417806	Al867277	Hs.183733	ESTs	2.7
	430698			gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
	441969	A1733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	446092	N33522	Hs.145894	ESTs	2.7
	456869		Hs.154294	discs, large (Drosophile) homolog 1	27
75	413617		Hs.279518	amyloid beta (A4) precursor-like protein	27
	444931		Hs.75113	general transcription factor tilA	27
	412236		101.0110	gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.7
	453264		Hs.271955	ESTs	
	438370		Hs.48523	ESTs	2.7
80	406092		Ha.40023	CUID	2.7
U U	454874		H- 2704 10	outcoolfular abreaust-1- FM IN A	2.7
			Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.7
	455880		II. 6600e*	gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2,7
	459275	AI808913	Hs.339352	Homo saplens brother of CDO (BCC) mRNA,	2.7

	411987 441884	AA375975 AW172630	Hs.193380 Hs.144884	ESTs, Moderately similar to ALU8_HUMAN A ESTs	2.7 2.7
	416211	R34625	13. 144009	gb;yg45c03.r1 Soares Infant brain 1NIB H	2.7
-	433128	AB021923	Hs.23367	EST-YD1 protein	27
5	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	2.7 2.7
	453696 456208	A1989482 AW299698	Hs.146266 Hs.334625	kinesin family member 13A Homo sapiens cDNA FLJ14690 fis, clone PL	2.7
	425876	AW005887	Hs.23405B	ESTs	2.7
1.0	450458	AA009926		gb:zi07e05,r1 Soares_fetal_liver_spleen_	27
10	406603	4)4cp440	LI- OCTOR	atalazania annutaha 4 (DO) 4 Ambidaga	2.7 2.7
	410181 410871	A1468210 D78367	Hs.261285 Hs.66739	pleiotropic regulator 1 (PRL1, Arabidops keratin 12 (Meesmann comeal dystrophy)	2.7
	412706	R97106	Hs.167546	ESTs	2.7
1.5	422897	AA679784	Hs.4290	ESTs	2.7
15	436329	A7798750	Hs.163960	Homo saptens heat shock transcription for ESTs, Weakly similar to unnamed protein	2.7 2.7
	436679 455992	A1127483 BE179015	Hs.120451	gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2,7
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	27
20	419296	AA236115	Hs.120785	ESTs	27
20	454747	AW818535		gb:RC1-ST0278-140300-016-05 ST0278 Homo	2.7 2.7
	455791 411409	BE090689 AW844803		gb:RC1-BT0720-280300-011-108 BT0720 Homo gb:RC3-CN0056-170300-015-108 CN0056 Homo	2.7
	426662	AA879474	Hs.122710	ESTs	2.7
25	400268				27
25	438782 443764		Hs.126733	ESTs gb:HSPD22980 HM3 Homo saplens cDNA clone	2.7 2.7
	412486	AF210650	Hs.150858	NAG19 protein	27
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	2.7
20	457900		Hs.291665	ESTs	2.7
30	417376 426682		Hs.154103 Hs.2056	UM protein (similar to rat protein kina UDP glycosyltransferase 1 femily, polype	2.7 2.7
	435608		Hs.250896	ESTs	2.7
		BE182082	Hs.246973	ESTs	2.7
35	432415		Hs.289014	ESTs, Weekly similar to A43932 mucin 2 p	2.7
33	445660 441396		Hs.201955 Hs.186890	ESTS ESTS	2.7 2.6
	452046		Hs.27657	KIAA0802 protein	2.6
	454936			gb:MR3-CT0176-081099-002-d01 CT0176 Homo	2.6
40	454434		Hs.261286	ESTs	2.6 2.6
40	436888 431613		Hs.187870 Hs.264482	ESTs Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	408812		Hs.254763	ESTs, Weakly similar to A42442 Integrin	2.6
	416690		Hs.108551	EST8	2,6
45	436471 425659		Hs.117662 Hs.158836	ESTs hypothetical protein FLJ20583	26 26
73	426237		Hs.168241	hypothetical protein FLJ10242	2.6
	458257		Hs.201219	ESTs, Weakly similar to \$18945 ultra hig	2.6
	455544			gb:RC3-BN0034-240400-017-d09 BN0034 Homo	26
50	407494 452821		Hs.160874	gb:Human forkhead family (AFX1) mRNA, pa ESTs	26 26
50	434222		Hs.283941	Horno sepiens PRO2591 mRNA, complete cds	2.6
	429864		Hs.286	ribosomai protein L4	26
	456273		Hs.1148	zinc (Inger proiein	2.6 2.6
55	402603 411162	AW819944		gb:QV0-\$T0294-240300-172-e03 ST0294 Homo	2.6
	420621			gb;zs79c09.r1 NCI_CGAP_GCB1 Homo saplens	26
	435113		Hs.117136	ESTs	2.6
	438186 438296		Hs.128859 Hs.37932	ESTs ESTs	2.6 2.6
60	450181		Hs.201198	ESTs	2.6
	43376		Hs.39982	ESTS	2.6
	433229		Hs.91625 Hs.221373	KIAA1492 protein ESTs	2.6 2.6
	443718 418248		Hs.121276	ESTs, Weakly similar to R5HU7A ribosomal	2.6
65	45393		Hs.36727	hypothetical protein FLJ10903	26
	40036		Hs.274501	H.saplens ACTH receptor mRNA 3'UTR	2.6
	41931 42852		Hs.291005	ESTs Cyt19 protein	2.6 2.6
	40445		Hs.34492	Olt is brown	26
70	44644	4 Al743737	Hs.24370	ESTs	2.6
	41135		Hs.288141	hypothetical protein MGC3156	2.6
	41791 41831		Hs.163754 Hs.86693	hypothetical protein FLJ12606 ESTs	2.6 2.6
	45448	1 AW794878	Hs.314230	ESTs, Highly similar to clock [H.saplens	2.6
75	,44121	6 BE299830	Hs.192908	ESTs	2,6
	43825		Hs.224794	ESTS	26
	44226 41950		Hs.263455 Hs.143061	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs	2.6 2.6
	41759		Hs,226823	ESTs, Moderately similar to 154374 gene	2.6
80	44355	5 N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	44451		Hs.146883	ESTs	2,6 2.6
	45486 45587		Hs.313803	gb:PM1-LT0018-250200-002-a09 LT0018 Homo ESTs, Highly similar to AF157833 1 nonci	2.6

	457630	AJ680803	Hs.112627	ESTs	2.6
	424210	T71397	Hs.222707	KIAA1718 protein	26
	447748	Al422023	Hs.161338	ESTs	2.6
_	411970	AA099142	Hs.13804	hypothetical protein dJ462O23.2	2.6
5	441233	AA972965	Hs.135568	ESTs	2.6
	400706	1170904	II- Oresto	COT-	26
	436033 440836	H75391	Hs.255748 Hs.222080	ESTs ESTs	26 26
	431086	AW370882 AI829692	Hs.211561	ESTS	2.6
10	455110	BE154505	115.2 (150)	gb:PM0-HT0343-281299-003-e06 HT0343 Homo	2.6
	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.6
	413088	BE064962		gb:RC1-BT0313-130400-018-c02 BT0313 Homo	2.6
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, ctone HE	26
4.5	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.6
15	432374	W68815	Hs.301885	Homo sapiens cDNA FL111346 fls, clone PL	2.6
	442690	Al014727	Hs.160047	ESTs, Weakly similar to B28096 fine-1 pr	2.6
	441700 410286	AA233556 AJ739159	Hs.126908	hypothetical protein FLJ12994	26 26
	403271	M193193	Hs.61898	DKFZP586N2124 protein	26
20	429761	A1276780	Hs.135173	ESTs	26
	437085	AA743935	Hs.202329	ESTs	2.6
	450822	AW771860	Hs.205130	ESTs	2.6
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	2.6
25	416585	X54162	Hs.79386	leiomadin 1 (smooth muscle)	2.6
25	430357	AW976789	Hs.165607	ESTs	2.6
	41724 9 423554	N58198	Hs.182898 Hs.1674	ESTs glutamine-fructose-6-phosphale transamin	2.6 2.6
	440400	M90516 AA994364	Hs.125594	ESTs, Weakly similar to 725472 hypotheti	2.6
	440460	H92571	Hs.234478	Homo sepiens cDNA: FUJ22648 fis, clone H	26
30	446302	Al285848	Hs.149757	ESTs	2.6
	424012	AW368377	Hs.137569	tumor protein 63 kDs with strong homolog	2.6
	428944	AA780181	Hs.41182	Homo sepiens DC47 mRNA, complete cds	2.6
	419647	AA348947	Hs.91816	hypothetical protein	26
35	455500	AW963582	11. 4 40000	gb:EST376655 MAGE resequences, MAGH Homo	2.6
33	419435 452450	A1200540 AW854891	Hs.14877 Hs.194720	ESTs, Weakly similar to (defiline not ava ATP-binding cessette, sub-family G (WHIT	2.6 2.6
	434699	AA643687	Hs.149425	Homo saplens cDNA FLJ11980 fis, clone HE	2.5
	436421	A1678031	Hs.122813	ESTs. Weakly similar to ZN22_HUMAN ZINC	2.6
4.0	447505	AL049266	Hs.18724	Homo sapiens mRNA; cONA DKFZp564F093 (fr	2.6
40	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	2.6
	42669B	AA394104	Hs.97489	ESTs	2.6
	446861	Al696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	26
	423025	AA831267	Hs.12244	hypothetical protein FU20097	2.5
45	447624 411736		Hs.62713	ESTs gb:MR1-CT0350-150200-002-d02 CT0350 Homo	2.5 2.5
٦,	416334		Hs.36271	ESTs	2.5
	446818	Al342668	Hs.279765	ESTs	2.5
	454836			gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
50	442278		Hs.166313	ESTS	2.5
50	453393		Hs.110976	ESTS	2.5
	420854		U- 30000	gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCI_CGAP_Su	2.5
	408729 455675		Hs.72639	ESTs gb:RC3-BT0319-120200-014-a06 BT0319 Homo	2.5 2.5
	411660			gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
55	455252			gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	409156		Hs.173518	M-phase phosphoprotein homolog	2.5
	423175		Hs.18653	hypothetical protein FLJ14627	2.5
	430291		Hs.238126	CGI-49 protein	2.5
60	401785 402369				2. 5 2.5
Q0	439079		Hs.38948	ESTs	2.5
	412566		. OFFICE	gb:EST374647 MAGE resequences, MAGG Homo	2.5
	411463	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homa	25
c=	413758			gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.5
65	404988				2.5
	409446		Hs.67688	ESTs	2.5
	412613		Hs.285711	hypothetical protein FLI13089	25 25
	417909 454743		Hs.79347	gb:yg66e08.r1 Soares Infant brain 1NIB H KIAA0211 gene product	2.5
70	406364		11001 9071	(dranazi i Bayo bioaser	2.5
, ,	404108				2,5
	411934			gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.5
	415747			gb:EST94257 Activated T-cells I Homo eap	2.5
75	443526		Hs.134002	ESTs	2.5
, ,	415319 454864		Hs.34955	Homo sepiens cDNA FLJ13485 fis, clone PL gb:QV4-LT0016-240200-110-304 LT0016 Homo	2,5 2.5
	454864 458771		Hs.163612	gb:QY4-110016-240200-110-304 110016 F0110 ESTs	2.5 2.5
	414349		110.100012	gb:601172298F1 NIH_MGC_15 Homo sepiens c	2,5
00	426589			gb:EST366530 MAGE resequences, MAGC Horro	2.5
80	42951	5 AL03122B	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	44361		Hs.7645	fibrinogen, B beta polypeptide	25
	411773 43478		Di. 404007	gb:QV4-HT0536-040500-193-605 HT0536 Homo ESTs	2.5 2.5
	4341 Q	1 (0000000	Hs.164007	Luia	2.5

					4.5
	429322	DB6984	Hs.199243	KIAA0231 protein	2.5
	446252	A1283125	Hs.150009	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
_	455276	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
5	449410	AA001356	Hs.18159	ESTs	25
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	25
	458861	A1630223		qb;ad06g08.rl Proliferating Erythroid Ca	2.5
	416944	N22809		gb:yw41a07.s1 Welzmann Olfactory Epithel	2.5
	423010	W25436	Hs.90725	ESTs. Moderately similar to 138022 hypot	2.5
10			Hs.21734	ESTs	2.5
10	412505	AA974491			25
	446399	A1298405	Hs.150080	ESTs	
	412139	BE044976		gb:hn25b10.x1 NOL_CGAP_Thy7 Homo saplens	2.5
	403691				2.5
	424025	A1701852	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, cloле L	2.5
15	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.5
	457770	BE065030	Hs.124179	ESTs	2.5
	427731	AA411750	Hs.20943	ESTs	25
20					2.5
20	426920	AA393351	Hs.132121	ESTs	
	427794	AA709186	Hs.282963	ESTs	2.5
	429903	AL134197	Hs.93597	cyclin-depandent kinase 5, regulatory su	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	25
~ =	414550	BE37980B		gb:601159567T1 NIH_MGC_53 Homo saplens c	25
25	436391	AJ227692	Hs.146274	EST8	2.5
	401989				2.5
	423346	A1267677	Hs.127416	synaptojanin i	2.5
	444905	AW135863	Hs.209228	ESTs	25
		L02911		activin A receptor, type I	2.5
30	424539	LU29	Hs.150402	activiti A receptor, type i	2.5
20	400861				
	458426	Al084514	Hs.249587	ESTs	25
	429520	AA160142	Hs.205058	hypothetical protein FLJ20075	2.5
	403568				2,5
	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.5
35	451078	A1927694	Hs.204470	ESTs	2.5
30	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.5
				ESTs	2.5
	427888	AA417088	Hs.137598		2.5
	425541	AA359119		gb:EST68172 Fetal lung II Homo septems c	
40	422B40	U4405 9	Hs.121481	thyrotrophic embryonic factor	2.5
40	404708				2.5
	405008				25
	453772	BE281431	Hs.16323	Homo sepiens, Similar to G antigen 8, cl	2.5
	411036		Hs.297007	membrane-bound transcription factor prot	2.5
	444575		Hs.22545	Homo saplens cDNA FLJ12935 fis, clone NT	2.5
45	449311		118.22040	gb:tl49a12x1 NCI_CGAP_GC6 Homo septens	2.5
70			Un 91742		2.6
	454277		Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	
	454566			gb:MR4-ST0098-120100-001-b05 ST0098 Homo	2.5
	454597			gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
	41620B	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.4
50	407851	NM_014496	Hs.40434	ribosomal protein S6 kinase, 90kD, polyp	2.4
	446554	AA151730	Hs.301789	nudlx (nucleoside diphosphate linked moi	2.4
	452850		Hs.22481	ESTs, Moderately similar to A46010 X-lin	24
	406468				2.4
	407300			gbzn43e07.s1 Stratagene HeLa cell s3 93	2.4
55	408617		LL 19/19R	ESTS	2.4
<i>ل ب</i>			Hs.124128	ESTS	2.4
	409827		Hs.313637		
	416665			gb:yu28a10.s1 Soares fetal liver spleen	24
	417404		Hs.82101	pleckstrin homology-like domain, family	2.4
C O	418994		Hs.89546	selectin E (endothelial adhesion molecui	2.4
60	428709		Hs.104916	hypothetical protein FLI21940	24
	429654		Hs.164318	ESTs	2.4
	432253		Hs.274174	transcription elongation factor (SIII) e	2.4
	439786		Hs.33756	Homo sepiens mRNA full length insert cDN	2.4
	445432			gb:AV853771 GLC Homo sapiens cDNA clone	2.4
65	453052		Hs.223813	ESTs	2.4
00					2.4
	454137		Hs.313876	ESTs, Weakly similar to 138022 hypotheti	2.4
	459600			gb:DKFZp761M141_r1 763 (syronym: hamy2)	
	45284		Hs.208320	ESTs	2.4
70	43322		Hs.238415	ESTs, Moderately similar to ALU8_RUMAN A	2.4
70	44969		Hs.34550	ESTs	2.4
	43153		Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	42596		Hs.4007	Sarcolemmal-associated protein	2.4
	40064		,		2.4
	43098		Hs.22217	Homo sepiens clone IMAGE:32106, mRNA seq	2.4
75					2.4
10	43280		Hs.278973	anglopoletin-3	24
	41084			gb:MR4-ST0062-180200-001-b04 ST0062 Homo	
	41156		Hs.285017	hypothetical protein FLJ21799	2.4
	42108		Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
	42351		Hs.129719	transglutaminese 5	2.4
80	43462		Hs.39311	ESTs	2.4
~~	43566		Hs.134273		2.4
	45587		110,107210	gb:PMO-HT0335-180400-008-e11 HT0335 Homo	2.4
			De goodes		2.4
	45179	7 AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.4
				276	

			D Fanna	ARA LARGE ALA	24
		AB033025	Hs.500B1 Hs.209602	KJAA1199 protein ESTs, Weakly similar to ublquitous TPR m	2.4
		AL039379 AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	24
	448889	BE140902	110.30131	gh:IL1-HT0028-240699-001-C11 HT0028 Homo	2.4
5	439481	AF086294	Hs.125844	ESTs	2.4
•	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.4
	403D53	R58624	Hs.2186	eukaryotic translation elongation factor	24
	409298	AA070211		gb:zm68c04.s1 Stratagene neuroepithelium	2.4
10	411322	AW887330	Hs.172405	cell division cycle 27	2.4
10	447640	Al417187		gb:tg75g11_x1 Soares_NhHMPu_S1 Homo sapi	2.4
	447849	A1538147	Hs.164277	ESTs	24 24
	458763	A1693417	Hs.293309	ESTs	24
	404638 413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.4
15	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.4
13	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.4
	408238	W95901		gb;ze43d11.r1 Soares retina N2b4HR Homo	2.4
	436747	AW977192	Hs.291343	ESTs	2.4
	43704B	AA743240	Hs,915B2	ESTs	2.4
20	413143	BE067232		gb:PM3-BT0347-170200-001-b05 BT0347 Homo	2.4
	404561				24
	444009	AJ380792	Hs.135104	ESTs	2.4 2.4
	400250				2.4
25	403891 417002	T79613	Hs.14613	ESTs	24
23	439446	AI927629	Hs.57873	ESTS	2.4
	441227	AW295407	Hs.128893	ESTs	2.4
	445038	A1635444	Hs.143917	dJ467N11.1 protein	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	24
30	458624	A1362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	2.4
	457652	AF116656	Hs.273809	Homo sepiens PRO1167 mRNA, complete cds	24 24
35	450068	AW207212	Hs.280925	ESTs ESTs	2.4
23	444750 414591	AW242584 AI888490	Hs.243623 Hs.55902	ESTS, Weakly similar to ALUS_HUMAN ALU S	24
	407264	L34727	H\$.00902	gb:Homo saplens T-cell receptor beta (TC	24
	443169	AR038687	Hs.133338	ESTs	2.4
	426536	A1949749	Hs.44441	ESTs	2.4
40	449752	AJ668626	Hs.61773	Homo sapiens cDNA FLJ11648 fls, clone HE	24
	459592	ALD37421	Hz.208746	ESTs, Moderately similar to pot. ORF 1 [2.4
	429504	X99133	Hs.204238	Epocalin 2 (oncogene 24p3)	2.4
	429053	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
45	430484	D82800	Hs.241548	RAS p21 protein activator 2	24 24
43	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.4
	447375 444230	A1376660 1495537	Hs.257822 Hs.146067	ESTs ESTs	2.4
	439911	AA854024	Hs.189110	ESTs	24
	421296	NM_002666	Hs.103253	perilipin .	24
50	449385		Hs.270370	ESTa	2,4
	430044		Hs.152B12	ESTs	2.4
	427131	AA44B460	Hs.112017	GE36 gene	24
	409103		Hs.112208	XAGE-1 protein	2.4
55	421354		Hs.269664	ESTs	2.4 2.4
33	423740 440048		Hs.293007 Hs.328797	aminopepidase puromycin sensilive ESTs, Weakly similar to envelope protein	2.4
	441358		Hs.129041	ESTS, WEEKLY SKINGS OF CHICAGO PRODUKT	2.4
	453857		Hs.35861	DKFZP586E1621 protein	2.4
_ م	414290		Hs.71721	ESTs	2,4
60	427342	AL110150	Hs_176680	Homo sapiena mRNA; cDNA DKFZp586D0724 (f	2.4
	459459			gb:zx66h11.rl Soares_total_felus_Nb2HF8_	2.4
	434638			gbyp86e06.r1 Soares fetal liver spleen	2.4
	442717 419637		Hs.180591	ESTs, Weakly similar to T23976 hypotheti gb;31h10 Human retina cDNA randomly prim	2.4 2.4
65	431169			gb:EST383329 MAGE resequences, MAGL Homo	2,4
U.J	449432		Hs.196529	ESTs	24
	458734		Hs.158794	ESTs	2.4
	449529		Hs.232033	ESTs	2.4
	4260B6		Hs.166196	ATPase, Class I, type 8B, member 1	2.4
70	420199	N44348	Hs.26243	Homo saplens cDNA FLJ11177 fts, clone FL	24
	41810		Hs.178000	ESTs. Weakly similar to FVI MOUSE FRIEND	24
	430957		Hs.55043	Homo sapiens cDNA FLI13277 fis, clone OV	2.4
	41818		Hs.151880	ESTs	24
75	424103		Hs.139410	dihydrolipeamide branched chain transacy	2.4 2.4
13	45432		Hs.52184	hypothetical protein FLJ20518 ESTs	2.4
	437369 45321		Hs.121742	gb:zh53f04.r1 Soares_fetal_liver_spleen_	2.4
	45321 45109		Hs.25954	interleukin 13 receptor, alpha 2	2.4
	40046		1 104800 007	attendents to recolour advise a	24
80	41369		Hs.47144	DKFZP586N0819 protein	2.4
	42175	5 AW169454	Hs.207422	ESTs, Weekly similar to S71949 metatlopr	2.4
	42419	5 U50536	Hs.142907		24
	43416	3 AW974720	Hs.25206	group XII secreted phospholipase A2	2.4
				277	

	435985	AA703154	Hs.191934	ESTs	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinasa, isoenzyme	24
	458661	Al299789	Hs.166999	ESTs, Moderately similar to 138344 titin	2,4
E	459023	AW968226	Rs,60798	ESTs	2.4
5	406005	AIDCOGGA	U- 040000	COT- March similar to TOOOEO broodhot	2.4 2.4
	456561 452151	AI868634 R43077	Hs.246358 Hs.221747	ESTs, Weakly similar to T32250 hypothed ESTs	24
	436590	At393115	Hs.127655	EST6	24
	430151	AW968203	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:EST380398 MAGE resequences, MAGJ Homo	2.4
10	445635	A1769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	433479	AW511459	Hs.249972	ESTs	2.4
	441676	BE564206	Hs.49889	ESTs	2.4 2.4
	407965 450682	W21483 Z42993	Hs.41707 Hs.25320	heat shock 27kD profein 3 Homo sapiens clone 25142 mRNA sequence	2.4
15	45295B	AA883929	Hs.40527	ESTs	2.4
~~	454032	W31790	Hs.194293	ESTs, Weakly similar to 154374 gene NF2	2.4
	405347				24
	440577	AA889945	Hs.326381	EST	2.4
20	455780	BE088828	11- 440454	gb:CM2-BT0693-230308-129-g09 BT0693 Homo	2.4
20	457024	AA397546	Hs.119151	ESTs	2.4 2.4
	404249 437511	A1807500	Hs.125247	ESTs	2.4
	421338	AA287443	12.120241	gb:zs52c10.r1 NCI_CGAP_GC81 Homo septens	2.4
~ -	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	2.4
25	428277	AA425220	Hs.179203	ESTs	2.4
	444870	A)200621	Hs.148504	ESTa	2.4
	402090	4)405300	L1. 6000F7	FOT-	2.4 2.4
	458507 443054	Al185703 Al745185	Hs.206957 Hs.8939	ESTs yes-associated protein 65 kOa	24
30	446534	Al307356	Hs.175225	ESTs	2.4
	453111	AB014598	Hs.31720	hephaestin	2.4
	405230			•	2.4
	405935				24
35	413642		11-404540	gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4 2.4
55	420724 436998		Hs.191540 Hs.291414	ESTs ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748		Hs.13252	Human EST clone 22453 mariner transposon	2.4
	434283		Hs.58715	thiamine pyrophosphokinase	23
40	407404			gb:Homo sapiens TNF receptor homolog mRN	2.3
40	440621		Hs.150434	ESTs	2.3
	423417		Hs.128342	potassium large conductance calcium-acti	23 23
	424131 450737		Hs.199665 Hs.203330	ESTs ESTs	23
	453687		Hs.283108	hemoglobia, gamma G	2.3
45	442704		Hs.130987	ESTs	2.3
	457756		Hs.38125	Interferon-induced protein 75, 52kD	23
	412732			gb:RC2-BN0033-180200-015-g06 BN0033 Homo	2.3
	418998		Hs.287849 Hs.93121	ESTs, Weakly similar to T22074 hypotheii KIAA0761 protein	2.3 2.3
50	419751 429485		Hs.99338	ESTa	2.3
	433377		Hs.43845	ESTs	2.3
	434896	AW022054	Hs.136591	ESTs	2.3
	441675		Hs.5451	ESTa	2.3
55	444711		Ha.148488	ESTs	23 23
JJ	445621 449182		Hs.145549 Hs.224160	ESTs ESTs	2.3
	430987		Hs.248190	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.3
	404068				2.3
<i>c</i> 0	414368			gb:601076456F1 NIH_MGC_12 Homo saplens c	2.3
60	438319		Hs.82419	ESTS Variable and the angle of the control of the c	2.3 2.3
	423161 447998		Hs.124776 Hs.304389	Homo sepiens mRNA; cDNA DKFZp564N1116 (f ESTs	2.3
	410150		Hs.6774	ESTs	23
	43279		Hs.278950	protocadherin beta 1	23
65	443363	A1792629	Hs.133293	ESTs	2.3
	44072		Hs.128204	ESTs	23
	41104		Hs.115325	RAB7, member RAS oncogene family-like 1	2.3 2.3
	45920 45912		Hs.45051 Hs.184592	ESTs projein kinase, lysine deficient 1	2.3
70	4586B		Hs.98655	hypothelical prolein FLI20909	2.3
	42796		Hs.8700	deleted in liver cancer 1	2.3
	40189				2.3
	43211		Hs.308538	ESTs	2.9
75	40419			-L-FIGS ST0400 320200 B40 LDS STA400 Dama	23 23
13	41099 41330			gb:RC3-ST0186-230300-019-h02 ST0186 Homo gb:4217 Human retina cDNA randomly prime	2.3
	41330 43026			gb:nc71f10.s1 NCI_CGAP_Pr1 Homo septens	2.3
	44348		Hs.250385	ESTs	2.3
00	45330	5 R39224	Hs.267997	EHM2 gene	23 23
80	45196		Hs.224952	ESTs	2.3
	45304		Hs.224277	ESTS	2.3 2.3
	43555 44072		Hs.42636 Hs.134268	zinc finger protein 277 ESTs, Wealdy similar to 2109260A B cell	2.3 2.3
	77012		1 104 104 10	and the state of t	

	434120	AI436050	Hs.143937	ESTs	2.3
	429768	AAB05719	Hs.192154	ESTs	23
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeal (LRR) protein	2.3
5	455841	BE145836		gb:MRQ-HT0208-101299-202-b08 HT0208 Homo	2.3 2.3
3	411093 430706	BE067650 NM_003540	Hs.247816	gb:MR4-BT0358-090300-003-e01 BT0358 Homo H4 histone family, member C	2.3
	428268	AA424957	Hs.294132	ESTs	23
	458833	AW236702	Hs.171431	ESTs, Weakly similar to A46010 X-linked	2.3
10	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	2.3
10	444109 428411	AI124553 AW291464	Hs.48965 Hs.10338	Homo sapiens cDNA: FLJ21693 fis, clone C ESTs	2.3 2.3
	433098	AW190593	Hs. 151143	ESTS	2.3
	424882	Al379461	Hs.153636	far upstream element (FUSE) binding prot	23
4.5	453178	AA496086	Hs.61648	ESTs	2.3
15	404569				2.3
	413841 424068	M34276 U50531	Hs,75576 Hs.138751	plasminogen Human BRCA2 region, mRNA sequence CG030	2.3 2.3
	433532	AW975367	H2.130/31	gb:EST387475 MAGE resequences, MAGN Homo	2.3
	442710	AI015631	Hs.23210	ESTs	23
20	444206	AW301017	Hs.146492	ESTs	2.3
	451264	A1768235		gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.3
	454784	AW820626))- 000F7	gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3 2.3
	429080 404166	AA446228	Ha.99057	ESTs	23
25	416327	R99822	Hs.36172	ESTs	23
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.3
	438504	AW665281	Hs.224625	ESTs	2,3
	435325	A1038388	Hs.119309	ESTs	23
30	421253	A1188102	Hs.31028	ESTs	2.3 2.3
50	427046 432711	BE246180 AA583785	Hs.121385 Hs.152465	ESTs ESTs, Weakly similar to 138022 hypotheti	2.3
	439715		Hs.42612	ESTs, Weakly similar to ALU1_RUMAN ALU S	2.3
	441398	88ESERAA	Hs.292036	ESTs, Weakly similar to 834087 hypotheti	23
25	448458		Hs.171054	ESTs	2.3
35	452542		11. 475500	gb:RC0-ST0174-191099-031-a07 ST0174 Homo	2.3
	417768 427374		Hs.175139 Hs.143686	ESTs ESTs	2.3 2.3
	446847		Hs.82845	Homo seplens cDNA: FLJ21930 fis, clone H	23
	423600		Hs.310359	ESTs	2.3
40	413006		Hs.34298	ESTS	2.3
	434698			gb:hm46f02.x1 NCL_CGAP_RDF1 Homo sapiens	2.3
	407639 455121		Hs.312830	ESTs gb:QV0-HT036B-940100-082-f06 HT0368 Homo	23 23
	448117		Hs.172982	ESTs	2.3
45	443931		Hs.22657	ESTs	2.3
	450795		Hs.60435	ESTs	23
	418632		Hs.9460	Homo saplens mRNA; cDNA DKFZp547C244 (fr	2.3
	419441 455067		Hs.274368	MSTP032 protein gb:RC3-CT0255-200100-024-b02 CT0255 Homo	2.3 2.3
50	418291		Hs.289038	hypothetical protein MGC4126	2.3
	455964			gb:CM4-HT0501-240300-519-101 HT0501 Homo	2.3
	445944		Hs.13480	Homo sapiens clone 24875 mRNA sequence	23
	424827		Hs.96867	Homo sapiens cDNA: FLJ23155 ffs, clone L	2.3
55	449272 445292		Hs.197645 Hs.13982	ESTs Home saplens cDNA FLJ14666 fis, clone NT	2.3 2.3
	415131		113.10502	gb:HUM158C118 Clontech human fetal brain	2.3
	444715		Hs.282464	ESTs	2.3
	439560		Hs.74899	hypothetical protein FL112820	2.3
60	444140		Hs.282383	ESTS	23
OU	423949 428434		Hs.130912 Hs.65551	ESTs Homo saptens, Similar to DNA segment, Ch	23 23
	445711		Hs.193691	ESTs	2.3
	424568	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.3
CE	455201			gb:PM1-MT0010-200300-001-g08 MT0010 Horno	23
65	429180		Hs.58893	ESTs	2.3
	416849 42552		Hs.53565 Hs.158244	Homo sapiens PIG-M mRNA for mannosyltran KIAA0479 protein	2.3 2.3
	41650		Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	23
	41933		Hs.209978	ESTS	2.3
70	41969		Hs.173044	ESTs, Weakly similar to 138022 hypotheti	2.3
	42897		Hs.194695	ras homolog gane family, member i	2.3
	43629 45892		Hs.281587	gb:zg07b07.s1 Soares_pinea(_gland_N3HPG Human (ctone CTG-A4) mRNA sequence	2.3 2.3
_	43393		Hs.254122	hypothetica) protein	2.3
75	45004		Hs.202273	ESTs	2.3
	45164	0 AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	23
	41667		Hs.394840	ESTs, Moderately similar to 178885 serin	2,3
	40592 40574				23 23
80	41210		Hs.94319	VPS10 domain receptor protein	2.3 2.3
	42045		Hs.191656	ESTs	2.3
	40772	6 AA435679	Hs.88594	ESTs	2.3
	42372	0 AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.3

	409517	X90780	Hs.120036	troponin I, cardiac	2,3
		AI066599	Hs.120893	ESTs	2.3
	435352				
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	23
_	444098	AV647969	Hs.109594	KIAA1451 protein	2.3
5	449276	AW241510	Hs.252713	ESTs	23
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.3
	449015	AL038958	Hs.22868	projekt tyrosine phosphatase, non-recept	23
			110.22000		23
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	
10	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.3
10	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.3
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	2.3
	407809		Hs.244106	ESTs	2.3
		AW082279			
	420478	AA521259	Hs.193796	ESTs	2.3
	424073	U03493	Hs.138959	gap Junction protein, alpha 7, 45kD (con	2.3
15	445117	Al208754	Hs.147369	EST8	2.3
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo saplens c	2.2
			U- 204100		2.2
	420230	AL034344	Hs.284186	forkhead box C1	
	411517	AW650267		gb:IL3-CT0219-161199-031-A09 CT0219 Homo	` 22
	403678				2.2
20	457003	S78234	Hs.172405	cell division cycle 27	2.2
	404531	Z25884	Hs.121483	chloride channel 1 , skeletal muscle (Th	2.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	2.2
	409427	AW389668		gb:RC2-ST0168-071299-013-106 ST0168 Hamo	2.2
	434745	AW974445	Hs.185155	ESTs, Weakly similar to T12482 hypotheti	2.2
25	400696				2.2
23		1.00050		at a time a Fall for a label to a consider	2.2
	407259	L02256		gb:Human Fab fragment binding syncytial	
	411B93	R82845	Hs.273789	EST\$	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384			2.2
30			11	gb:yc14f05.r1 Stratagene lung (937210) H	
3 0	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	458303	A1264628	Hs.125428	ESTs	2.2
	405692				2.2
	403572				22
		£020=0	11- 40005		
36	415380	F07953	Hs.16085	putative G-protein coupled receptor	22
35	433014	NM_014711	Hs.279912	K!AA0419 gene product	2.2
	417859	T26453		gb:AB214F6R Infant brein, LUNL array of	2.2
	456472	AK001714	Hs.95744	hypothetical protein similar to ankyrin	2.2
	444106	A1123922	Hs.138215	Hamo saplens cDNA FLJ11400 fis, clone HE	2.2
40	428231	U17989	Hs.183105	nuclear autoantigen	2.2
40	454086	AW885909	Hs.6975	PRO1073 protein	2.2
	425071	NM_013989	Hs.154424	deixidinase, lodothyronine, type li	2.2
					2.2
	416348	H65887	Hs.272163	ESTs	
	403780				2.2
	414262	AW975616	Hs.291469	ESTs	2.2
45	419423		Hs.90315	KIAA0007 protein	2.2
	44207B			ESTs .	2.2
			Hs.262629		
	452975		Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2,2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
	416568	H66558		gb:yu16e04.r1 Soares fetal liver spicen	2.2
50	42536B		Hs.155976	cullin 4B	2.2
50					
	425686		Hs.1937	relinal degeneration, slow (relinitis pi	2.2
	441638	AW293202	Hs.133451	ESTs	2.2
	446845	Al343645	Hs.158108	ESTs	22
	422563		Hs.1934B	hypothetical protein FLJ13119	2.2
55	436574		Hs.126465		2.2
				ESTs COX-	
	424584		Hs.13310	ESTs	2.2
	456347		Hs.89426	fyn-related kinase	22
	446901	Al347274		gb:tc05d02.x1 NC3_CGAP_Co16 Homo saptens	2.2
	459364			gb;zd46c03.r1 Soares_fetal_heart_NbHH19W	2,2
60	430686		Hs.2633		2.2
00				desmoglein 1	
	414831		Hs.77439	protein kinase, cAMP-dependent, regulato	2.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.2
	403525			·	2.2
	453343		Hs.121622	ESTs	2.2
65	421574				2.2
UJ			Hs.105924	defensin, beta 2	
	449327		Hs.224672	ESTs	22
	454769	AWB19848		gb:QV0-ST0294-070300-151-b04 ST0294 Homo	2.2
	420493		Hs.270366	ESTs, Weakly similar to 178985 serine/th	2.2
	401614				22
70					2.2
70	404767				22
	403534				2.2
	410594	AW770778	Hs,281238	ESTs	2.2
	436193		Hs.255286	ESTs	2.2
	439628		Hs.189080	ESTs	22
75					
13	456481		Hs.108110	DKFZP547E2110 protein	2.2
	441453	AW176106	Hs.285459	ESTs	2.2
	424946		Hs.153932	protein tyrosine phosphatase, non-recept	2.2
	437332			gb:cc07d06.s1 NCL_CGAP_GCB1 Home sapiens	2.2
			Lin ganger		
QΛ	454419		Hs.233936	myosin, light polypeptide, regulatory, n	22
80	41522		Hs.188684	ESTs, Weakly similar to PC4259 femilin	2.2
	450579	AW136774	Hs.48614	ESTs	2,2
	400664			·	22
	44761		Hs.33363	DKF2P434N093 protein	2.2
	-7101		1 191999103	MA EL TOTATOGO PIONIA	Z.Z.

	400000	41/00/224	H- 45 470	and the size of th	2.2
		AK001334 AF053748	Hs.15470 Hs.248114	petative ring zinc finger protein NY-REN glief cell derived neurotrophic factor	2.2
	432797	AA565264	Hs.136443	ESTs	2.2
	405608	, 1,	11011007710		2.2
5		AA376667	Hs.10283	RNA binding motif protein 6B	2.2
	405634				2.2
	423646	H02364		gb:yj35d06.c1 Soares placenta Nb2HP Homo	2.2
		Al867679	Hs.148410	ESTs	2.2
10	436672	AA723274	Hs.279596	ESTs	2.2
10	447044	AF030107	Hs.17165	regulator of G-protein signaling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2 2.2
	457802 444585	178013 AW170015	Hs.167279 Hs.6594	FYVE-finger-containing Rab5 effector pro	2.2
	433781	AA609379	Hs.192083	ESTS ESTS	2.2
15	450587	A1828854	Hs.258538	striatin, calmodulin-binding protein	2.2
	434077	AF116659	Hs.321151	Homo sepiens PRO1412 mRNA, complete cds	2.2
	448756	Al739241	Hs.171480	ESTs	22
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.2
-00	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.2
20	419107	AW085152	Hs.292987	ESTs	2.2
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.2
	416548	H62953	13- 40000	gb:yr47f05.r1 Soares fetal liver spleen	2.2 2.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigms	2.2
25	456056 409998	AA463550 M78345	Hs.337532 Hs.98265	ESTs, Weakly similar to A47582 B-cell gr KIAA1877 protein	2.2
23	422352	AA766296	Hs.99200	ESTs	2.2
	409191	AWB18390	Hs.175613	homolog of Xenopus Clespin	2.2
	433919	AA746311	12.110210	gb:oa56d12.r1 NCI_CGAP_GCB1 Homo sepiens	22
	455771	BE064820	Hs.186711	hypothetical protein FL120070	2.2
30	431632	AK000992	Hs.333144	Homo sapiens cDNA FLI10130 fis, clone HE	2.2
	454716	AWB50684		gb:)L3-CT0219-160200-063-D12 CT0219 Homo	2.2
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	2.2
	458037	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	22
25	434239	AF119910	Hs.283047	hypothetical protein PRO2964	22
35	435133	AJ010482	Hs.31412	Homo sepiens cDNA FL311422 fis, clone HE	2.2 2.2
	442772 400697	AW503680	Hs.5957	Homo sapiens cione 24416 mRNA sequence	2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Hamo	2.2
	447039	AV661798	Hs.282915	ESTs	2,2
40	404593	***************************************	110.202010	2015	2.2
• •	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.2
	421976	AL138443	Hs.23450	mitochondrial ribosomal protein S25	2.2
	401673			·	2.2
4.5	42500t	U55184	Hs.154145	hypothetical protein FLJ11585	2.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	2.2
	416143	A1955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	22
	419118	AA234223	Hs.139204	ESTs	2.2
	426261	AW242243	Hs.168670	peroxisomal famesylated protein	22
50	449808 454749	AA694220 AW818649	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A gb:RC1-ST0278-040400-018-802 ST0278 Homo	2.2 2.2
50	456933	AA363946	Hs.20969	ESTs	2.2
	402942	700000515	118,20303	LOIG	2.2
	437064	A)023264		gbzov64h08.s1 Soares_testis_NHT Homo sap	2.2
	458623	A1305223	Hs.148056	ESTs	2.2
55	415257	F03016	Hs.27513	ESTs	2.2
	426269		Hs.168950	Homo sapiens mRNA; cDNA DKFZp586A1046 (f	2.2
	442783		Hs.131181	ESTs .	2.2
	444313		Hs.197955	KIAA0704 protein	2.2
60	453444		Un comes	gb:DKFZp564l1162_r1 664 (synonym: h/br2)	2.2
UU	422757 430013	A1909935	Hs.66551 Hs.151275	Homo sepiens, Sknilar to DNA segment, Ch ESTs, Weakly similar to TRHY_HUMAN TRICH	2.2 2.2
	43713B		Hs.271245	ESTs	2.2
	406298		18,211210	COIS	2.2
	409723		Hs.257862	ESTs	2.2
65	414481		Hs.8383	bromodomain adjacent to zinc finger doma	22
	433266		Hs.31476	Homo sapiens cONA FLI13872 fis, clone TH	2.2
	435090		Hs.149595	ESTs	2.2
	457187		Hs.144360	EST	2.2
70	445061		Hs.145227	ESTs	2.2
70	442617		Hs.130538	ESTs .	2.2
	438298		Hs.181768	ESTS	2.2 2.2
	454916 428017		Hs.98312	gb:PM1-BT0348-151299-001-d04 BT0348 Homo ESTs	2.2
	451149		Hs.10283	RNA binding motif protein 8B	2.2
75	418078		Hs.6724	ESTs	2.2
	403306		Hs.74368	transmembrane protein (63kD), endoplasmi	2.2
	441811		Hs.164597	ESTs	2.2
	434763			gb:ns07a11.r1 NCL_CGAP_Ew1 Homo septens	2.2
DΛ	447453		Hs.18800	hypothetical protein FLJ20281	22
80	420931		Hs.100431	small inducible cytokine 8 subfamily (Cy	2.2
	415424		17	gb:HSC28G081 normalized infant brain cDN	2.2
	408332 421216		Hs.234794	Homo sepiens mRNA; cDNA DKFZp564B083 (fr veslcle-associated membrane protein 4	22 22
	421210	5 AV649282	Hs.102664	voolad-assurated interior and patent 4	46

	400000	4F00DD40	11- 040000	and and business makes to with harmology to	22
	429609 448700	AF002246 BE614182	Hs.210863 Hs.123075	cell adhasion molecule with homology to ESTs	2.2
	457741	BE044740	110,120010	gb:hm55g10.x1 NCI_CGAP_RDF1 Homo saplens	2.2
_	437927	AI039789	Hs.25982	hypothetical protein FLJ21031	2.2
5	401694			a was a landana	22
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2 2.2
	424419 436640	AK001563 AA724411	Hs.146589 Hs.156065	hypothetical protein FLJ10701 ESTs	2.2
	43B290	AA843719	Hs.122341	ESTs	2.2
10	445908	R13580	Hs.13436	Homo sapiens done 24425 mRNA sequence	2.2
	455735	BE161124		gb:PMC-HT0425-141299-001-A06 HT0425 Homo	2.2
	458455	AV648310	Hs.213488	ESTs	2.2 2.2
	430680	AW138724	Hs.168974 Hs.292815	ESTs, Highly similar to ALU7_HUMAN ALU S ESTs, Weakly similar to T23482 hypotheti	22
15	447147 424063	AA910353 NM_002019	Hs.138671	fins-related tyrosine kinase 1 (vascular	2.2
13	441B74	AA970389	Hs.126055	ESTs	2.2
	448045	AJ297436	Hs.20166	prostate etem cell antigen	2.2
	433629	R13140	Hs.13359	ESTs	2.2
20	415266	AA164199	Hs.270152	ESTs	2.2 2.2
20	440633	A1140586	Hs.263320 Hs.131191	ESTs ESTs, Weakly similar to ALU7_HUMAN ALU S	22
	442789 417563	AW904361 AA203701	PE.131131	gb:zx52a10.r1 Soares_felal_liver_spleen_	22
	407768	BE514982	Hs.38991	S100 calcium-binding protein A2	2.2
	401240				2,2
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	22
	411151	AW868497	11 000	gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2 2.2
	414275	AW970254	Hs.889 Hs.120750	Charol-Leyden crystal protein ESTs	2.2
	436992 439634	AA741074 W79377	Hs.167	microtubule-associated protein 2	2.2
30	411770	NM_014278	Hs.71992	heat shock protein (hsp 110 family)	2.1
•	400040				2.1
	458762			gb:IL2-UM0076-030400-051-H01 UM0076 Homo	2.1 2.1
	424736		Hs.152701	microtubule-interacting protein that ass	21
35	419953 410648		Hs.125752	ESTs gb:CM0-UM0001-010300-258-c05 UM0001 Homo	2.1
55	423717		Ha.152003	ESTs	2.1
	436683		Hs.57787	ESTs	21
	445225		Hs.202398	ESTS	21
40	410991		1- 40000	gb:RC3-ST0186-141299-014-p08 ST0186 Homo	2.1 2.1
40	412639 447777		Hs.296235	ESTs gb:te95a05.x1 NCI_CGAP_Py28 Homo sapiens	21
	451270		Hs.235795	ESTs	2.1
	404526		Hs.157195	peptide YY, 2 (seminalplasmin)	2.1
4 10	452492			gb:CM4-BT0266-091199-039-a02 BT0266 Homo	21
45	417154		Hs.21388	ESTS	2.1 2.1
	428152 442312		Hs.129216	gb:zv26h05.rt Soares_NhHMPu_S1 Horto sapl ESTs, Weakly similar to ALU1_HUMAN ALU S	21
	456513		Hs.88561	ESTs	21
	430712		Hs.196284	ESTs	2.1
50	44144		Hs.187937	ESTs	2.1
	42028		Hs.245558	ESTS	21 21
	412329 447033		Hs.157601	gb:QV3-DT0043-090200-080-c09 DT0043 Homa ESTs	2.1
	43685		Hs.148681	ESTs	2.1
55	45518			gb:PMO-SN0014-260400-002-b08 SN0014 Homo	2.1
	43089		Hs.183528	hypothetical protein FLJ 14906	21
	45835		Hs.131575	ESTs	2.1 2.1
	45704 42448		Hs.173717 Hs.205299	phosphatidic acid phosphatase type 28 ESTs	21
60	40331		Hs.385	fms-related tyrosine kinase 3	2.1
-	40601		(121000		2.1
	41056		Hs.43047	Homo saplens cDNA FLJ13585 fis, clone PL	21
	41380		Hs.35406	ESTs, Highly similar to unnamed protein	2.1 2.1
65	41587 41674		Hs.283309 Hs.15929	ESTs, Moderately similar to ALU1_HUMAN A hypothetical protein FLJ12910	2.1 2.1
UJ	41772		Hs.21503	ESTS	2.1
	42485		Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.1
	43947	4 A1824060	Hs.211501	ESTs	2.1
70	44689		Hs.282803	ESTS	21
70	44858		Hs.94812	ESTs ESTs	2.1 2.1
	45278 44243		Hs.61486 Hs.48320	double ring-linger protein, Dorlin	21
	42890		Hs.144955	ESTs	2.1
	42733	35 AA448542	Hs.251677	Gantigen 7B	2.1
75	4283	36 AA503115	Hs.183752	microseminoprotein, beta-	2.1
	41929		Hs.112885	spinal cord-derived growth factor-8 ESTs, Moderately similar to S65657 alpha	2.1 2.1
	4169: 4399:		Hs.190765 Hs.293561	ESTs Wooderziely Similar to Sociost Signal	2.1
	4582		Hs.181340		2.1
80	4471		Hs.157299	ESTs	2.1
	4549	50 AW847460		gb:RC3-CT0208-270999-021-e04 CT0208 Homo	2.1
	4044 4208			gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sepiens	2.1 2.1
	4200	N-0300ZZ		guilleassat Noi_oon _ 11 mile septins	

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		AA580748	Hs.130658 Hs.30715	ESTs potassium voltage-gated channel, lsk-rel	2.1 2.1
		W28418 BE149423	Hs.10554	hypothetical protein FLJ12761	2.1
		A1168422	16.10001	gb:ok30e11x1 Soares_NSF_F8_9W_OT_PA_P_S	2.1
5		AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	21
		AL040600	Hs.188083	ESTs	2.1
		AL121282	Hs.257786	ESTs	21 21
	401645	1101771	Hs.17643	ESTs	2.1
10		WB4774 AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.1
10		N94037	Hs.312938	ESTs, Weakly similar to ALU1_HUMAN ALU S	21
		A1554545	Hs.68301	ESTs	2.1
		A1792557	Hs.133107	ESTs	2.1
1.5		AF151852	Hs.111449	CGI-94 protein	21 21
15	402333	CD7002	Ds 40004	ESTs	2.1
		R87083 NM_000406	Hs.19081 Hs.73064	douglopobiu-telessing posmone receblor ,	21
		AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	21
		H18072	Hs.92576	ESTs	2.1
20		AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
		AA773B66	Hs.244569	esophagus cancer-related gene-2	2.1 2.1
	452374	AL037405	Hs.339639	ESTs ESTs	2.1
	450061 450180	A1797034 AW449644	Hs.201115 Hs.257182	ESTs	2.1
25	405120	A11713011	110.201 (02	2010	2.1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypol	2,1
	458890	AW855523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.1
	435600	AL047034	Hs.119747	ESTS	21
20	440964	A\733106	Hs.13021B	ESTs ESTs, Weakly similar to CA2B_HUMAN COLLA	2.1 2.1
30	417455 436461	AW007066 AW511956	Hs.18949 Hs.293261	ESTs	2.1
	436777	AA731199	Hs.293130	ESTS	21
	427521	AW973352	Hs.290585	ESTs .	2.1
0.5	413646	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	2.1
35	413231	D87461	Hs.75244	BGL2-like 2	21
	423969	A)B30571	Hs.331633	hypothetical protein DKFZp566N034 gb:1L3-CT0219-291099-021-E07 CT0219 Homo	2.1 2.1
	411518 443777	AW850246 AV646510	Hs.41185	Homo saplens mRNA; cDNA DKFZp564O1262 (f	21
	416148	H22453	Hs.169187	ESTs	2.1
40	402528				2.1
	431215	AA495078	Hs.121554	Human DNA sequence from clone RP11-218C1	2.1
	436820	A1684535	Hs.200811	ESTs ESTs	2.1 2.1
	446209 453362	Al375025 H14988	Hs.153368 Hs.107375	ESTS	2.1
45	417430	AA984546	113.101010	gb:am88e08.s1 Stratagene schizo brain S1	21
	401069	, , , , , , , , , , , , , , , , , , , ,			21
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.1
	410966	AW812088	12- 471400	gb:RC4-ST0173-191099-032-a07 ST0173 Homo	21 21
50	447124 449939	AW976438 T86420	Hs,17428 Hs,272139	RSP1-like protein ESTs	2.1
50	411693	AW857271	113,212100	gb:CMO-CT0307-210100-158-g09 CT0307 Homo	21
	438005	BE151746		gb:PM1-HTD305-061299-003-a06 HTD305 Homo	2.1
	443486	NM_003428	Hs.9450	zinc (Inger protein 84 (HPF2)	2.1
55	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	2.1 2.1
55	404694	T62745	Hs.184411	albumin	21
	406668 441092		Hs.128556	EST	2.1
	454543			gb:RC2-BN0127-240300-011-d05 BN0127 Homo	2.1
~	426646		Hs.122713	ESTs	21
60	431605		11- 00000	gixEST384498 MAGE resequences, MAGL Homo	2.t 2.1
	414452		Hs.29032	ESTs	21
	401991 457176			gb:zv57g07.s1 Soares_testis_NHT Homo sap	2.1
- -	436464		Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
65	428208	AA442327	Hs.104854	ESTs	21
	445049			gb:AV652718 GLC Homo septens cDNA clone	21
	419116		Hs.283093	neuromedin U receptor 2	2.1 2.1
	427894 424298		Hs.28921 Hs.155140	zinc finger protein casein kinase 2, alpha 1 polypeptide	21
70	424323		Hs.177788	ESTs	2.1
	404582				2.1
	418631		Hs.115105	ESTs	2.1
	424872		11- 100=	glxEST54302 Fetal heart II Homo sapiens	2.1
75	452539		Hs.49367	ESTs	2.1 2.1
13	454658 440310		Hs.11123 Hs.125408	DKFZP564G092 protein ESTs	21
	433297		Hs.282633		2.1
	41090			gb:MR4-ST0124-040500-007-h07 ST0124 Homo	21
00	41938	B AA236B67	Hs.143868	ESTs, Weakly similar to 138022 hypotheti	21
80	40245		LI_ nžanna	tuinted exclusion	2.1 2.1
	447841 45388		Hs.247302 Hs.28462	twisted gastrulation ESTs, Waskly similar to I38022 hypotheti	2.1 21
	42518		113,20402	gb:ym26c07,r1 Soares Infant brain 1NIB H	21
	72.010			V	

	457225 400612	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	21 21
	402318				2.1
5	410534	AW905138	11- 04 10 10	gb:CVO-NN1071-280400-207-g07 NN1071 Homo	2.1
5	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.1 2.1
	412029 414494	AW886238 AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	Al924294	Hs.173259	uncharacterized bone marrow protein 8M03	2.1
	444498	AI151413	Hs.26330	ESTs	21
10	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	21
	425324	M89470	Hs.155644	paired box gene 2	2.1
	430719	AA488988	Hs.293796	ESTs	2.1
	432577	BE208545	Hs.317590	hypothetical protein FL) 14640	2.1
1.5	407593	AW044083	Hs.237008	ESTs	2.1
15	401098				2.1
	440299	A1871778	Hs.250112	ESTs	21 21
	414146	BE549372	Hs.317596 Hs.187660	Homo saplens cDNA FLJ12927 fis, clone NT	21
	428527 451806	BE002993 NM_003729	Hs,27076	putative Rab5 GDP/GTP exchange factor he RNA 3-terminal phosphate cyclase	21
20	431912	A1660552	Hs.154903	ESTs, Weakly similar to A56154 Abi subst	2.1
20	439831	AW136488	Hs.25545	ESTs	2.1
	451829	AW964081	Hs.247377	ESTs	2.1
	404595				2,1
o. =	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
25	456083	U46922	Hs.77252	tragile histidine triad gene	21
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	2.1
	406413	T0000	1) 50000	11	2.1
	439483	T69980	Hs.58323	Homo saplens cDNA FLJ11613 fls, clone HE	2.1 2.1
30	446242	N66336	Hs.7360 Hs.23796	ESTs	21
20	449625 457938	NM_014253 AI373638	Hs.133900	odz (odd Oz/ten-m, Drosophila) homolog 1 ESTs	2.1
	413101	BE065215	1 100 100 000	gb:RC1-BT0314-310300-015-f01 BT0314 Homo	. 2.1
	40B350	AW183350	Hs.250127	ESTs	2.1
	419812	NM_000562	Hs.93210	complement component 8, alpha polypepild	2.1
35	430881	NM_000809	Hs.248112	gamma-aminobulyric acid (GABA) A recepto	2.1
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.1
	409955	U60665	Hs.57692	chromosome 6 open reading frame 10	21
	435579	Al332373	Hs.156924	ESTs	2.1
40	436088	AA704687	Hs.191294	EST8	2.1 2.1
40	430223	NM_002514	Hs.235935 Hs.26B799	nephroblastoma overexpressed gene ESTs	2.1
	418100 403218	H18700 Al.134878	Hs.119500	ribosomal protein, large P2	21
	409747	H60964	Hs.331250	ESTs	2.1
	428764		1 ENGO I E GO	gb:zb52f12.r1 Soares_fetal_lung_NbHL19W	21
45	425075	AA506324	Hs.1852	acki phosphatase, prostate	21
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.1
	428299	AL038004	Hs.29419	ESTs	2.1
	406817			gb:wo47a09.x1 NCI_CGAP_Gas4 Homo saplens	2.1
50	411940		11. 88469	gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
30	412446		Hs.92127	ESTs .	2.1 2.1
	414012 421966		Hs.128148 Hs.130710	ESTs ESTs	2.1
	430566		Hs.190149	ESTS	21
	456606		Hs.275369	ESTs	21
55	451604		Hs.172851	arginase, type il	2.0
	440926	AW196772	Hs.131923	ESTs	2.0
	4206B?		Hs.8B605	Homo sapiens cDNA FLJ13427 fis, cione PL	2.0
	459082		Hs.282149	ESTs	2.0
60	413241		Hs.302414	Homo sapiens clone FLBB945 PRO2411 mRNA,	2.0
vv	426917 447552		Hs.172854 Hs.160413	DKFZP586B0923 protein ESTs	2.0 2.0
	420905		Hs.186651	EST'S	20
	428052		Hs,26993	ESTs	2.0
	424308		Hs.154443	minichromosome maintenance deficient (S.	2.0
65	432527		Hs.102754	ESTs	2.0
	430202			gb:yd60g02.r1 Soares fetal liver spieen	2.0
	446610		Hs.282984	ESTs, Weakly similar to I38022 hypotheti	2.0
	427961		Hs.143134	ESTs	2,0
70	455290			gb:HSU75810 Human Homo sepiens cDNA clon	20
70	445664		Hs.12896	KIAA1034 protein	20
	412811 413783		Hs.21400	ESTs ribosomai protein S7	2.0 2.0
	423867		Hs.301547	gb:EST35757 Embryo, 8 week I Homo sapien	2.0
	42941		Hs.118769	GD:Eat50757 Ettim yo, a week t Flotito sapieti ESTs	2.0
75	43151		Hs.258581	Homo sapiens p95 paxillin-kinase linker	2.0
	44582		Hs.145526	ESTs	2.0
	45236		Hs.29276	hypothetical protein FL320457	2.0
	45312	3 Al953718	Hs.221849	ESTs	2.0
QΛ	45540			gb:QV4-DT0021-301299-071-d07 DY0021 Home	20
80	40666		Hs.1B4411	albumin	2.0
	44568 44613		Hs.153244 Hs.290	ESTs phospholipase A2, group V	2.Q 2.0
	44038		Hs.223000	prosprompase Az, group v ESTs	20
				-	

	457128	AI932995	Hs. 183475	Homo sapians clone 25061 mRNA sequence	2.0
	404416				2.0
	444187	AW13B466	Hs.151274	ESTs	2.0
_	431552	A1815863	Hs.259873	axonal transport of synaptic vesicles	20
5	455814	BE141689		gb:CM1-HT0092-220999-016-b09 HT0092 Homo	20
	454759	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	2.0
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.0
	404420				2.0
	408112	AW451982	Hs.248613	ESTs	20
10	432702	AW973953	Hs.293744	ESTS	20
	448587	A1539652	Hs.28338	KIAA1546 protein	2.0
	446854	BE268103	Hs.208914	hypothetical protein MGC10999	20
	410569	AA766825	Hs.205675	EŜTs	2.0
	432596	AJ224741	Hs.278461	matrifin 3	2.0
15	402341				20
	452919	AW962167		gb:EST374240 MAGE resequences, MAGG Horno	20
	433632	AA649921	Hs.112553	ESTs	2.0
	435079	AA654192		gb:ac05b03.s1 Stratagene lung (937210) H	2.0
	451927	AL355687	Hs.27261	Homo saplens mRNA full langth insert cDN	2.0
20	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	20
	450895	N66727	Hs.10957	ESTs	2.0
	408459	H09701	Hs.278366	ESTs, Wealdy similar to 138022 hypotheti	2.0
	400842				2.0
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.0
25	400859				20
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
	416093	R60685	Hs.266698	ESTs, Moderately similar to ALUC_HUMAN I	20
30	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	428002	AA418703	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapl	20
	437733	A)792574	Hs.122876	ESTs .	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobóx (Drosophila) homolo	2.0
35	454578	AW809178		gb;MR4-ST0118-261099-012-c07 ST0118 Homo	2.0
~~	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	2.0
	419986	A1345455	Hs.78915	GA-binding protein transcription factor,	2.0
	415173	AW501735	Hs.253015	ESTs	2.0
	449011	Al655376	Hs.192693	ESTs	20
40	410365	AI287518	Hs.62669	Homo sepiens mRNA; cDNA DKFZpS8600923 (f	2.0
	416057	A1927382	Hs.29857	ESTs	20
	45568B	BE06723B		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.0
	408531	AW207553	Hs.253639	ESTs	2.0
	434663	AA641972	Hs.130055	ESTs	2.0
45	428085	AA4210B1	Hs.12388	ESTs	20
	425006	R38685	Hs.332622	ESTs	2.0
	446139	H77395	Hs.39749	ESTs	2.0
	400049	1111000	VIOLEGI 10		2.0
	428333	AW972668	Hs.293044	ESTs	20
50	429458	BE161832	Hs.292689	ESTs .	2.0
	425087	R62424	Hs.126059	ESTs	2.0
	457122	A)026157	Hs.33728	ESTs, Weakly similar to ALU1_HUMAN ALU S	2,0
	400310	X63966	Hs.135631	H.sapiens synthetic gene for platelet-de	20
	451805		Hs.208220	ESTs	2.0
55	401986				20
•	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cet	2.0
	417756			gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW978201	Hs.53913	hypothetical protein FLJ10252	2.0
	424698		Hs.151973	hypothetical protein FLJ23511	20
60	429110	1.29301	Hs.2353	oplaid receptor, mu 1	2.0
	433755		Hs.120868	ESTs	2.0
	434118	AF116715	Hs.256256	Homo saplens PRO2829 mRNA, complete cds	2.0
	435413		Ha.46669	ESTs	2.0
	443748			gb;UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	20
65	445205		Hs.12413	KIAA0191 protein	2.0
	45B175		Hs.150434	ESTs	2.0
	446419		Ha.160728	Homo saplens cDNA FLJ11680 fis, clone HE	2,0
	441627		Hs.58086	ESTs	2.0
	457653		Hs,154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.0
70	455614		Hs,202274	ESTs	2.0
	449899		Hs.103280	ESTs	2.0
	420111			gb:zs2th11.rl NCI_CGAP_GCB1 Homo sapiens	2.0
	437354		Hs.291886	ESTs	20
	412228		Hs.73792	complement component (3d/Epsteln Barr vi	20
75	419691		Hs.193521	ESTs	2.0
	43972		Hs.60351	EST	2.0
	413362			gb:CM2-BT0693-230300-129-d08 BT0693 Homo	2.0
	453657		Hs.28368	ESTs, Moderately similar to \$65657 alpha	20
	43436		Hs.117772		2.0
80	44247			gb:AF059484 Homo sapiens astrocytoma lib	2.0
•	41355		Hs.75426	secretogranin II (chromogranin C)	2.0
	45932			gb:MR0-CT0065-100899-001-d01 CT0066 Homo	20
	44943		Hs.554	Sjogren syndroma antigen A2 (60kD, ribon	2.0
				205	

	400285			م المتابعة ا	2.0	
		AF050198		gb:Homo sapiens putative mitochondrial s	2.0	
	411459	BE142707	13- 400400	gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0 2.0	
5	417383	W02842	Hs.136102	KIAA0853 protein	2.0	
3	447153	AA805202	Hs.315562	ESTS	2.0	
	447313 455005	U92981	Hs.18081	Homo sapiens clone DT1P 186 mRNA, CAG rep gb:RC0-BT0362-021299-031-505 BT0362 Homo	2.0	
	455696	BE067870	Hs.99423	ATP-dependent RNA helicase	2.0	
	456510	AK001652	Hs.199739	ESTs	2.0	
10	449815 425398	A1671000 AL049689	Hs.156369	hypothetical protein similar to tenascin	2.0	
10	420038	AL049003	J.S. 130303	HANGE IBRICAL PROTEST SATISFAS TO SELECTION	2.0	
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.0	
		AW291389	Hs.13058	hypothetical protein FLJ13920	2.0	
	455221	AW867751	ris. 13000	gb:MR0-SN0038-290300-001-203 SN003B Homo	2.0	
15	413174	AA723564	Hs.191343	ESTs	2.0	
1.0	435810	BE349853	Hs.2785	keratin 17	2.0	
	4186B7	R61650	Hs.22581	ESTs	2.0	
		AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-finked	2.0	
	431750		Hs.283705	ESTs	2.0	
20		T98327	Hs.18343	ESTs	2.0	
	437074	A1286235	Hs.128905	hypothetical protein FLJ13204	2.0	
	459411	N52920		gb:yv34h09.s1 Soares fetal liver spleen	2.0	
	424834	AK001432	Hs.15340B	Homo sapiens cDNA FLJ10570 fis, clone NT	2.0	
	409929	R38772	Hs.172619	myelin transcription factor 1-like	20	
25	405378				2.0	
	459208	BE261314	Hs.149039	ESTs, Weakly similar to 138022 hypotheti	2.0	
	445260	A)218133	Hs.147617	ESTs	20	
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.0	
	445020	Al205655	Hs.147221	ESTs	2.0	
30	402048			Charles de la	2.0	
		AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	20	
		R94725	Hs.35354	ESTs 4	2.0	
	423347		Hs.234557	ESTs	2.0	
25		AA416642	Hs.116176	ESTs	2.0	
35		AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	20	
		AW247145	Hs.192729	ESTs	2.0	
		Al733011	Hs.127678	ESTs	2.0 2.0	
	442901		Hs.114191	ESTS	2.0	
40	444097		Hs.150757	ESTS	2.0	
40	447278		Hs.158869	ESTs gb:zt52f02.r1 Soares retina N2b4HR Homo	2.0	
	451361		11- 27-122		2.0	
	451813		Hs.27182	phospholipase A2-activating protein gb;RC4-CN0048-140100-011-a04 CN0048 Homo		
	454423		LL_ 270000	ESTs, Weakly similar to C Chain C, Human	20	
45	458801	N98548	Hs.276860	E318, Weakly Stilled to C Chart C, Italian	20	
73						
	TABLE	30B				
	174544	V				
50	Pkey:	Unique Fo	s probeset ideni	ifier number		
		mber: Gene clust				
		ion: Genbank a		ers		
	Pkey	CAT numb	er Accessk	on .		
55						
	407593	1003161_	1 AW0440	B3 AW044094 AW370634		
	407594			84 AW057585 AW044153 R34370		
	407639			69 AW058599 AW20760B		
	407678	1008294_	1 AVVC641	11 AW064450 AW064429		
60	407721	10108_1	Y12735	NM_003582 AW238970 R38268 R41411 R41419 T10	16717 AA002193 H62028 AI359545 AW105201 AW087158 AA699728 AI095264	ł
				65 H62029 Al289101 AABB4804 AA904950 AA60967		
	407726	101126_1	AA4356	79 AA470656 H22526 AA044031 AA876426 W63767	7 A1421140 A141B990 H42329 H88910 AL041056 H88909 W94610 AW952277 V	N94848
					353 H41626 H22525 R58582 AW297645 C75230 AW368034 AW468904 AI2727	/50
~~	407763			338 AA346882 AW866803 AA361281 AW963163 AAC	JU44373 AA136765	
65	40776			47 BE008320 BE0B3307 BE083311 AW075968		
	40778	B 10163_1	BE5149	B2 BE614814 AW393078 AWZ3848U AAU55637 N27	7644 AA64115B M97068 AA161019 AA161003 AA567315 AA716746 AA593632	100717
			Al35487	O AW183492 Y07755 NM_UU5978 AW872948 AIGUS	8987 H64656 AF086003 AA643149 A1819402 H64565 AA858398 AA594985 A14	20141
					54004 AW23823B AI971395 AA459074 AA458884 AIG08591 BE181995 BE1819	.10
70				797 C00271 BE182043		
70	40780			681 N36967 N36959		
	40780		_1 AYYU8Z	279 AW082688	13372 H99469 N35377 AW151676 A1678451 AW078795 AW087935 A1884505	
	40781	1 10180_1	AVVISO	902 AUGUZ100 AUG 1030 AUG1001 AFT (VIGT NATU). Ang appagang appapagn albatag Alama	6403 AI910477 AA373348 AA373673 AI752124 AL359060 W48619 AA373298 A	AA373975
			AVVU44	002 M0032312 M1040000 M021 103 M1 30310 MM310 M	A373557 AW956164 AW853798 Al750595 Al359059 AA344024 N31127 AW58	0737
75			PODANA PODANA	MAN GERMAN PETERENA CUBGOCAPA PURPUGAPA LANGO IN 10 PM	1 AA112124 AI940705 W52686 AA084001 C01826 AI940729 AA373544 AW957	/491
13			N2/U4L	i i ocopyy sebopy i voecema ugugulya ari i swya i Madeerna sebopyi i voecema ugugula aregenia are	1 AA 112124 AI940705 W32666 AA06400 CO 1626 AI940729 PAST3544 A1754387 1 W842507 AI940795 H80042 AW631118 W47324 W42884 A1750594 A1754387	AI753734
					00082 Al041803 W51909 W25447 Al521673 Al087351 AA670070 W47325 AAU	
			MA3/21 W/1970	1 AINDNAUL POERICA 1970 II 2012 I	30 AW069485 AI754608 AA373014 BE140150 BE140166 BE140102 BE140143	
			114219 DC1JA	1 ANDROOD MICHOLOGY ANDREED AND DIE 23 ANDROOMS 147 DE 140117 RE140008 AWMRQ43 RE140108 DE1.	140176 BE140171 BE140144 BE140175 BE140160 BE140152 BE140099 BE14	0177
80			DC 140	167 RE140145 RE140109 RE140163 RE140177 RE14	40161 BE140179 BE140147 BE140107 BE140146 BE140155 BE140173 BE140	0148
30			RF140	174 RE14015B RE140149 BE140118 BE140156 BE14	40105 BE140103 BE140164 AW 138508 BE140153 AW806557 BE140121 BE14	40162
			00195	AW806500 BE140124 AA329219 AW955642 AW06	69165 AI968107 NZ1113 AI754594 AW069264 AI754660 BE551937 AA549066	AA703927
			AW190	486 Al814434 Al924946 AA789056 AW173667 AW0	069841 AUD22286 A17535Z3 A175355B A1753482 AVV068940 A1753002 AA66966	6

			A1753593 A1753469 A1753506 AW008360 A1753255 A1949111 A1752123 W19275 A1679006 A1888455 A1677772 A1589279 A1968546 AW069588 A1754028 N20040 A1754354 A1752878 AA836970 AW631283 A1440410 AW016646 A1801326 A1610424 A1521669 A1446171 A1453455 A1753087 AA670062 AA598863 A1753821 A1802571 A1537325 AA669978 A1921732 A1811571 A1309543 H80043 A1623845 A1623852 A1075634 A1919521
_			AA729459 C01795 AA577421 AA668620 AA600003 AA653400 AI445339 AW466974 AW130343 AA600104 AW970482 AW806815 BE140122
5	407834 407851	1020170_1 10212_1	AW084991 R54179 N64486 NM 014496 AF184965 H82896 H82897
	407884	1023626_1	PERZESIS ANNONASO AWS90A17 HA7391 D61911 9F173752
	407938	102759_1	ASIDSIGN AKT34242 BECN4545 NB5431 AA344041 C03245 AW963097 AL567324 AA045934 AW079233 R58274 AKT44425 AL167427 R58176 R58598 AL569945 AL921684 AW013884 AL204559 AA909648 NB4115 AA897468 AL668637 BE221753 AL355307 AL139542 N80934
10	407965	10298_1	WOLARI LISSIN NM 00630B NS6344 AA126678 AA426507 Y 17782 W24740 W05052 W21042 AA649552 AA093507 AA09208B AA476830 N88299
10	107300	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	AAA29999 AA699643 AI224915 AA443775 AI204315 AI333690 AA666584 AI275037 AI193915 AA659647 TB2641 AA136048 T82643 T82647
			F36041 N74099 Al572217 T82650 T82642 T82640 R47360 R47361 R47357 N74672 R47356 R47355 N93086 R47354 R47353 R47342 R47362 R47358 N93441 N56304 N93566 T82622 T82618
	407995	103177_1	ALCOATAR AMIZATTOT AITEOTRE TAGEOR AIRIAAAA AIAZ1977 AIAZ3762 NT3686 T31392 AAB46406
15	408000	1031_1	1.1690 NM_001723 M59223 H99965 AI750395 BE000199 M63618 N31521 AA112876 AW266395 AA0B8909 N21507 X58677 U04850 AW864903 AI830854 AW361101 AW379366 AA301170 T29232 AW966998 H26216 H44230 H44784 AA808916 AA514765 H44575 AA705179 AA586735
			ANS89403 H25843 AA664993 AI783828 BE087370
	408112	1039850_1	AW451982 AW157117 AW161544
20	408172	1044105_1	WD24BB AW167479 AW361027 AW833243 AA912183 AA541622 Al673341 Al266109 Al335896 Al421010 AA053327 Al982962 Al372854 Al674348 AA531087 Al801016 Al372855 Al817816
20	408221	104826_1	N52151 D62928 A1401633 A1378549 A1378800 A1337972 D62536 AW972977 AA135826 BE222491 D62195 BE326453 AA225293 AA236461
			R85586 AA625141 AA058641 AA135825 AA234644 H50784 R71863
	408235	1048681 104872_1	AAD53381 W96901 AAD53387 AA121501
25	408238 408243	1048_1	V00787 N28130 D14283 RE439795 RE439924 NA362187 BE439515 M17017 C05929 NA381897 NA346136 NA381472 C06304 NA381670
		_	AA381679 AA381965 T11274 AA381318 AA381601 AA381700 AA381952 AW950718 AA381992 D82198 AA381914 AV653399 AA362140
			AA3B1592 AA3B1967 AA3B1454 M263B3 AA362188 AA3E2D57 AA3B1781 AA362246 AA3B1669 AA3B1395 AA3B1845 AA3B1848 AA3B1603 W40425 AW66323B AA3B1702 AA3B1355 AA3B1356 AA3B1653 AA362127 AA374516 AA3B1426 AA3B1767 AA362270 AA3B1459 AA362358
			A AGGGGG A AGGMAA 1 TOZARO DRGRAR A AGGGGGZ AAGGGGGG DRGRS 1 AAGGGGGG AAGGGGGGGA AAGGGGGGA AAGGGGGGA AAGGGGGG
30			AA352107 AA363589 AA296403 T11316 D82218 AA381456 W56111 AA381435 W40163 T11379 W40283 D82615 AA382121 W40401 AA381699 T68485 D82618 W52968 W39356 T27467 D83813 Z11686 T10915 AW367405 AW604306 AA363550 AA363514 BE004230 AA381218 W40279
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	421330	21131_1	AA448542 NM_001474 U19145 NM_001476 U19147 NM_001472 U19143 AF058988 U19146 NM_001475 AF055473 NM_012196 NM_001477
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			AA662333 F35933 F34419 F23435 F19078 F25502 F28223 AW573178 F36429 AI972305 F25248 H16233 AI927622 AI932901 H03779 R58599
			AA028651
70	435191	4022_1	R15912 Z45805 R56366 H0968B H28908 Z42110 AF070577 H15499 Z45171 T80013 R19744 R12077 H41631 M52055 H28907 AI670949 H15441
70			N59804 AW015150 AI655738 Y17312 H42324 R37140 R15911 AI361490 R42494 AA912236 Z40896 F04673 AI217847 R56270 R45163 T03442
	40-0-0	400-0- 4	F01647 N72748 H42333 H41621
	435202	402737_1	AI971313 AW855041 AW991934 BE005447 R59093 AA670383 N79509
	435256	40352_1	AF193766 AA448744 T82006 T93181 AI742654 AA460463 H61567 AA701618 H57113 AI127309 AI633508 AI571380 T90634 AA233071 AA448648
75	*****		AA897786 Al206655 Al589742
75	435325	404382_1	AI038388 AA677963 TB6982
	435352	404634_1	AI056599 AA67823B AA704443 AA704720
	435413	405993_1	A/267476 A/565484 A/866193 AA680045 N47090
	435434	406256_1	AAGB0387 A)140534 AA704460 AA703562
QΛ	435451	40646_1	AF195420 AA702693 A1076124 N73156
80	435463	406582_1	AA682507 AW851124
	435559	40812_1	AF209198 AA251397 D81981 AA082116 BE536905 W81660 AI872970 H82577 W15613 AA102582 AW966886 AW967510 W81219 AI635559
			N27946 N24381 AU77944 Al763038 W61334 Al624272 Al972115 Al375967 Al378124 Al086015 AW028141 H99133 AW971529 Al198751 Al671325
			N90026 Al241170 AW207070 Al423885 Al865150 AA626093 AA554588 Al222670 Al927421 Al193218 AW305284 AA251239 Al638572 AA486306

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		-	AA918939 AI671678 AI700871 AA059043 AI580406 AI302080 AI796223 AI300071 BE466467 AI671399 AI913595
	435579	408457_1	AL332373 AL333796 AA688232 AW975345 AW592953
_	435586	408547_1	A1279137 A1290738 AA688341 N66427
5	435600	408804_1	AL047034 AA889487 Al821857
	435608	409071_1	AW183971 AW341427 AA693524
	435634	409239_1	T82394 R05307 AA593714 A1003077 AA59340 AUXT590
	435663 435766	409442_1 410653_1	AIO23707 AA693940 AI075300 R11673 AA693970 R00740
10	435793	4108_1	AB037734 AJ360749 Z39942 F01814 H13007 H05896 Z45594 H12106 H18730 AA249485 Z42339 R14983 R55164 AW957717 R54369 W6D887
10	4771 37	4100_1	AA010504 AA099463 W60805 R49440 AW901726 R39025 Al367370 Al537878 BE503519 AW167870 H44902 AW130792 Al740821 T03753
			AA010505 R54824 AA708629 AA443681 R45674 Al284956 R45286 F09255 AA729642 T16068 Al564764 T33869 AA099384 Z38565 H18644
			AA447058 F11599 R25922 H06346 H06936 T78310 H06937 R56539 R20468
	435810	411064_2	BE349853 AA771928 AA700433
15	435878	411895_1	RD8330 AA701418 WB8583 WB8497
	435985	413228_1	AA703154 W80635 R0B362
	436020	413539_1	AA778177 AA777469 AA703516
	436033	413663_1	H75391 AW298387 AW854959 AA703650
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20	436149	415010_1	AF754308 AW069285 T71338 AB378245 AA705384 AA973318 N74598
	436154	415063_1	AA764950 AW418719 AI420075 AW084601 AW977003 AA706446
	436168	41524_1	AK00883 AW799155 AW789153 AA300122
	436187	41550_1	AK000998 BE157076 BE157298
25	436193 436194	415573_1 41557_1	AA706059 BE218269 AW294253 AK001074 AA354117
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	436250	41647_1	AY0048BT Al\$13270 AA349423
	436269	416768_1	AA707472 A(684396 A)283634
	436294	417339_1	AA708310 H52584 H62175
30	436298	417417. 1	AW293496 A1188642 AA716002 AA708470 AA708756
	435329	417990_3	A1798750 A1221709 AA709226
	436332	41800_1	AL049679 AA577969 BE166265 AA315706 AA329923 AW962505
	436391	41899_1	AJ227892 AA338715 BE074475 BE074469 BE074474 AW006182 AW572953 Al831725 Al762923 Al341466 AW449335 BE551686 Al692895
25			Al040410 Al276881 Al89100B
35	436397	419098_1	AA715013 AW468194 AI476329 AA992943
	436421	419635_5	Al678031 AW173312 AA812698 AA729849 Al380375 W25689 Al344299
	436461	420667_1	AW511956 AA719438 BE071580 AW748028 AW696108
	436464	420676_1	A016176 A0091255 AA719507 A1128614
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	436572	423035_1	AA73274 BE503172 A457238 BE467884 BE221090
	436574	423192_1	AW259527 H30281 Al628505 AW073905 AW087393 Al092824 Al208455 AW338087 Al935381 Al434683 AW007605 BE327828 AA913315
	100017	420101_1	AJ749624 AJ457483 AJ348298 AJ348270 H30323 AA723461
45	436577	42320_1	W84774 AJQQ9B17 N29755 AA834395 AJ249064 H54235 T95647
	436590	423462_1	Al393115 AA961280 AA723779
	436637	423940_1	AJ783629 AJ837609 AJ655377 AW074703 AW449028 AA890668 R60313 AW243019 BE464436 AA973133 AJ263065 AJ582600 F03414 AW236442
			AAB7386B Z38275 AA724332 W23675 W153B8
F0	436638	423997_2	AJ271945 AJ27181B AW235681 AW051010
50	436640	424008_1	AA724411 AI286124 AW340053
	436679	424709_1	A1127489 AA725246 AA7252B1 A1676162 A1744107 A1745374 AA838337 A1675430
	436683	424793_2	AW991278 AA771917 AA725349 AW818293 A1744435 BE085750
	436720	425676_1	AW975902 AA729344 A1657342 AN075400 AA729067 A1734 445
55	436747 436777	426172_1 426966_1	AW977192 AA730050 AA731416 AA731199 AW975817 AW241735
J.J	436B20	427433_1	A184535 A1834666 A193856 A731767
	436853	42803_1	BE326074 A1700552 BEA67938 BE218350 A1807702
	436888	42876B_1	AI942357 AI253135 AA761673 AA736676 AA748004 AAB14004 AW978076 AW978086
	436902	429024_1	AW247145 AA737014 AW592475 AAB4390 AAB33987 AA905207 AW976117 AW976124
60	436938	429795_1	AW139680 AI934979 AI480295 AI809768 AA738123 AI080339 AI423832
	436982	4306_1	AB018305 BE315203 Al569725 AL133797 AK001584 H09449 F08408 AW998309 R25793 AA449547 H38279 Al871669 M78530 R57626 AA244349
			AA244163 AI700043 AI632669 AI632660 AA622344 T23690 AI567994 AW044114 AI664454 BE047014 AW594714 Z41397 C15384 H51875 H24153
			N77073 AA127579 AA453668 R67153 AW390446 AW390451 W93800 AA358644 AW359169 AA034237 Al689608 AW197421 R91784 AW088291
C 5			AW194393 BE049402 AA534904 AA428038 AW662968 R27202 H01251 H13082 N42254 N57202 R82261 AJ972558 BE464017 BE348770
65			AA449113 AW152432 AI2D5902 N32810 W93989 AI799502 AW665638 AW571858 AI423145 AW514573 AW197663 AA053930 AW665686
			AI376513 AI479838 AI218225 AI656541 AI128371 AA127466 R59973 AA427824 AA776360 AI817703 AWU88405 AI361608 AI859002 R27203
			H355900 AIB24832 AW190556 AW470416 AI568066 AI858842 AI674914 BE463424 R91795 AI401062 AW103934 AW276699 AI809596 AW628378
			AW071548 A1189019 A1002857 AW206484 AA364666 H01166 N59385 AA773930 AW027775 N29781 AW953931 AA447735 A1285163 A1633932 A1290045 A1360254 R82206 A1633501 A1690373 BE222634 AW027793 AW027950 AW182096 AW592206 H24046 A1811625 A1885290 A1744720
70			ALEQUIDO ADDIGOS POZADA RIDOSO I RIGUEZO SE REVOLEZOS ARROLEZOS AR
70			ALZ-1455 AW451191 AA502440 A1145651 AW276821 AW276831 AW51595 AA95340 D25758 AA327290
	436992	430854_1	AA741074 AW449312 AIB27330 Z44512 AW779392 AI76142B AW295099 AL134768 AI627818
	436998	430929_1	AA745625 AA743054 AA741154
	437048	432140_1	AA743240 AI458566 AW613503 T25344 T40899 AW976433 BE350724 AI954132 AA830804
75	437064	43234_1	AK023264 AA161185 X52350
	437073	432564_1	AI885608 AA743734 AI034154 AI075224 AI656815 AI887898 AW243126 AI950513 AI869093 AI273184 AA912285 AA912258 AW976672 AI335673
			A(080389 N79728
	437074	432577_1	AI2B6235 AI767243 AA761662 AI672630 BE047809
on	437085	432740_1	AA743935 AW341613 AI700300
80	437138	433575_1	ANSISSEZ ANTASISS ANTASISS 4
	437183	434235_1	AI928184 BEO48934 AA74605T AI206024 D57453 AI076908 Aĭ089589 AI283431 W58768 AA778157
	437263 437332	435353_1	AA747822 AA836580 AW976205 AA814943 AA748879 AW976617
	431332	436150_1	ווטטנפווויסיוטדער איין אריסיו איין אריסיו איין

	419543 455657	251903_1 1490185_1	BE065209	AA244170 AA244355 BE065364 BE065110 BE065111
5	414405	112689_1	AW612409 BG283489	AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090596 AI927369 AI669226 AI369437 AI371075 9 AI636711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 079312 AI375558 H61111 9 BE090666 BE090664 BE090862 H26545
	409010	10331_1	AA059411 Al580336	AL551714 BM014781 BG542863 BG771232 AA429722 A1377511 A1770155 AA716665 BG003427 AA810B1 AA442760 AA128610 A1796263 AM94075 A1572127 AA420992 BF436083 IA648675 AA878813 BI488614 BG700886 AA128609 AV702879 AA731146 A1373224 AA919169 A1758175 AA976350 BG701414 BF057794 AW136598 AA062683 BI549631 A118697 A9333879 AW024454 AA045194 BG928396 BE856883 BF435859 AA196423 AW237471 R99289 D61992 BE856637 BF366270 AA194236 N53319 AA383499
10	411962	2307710_1		G548812 BF027898 BG779448 I AA099525 T47733
	434982	121871_1	AW97508	4T90204 AA658177
	432676 437838	3503_22 2512601, 1		AA618478 AA558869 AJ307229 AA769348
15	446019	658727_1	A1362520	NJS01229 NATOSHIO DZ5917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793036 AW610540 AW362220 AW362166 AW362214 5 AW362228 AL119827
	454042	30254_1	AW24142	AIO18523 AA705686 BF049633 AL119553 BF945960 AIO81305 AAO41432 AI921013 AI684910 AI654847 AW874199 AI206120 8 RA3035 T66767 AW103715 W28478 BF963052 PA5926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350
20			Al431587	145331 BIS49761 R53955 BIS49855 BG991568 BI491075 AW020049 AW129293 146263 AA410309 AA340613 R42410 AA707199 BEB58679 AW292267 AI421678 AA041195 BE466753 A1243B13 A1358B94 AW137298 A1366468 N64350 AA779107 AW025959 R49056 I R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 A1880103 AW771447 A1202561 AA788851 A1494436 BF856114 H22570
	432954	2159612_1		A1887648 AA572691
25	446126	610_2	AA336407 AI458885 AI000008) BF946218 BF861494 AL536879 AA457150 AI590194 AI582629 AA464515 AA916242 AA337109 AA338509 N46908 AA336322 7 AA337222 AA319240 BI026817 BI027058 AL536880 AI693827 AA551730 AI701013 BM066789 AW339506 AA293021 BF891008 AW361203 AW974652 AI761251 AI655763 AA628063 BE047125 AW085916 AI129687 N52070 AW172361 AA052951 AW085909 AA962570 AI371342 AI364207 AA464514 AI962506 AI824603 AW376300 AA058439 AW381192 AV656660 N50282 BF820514 BF891008 IF891112 BE708029 AW043667 AA056762
30	419145 409245	248375_1 3199_2	BM45660 AF030234 AW46702 AW96084	2 AV705711 BF379357 H90994 AA234436 AA558020 BF351723 AA328271 R94815 N99638 BG223375 AW973750 N59599 4 BC017465 BG008626 AW505560 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 17 AI742080 A624350 H58206 AA478516 AW439937 AW393656 AW393523 AI659763 A/808732 R66856 H01374 BI257369 BI259830 15 BM468252 AW956813 BE768647 AV668853 BM056248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024
			BE76851	1 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87696 H87599 BF691752 1 BG940948 W37195 BF372041 BE683796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492668 BI495144 AA921846
35				: A1652147 A1435449 N47325 A1434429 AA573137 A1183429 A1829962 A1332526 BF613937 A1189561 A1221962 A1378034 AW118897 I7 AW340077 N41605 AA478519 AA463875 A1858260 AA483379 A1292305 BE045947 AA971089 A1125820 BG940947 A1080245
40	437856	34257_1	AA88495- AA94847: O56772 A H16217 H	4 A1125702 A1382934 AA931835 A1358631 AW439905 A1027833 A1399648 A1014533 AA347851 AA738261 NG7374 N69081 A1768687 2 A1819214 AA293133 A1186725 AA889214 A1222635 B1495143 N29605 N48812 AA769041 A1492769 D56771 AA096911 BE222062 A1819218 AA293133 A1186725 AA889214 A1222635 B1495143 N29605 N48812 AA769041 A1492769 D56771 AA096911 BE222062 A1827265 BM054985 D12465 BG534562 AW003511 H67486 H42880 AW190293 BF597676 H22047 B122047 B1255749 B1492848 A1827265 BM054985 D12465 BG334562 AW003511 H67486 H42880 AW190293 BF597671 H22047 B122047 B1255749 B1492848 A1827265 BM054985 D12465 BG334562 AW003511 H67486 B12880 AW190293 BF597671 H22047 B12047 B1
70	•	_	BM19413 AA83748 AA15678	M AW966609 W84374 BF916360 AA385173 W84366 AA383743 BF803698 AA043776 W84421 AA778446 AW444904 BF446960 17 AV755539 AW468444 AW468002 AA811830 AA581806 A1866686 A1572124 AA687333 D20160 AA812489 AU185248 AU186004 18 A1536733 BM144850 A1471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 B1022546 B1021204
45	458332 459513	1139685_1 417837_1		I AL766341 AW873274 12 BE162284 Al032945 BF360636
	449328	3030726_1	A1884781	1 AI652306 AI851694 AI638744 AI962493
	406685 417258	0_0 400B35_1	M18728 9G11678	31 BI914326 BI030196 N5B885 N63406 AV683374 N58892 BG110501 AA333708 AA359583 AW983123 N95562 N95696 N95587
50	447881	44623_1	AK07429 AA72218 AW81419 AW3165	M AW293424 BE576135 AI832125 BE019146 BE465019 AT61124 AA617778 AI279232 AW575697 AI672039 F28618 BF924261 M BF934174 BE004328 AV749301 BE680282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 95 BE879126 AI697926 BF694155 BE205787 BF063513 N35828 AI948557 AI433839 AI378679 BC056182 AI589094 N23123 AA688805 81 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 66 W01350 H05495 AI247785 Z38622 AA887432 AI350659 R46102
EE	425481	334120_2	AL52049	6 AW978162 AI610475 AI688990 AW470054 AA609426 AI167391 AA815231 AA358241
55	44063B 442495	371165_1 928718_1		00 Al376551 AA897445 T87714 7 AW518883 AF121173
	416311	1280744_1	AA17944	46 AA357794 D81719 DB0529 C14B33
	431926 435154	1237041_1 126506_1		24 AA877998 AA522631 AU185388 63 AA668764 AA804491 AW665688 AA765069
60	437908	13268_11		6 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676
	TABLE 330	:		
65	Pkey:			ending to an Eos probeset
65	Ref: Strand:	human chr	отоѕоте 22°	7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of Dunham, et al." refers to the publication entitled "The DNA sequence of Dunham, et al. (1999) Nature 402-489-495. In which exons were predicted.
	Nt_position			litions of predicted exons.
70	Pkey	Ref	Strand	Nt_position
	401403 406387	7710966 9256180	Plus Plus	146180-146294 118229-116371,117512-117651
	405268	4156151	Minus	24404-24521
75	406122 402550	9144087 7652009	Minus Minus	30940-31386 80413-80673
. •				

80 TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific intensitial pneumonitis

Pkey: ExAcon:

Unique Eos probeset Mentifier number Exemplar Accession number, Genbank accession number

	439560	47377_1	BE565647 AA384580 Al985958 AW118400 AA131255 Al017605 BE546585 AA131345 AA318529 AA316901 AW014441 Al632144 Al785495 AJ745695 AW473885 AJ263026 AJ377804 AW664079 Al806774 D20313 AA864830 AA993300 Al991497 Al092233 AJ253607 AW237133 Al638158
			AI223187 AAGS3544 AI972790 AW966478 BE175948
_	439567	47389_2	A(055618 A)076321 W79643 AF085386 A)418395 A)743471 A)744094 W74123 BE549611 A)796878
5	439606	47435_3	W79123 AF086432 W79920 AW873727 Al611298
	439626	474565_1	N22415 AA838783 AW450533
	439634	47465 1	W79377 AF088055 BE348731 AL119650 AA 165648 AW016476 W81285 AA258105 AL119947 AA331387 AW965247 R53043 AA290926
	439693	475350 1	AI741816 AI761457 AI453831 AA888796 AI051065 AI075210 AA843898 H87971 AW004862
	439702	475444_1	AW085525 AL043B07 Al435445 AA844005 Al079684
10	439703	47545_1	AF086538 W95969 Al631911 W95835
LV	439715	47556_1	AA524504 AF086549 AA931946 A(052102 W94492
	439724		AFD86565 AAD10136 AA010138
	439780	47571_1	AL109888 R23665 R25678
	439786	47673_1	AL 109000 72007 A 6693817 AV647943 N59453 N70232 N94146 R92830 AL359654 N76783 H73446 H74127 H40442 R97678 H82906 W01021 W03283
15	439700	47682_1	AV05ZFUF AA053D17 AV05793 R05453 NCV22C N97490 R9250 PL3350524 WCG S RC7490 R742C PT-PV-P4C R97670 R02503 WCUCLY WUX2503 AA007552 T81163 N63799 T68818 A1768510 H73934 N63729 H40443 R93048 T55956 H63716 T95962 AV69374 N82507 R97679 T80688
13	*****	17701 0	
	439818	47731_3	AL360137 AA455730 AL138067 AW978717 AI741559 Al034231 Al679611 BE044415 AAB24642 Al350608 Al683265 AA598951
	439831	477578_1	AW136488 AA854689 AI299060 W37504 N38890 AI970972 AI936400 R48273
	439871	478212_1	R88518 AA847584 AI940762 AI940747
00	439911	480063_1	AA854024 AA869110
20	439950	48 1368_1	AW937417 AW979195 AA856979 AW999881
	439953	481468_1	AA918129 A)732900 A1272847 A1278764 A1285200 A1339550 AA85711B A1263965 A1793166 A1952997
	440046	4839_1	AW402306 AK001345 Al693653 AA465467 AW974459 AA081718 AA648460 AA927610 AA764878 Al636548 AA465468 AA449153 AA989477
			AA356060 R14621 Z42414 H12254 AA563805 AI625726 H48597 H08479 AW080101 AW080074 AA322400 H62103 W94460 H80467 AA295083
			AA045999 AA322642 AW021802 AA040820 AA336467 AW952566 AI476789 AY744598 AI608724 AI271619 AI961091 AI884709 AI744653 AI978846
25			AI660134 AW900463 AA700728 BE220512 W94351 AA749238 AA970837 AW057695 AW571668 AA831554 AW043767 AA040157 AI810228
			H48791 H81387 AA045104 Al813379 AI026643 AW102687 AI095327 AI015840 AI277634 AA835199 AA640450 T17078 H12255 AI338417
			AA854569 AA836209 AI061248 BE242097 AI298338 AA838341 AA643527 AI061232 AI915382 BE243602 AI915493 AW999552 H61198 Z38620
			ABBB473 Al47/191 AA668039 F02599 R49291 R46153 R13438 R21307 R40949 R45508
	44004B	484235_1	AA897461 AJ376920 AB09991 AW061854 AI829714 AW572368 AA862176
30	440122	486363 1	A1733011 AA865542 A1791407
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	440129	486597_1	AA865B18 Al732997 AA977633 AB002297 R21018 R24849 Z46003 R53332 R35190 AL118982 AA355887 Z43686 T78686 F11356 AA888981 AA412141 M78951 AA394289
	440184	4877_1	
			R50850 R53937 AW303583 AIG56559 AW589917 AIG21051 AI933711 AIB25042 R44552 R39312 R46134 AI302700 N51360 AIG51758 T17357
25			A1161203 Z38651 A1961153 N50920 AW090632 AI423054 A1167950 AA976204 Al360906 M79104 R39087 F09016 Z39744 T80400 AL040356
35			AW893434 T05544
	440209	468434_1	H05049 A1129949 D60235 AW517611 Z40823 C15241 D81133 H23669 D50505 AAB72685 D79646 D62470 H23868 H23914 D61233 D60722
			061106 60930
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35	458175	498744_1	AW296024 AA897109 AI015000
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60			AA986654 AA826438 Al002431 Al299721
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	459207	926704_1	AW138410 AI912712 N40185
	459208	92717_1	BE261314 A1243406 AA027322
	459275	97318_1	Alborenia Awozesako wanzinzo Alborenia Awozesako wanzenia Alborenia Akostoti witeber rabiti nateor alborenia Rabitez Awozaren Alborenia Akostoti witeber alborenia alborenia Akostoti
	459278	9751_1	A000913 AW020342 W01290 AID7 IS19 A0302000 RA031011 W19080 R40151 NS1008 AIB10253 R40752 AW024095 AIS353564 AW294659 AI204928 AA351653 H51220 R86843 AA993182 U79298 R16294 F05089 Z42963 R17818 T77498 AA332319 W56049 AA331588
70	409270	3(0)"!	
, 0			AW881873 AW881865 AW881976 R32345 AI652070 AA400044 AA401512 T08151 W05466 N69378 T33846 AI190920 R43021 AI949980 Z39084 T59443 H27505 F04949 R09360 AI45464 AM841579 A1460414 AIRFORD A A450665 AI6546 AIRFORD AIFE AIRFORD AIRFORD AIFE AIRFORD AIRFOR
			T63413 W37269 F01343 R88669 AI621055 AW117593 AI193211 AW297932 AI500709 AA400056
75	Table 30C		
	JUL SILE :		
	Pkey:	linione orm	iber corresponding to an Eos probeset
	Ref:	Seguence er	purce. The 7 digit emphasize this column are Centrally Interffice (Cl) numbers. The his purpose to the publication entitled "The DMA sequence of

Prey: Unique number corresponding to an Los probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Durcham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402-489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

80

Pkey Ref Strend Nt_position

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5	403891	7331467	Minus	191508-193220
,	403937	7711761	Minus	12609-12773
	404042 404043	9558573 9558573	Plus	5140-5208,8633-8763
	40406B	3168621	Plus Minus	29042-29135,46597-46699
	404108	8247074	Minus	18123-18766 63603-64942
10	404166	7596822	Plus	86147-86509
	404193	3881948	Minus	94185-94322
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
15	404367	9965011	Minus	114391-114628
1.0	404404	7272262	Plus	82112-82244
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	404420	7407952	Minus Minus	143042-143216,144704-144853,145800-146048 129817-130586
	404443	7579073	Minus	87198-87441
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	404476	8080699	Pius	101841-102043
	404518	8151988	Plus	84494-84603
	404526	8152087	Plus	121918-122123,125198-125348
25	404531	8247909	Plus	20152-20352
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	404582	9739220	Plus	104257-104348,104822-104970 53230-53424
	404587	8696840	Minus	69781-70096
	404588	6456726	Minus	40059-40210
30	404593	9944086	Minus	74922-75788
	404595	9958262	Minus	16784-16900
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35	404694 404708	9799957 9800828	Minus	128092-128227
55	404731	7230299	Plus Minus	77522-77658 169600 150704 469054 469004
	404767	7882627	Minus	168609-168781,182951-183081 23244-23759
	404793	7232206	Minus	61087-61590
40	404822	3810614	Plus	7541-8132
40	404834	6911603	Minus	37948-38226
	404957	7407927	Plus	147512-148011
	404987 404988	7523744 4662677	Minus	89944-90729
	405001	6015406	Minus Minus	72406-72600,72779-72856
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	405120	8099940	Plus	140176-140340
	405229	7249019	Plus	51081-51701
50	405230	7249032	Minus	97493-97682
20	405302	2078453	Minus	121698-121840
	405347 405443	2979602 7408143	Minus Plus	977-1116
	405455	7656875	Plus	90716-90887,101420-101577 134112-134671
	405456	7656676	Pkis	150052-150208
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	405523	9454643	Plus	114550-114688,117265-117497,119490-119599,123237-123395,131140-131217
	405605	5836195	Minus	11/0/0-117270
60	405608 405634	5815499 530628B	Minus	66822-66925
~~	405654	4895155	Plus Minus	17858-17957,18302-18412,18837-18927,22790-22989 53624-53759
	405692	4314424	Plus	61379-62562
	40573B	994399B	Plus	44370-45410
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65	405780	7248203	Minus	48204-48371
	405783	5738434	Minus	27238-27885
	405784 405829	7417368 7109593	Minus	77798-78000
	405920	675B795	Minus Pius	15628-16127
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	405970	8247789	Minus	45795-46295
	406005	8247BQ1	Minus	39912-40220
	406018	6758904	Minus	37795-38168
75	406076	9123123	Plus	89972-90319
, ,	406092 406190	9123919 7289992	Plus	251370-251797,252168-252882
	406288	7209992 7549820	Minus Pius	22395-22901 111718-112008
	406298	5686278	Minus	30084-30770
DΔ	406333	9213235	Plus	64889-64798
80	406354	9256114	Minus	50715-50833
	406378	9256142	Minus	126408-126800
	406413 406468	9258407 9795553	Plus	43858-44003,46993-47136
	*********	97 33333	Ptus	4373-4616,8870-9046,11366-11509,11625-11880

406603 8272659 Minus 39506-39694

5 TABLE 31A: ABOUT 1884 GENES UP-REGULATED IN IPF COMPARED TO NSIP

Table 31A lists about 1884 geneswhose expression levels are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with non-specific intersitial pneumonia (NSIP) samples.

These were selected from about 59680 probesets on an Affyrnetrix/Eos Hu03 GeneChip array such that the ratio of "average" kilopathic pulmonary fibrosis sample expression level to "average" non-specific intersitial pneumonia sample expression was greater than or equal to about 2.0. The "average" kilopathic pulmonary fibrosis level was set to the 90th percentile amongst mon-specific intersitial pneumonia level was set to the 90th percentile amongst non-specific 10 interstifal pneumonia samples.

15

Pkey: Unique Eos probeset identifier number

Exacca: Examplar Accession number, Genbank accession number
Unique BD: Unique a number
Unique Title: Unique gene title
R1: Ratio of IPF (Kilopahic pulmonary fibrosis) to NSIP (non-specific intenstitlal pneumonia)

20	Pkey	ExAcen	Unigene ID	Unigene Title	RI
20	4110.4110				
	450478	AW451709	Hs.271200	ESTs	20.2
	405654	A1/004400	11- 074440	1 11 77 3 3 4 77 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	16.1
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
25	403637	A100 4070	11-0744		11.2
23	431548 407811	A1834273	Hs.9711	novel protein	10.8
	439606	AW190902 W79123	Hs.40098	cysteine knot superfamily 1, BMP antagon	10.4
		4419123	Hs.58561	G protein-coupled receptor 87	10.3
	403574 416653	A 8700002	11. 7/470		10.1
30	441233	AA768553	Hs.74170	metallothioneln 1E (functional)	9.3
50	415817	AA972965 U88967	Hs.135568	ESTs	9.1
	409632		Hs.78867	protein tyrosine phosphatese, receptor-t	8.8
	432437	W74001 W07088	Hs.55279 Hs.293685	serins (or cysteine) proteinese inhibito	8.4
	407266	AJ235664	NS.283000	ESTs	8.3
35	423017	AW178761	Hs.227948	gb:Homo saplens mRNA for immunoglobulin	8.2
<i>J J</i> .	403329	W41210101	19.221340	serine (or cysteine) proteinase inhibito	8.1
	429529	B£501732	Hs.30622	Nome analysis of MA CL 142040 61 NT	8.0
	441519	AA972740	Hs.127092	Homo sapiens cDNA FLJ13010 fis, clone NT ESTs	8.0
	453823	AL137967	115.121032		7.9
40	406690	M29540	Hs.220529	gb:DKFZp761D2315_r1 761 (synonym: hamy2) carcinoembryonic antigen-related cell ad	7.8
- •	416379	N38857	Hs.203933	ESTs	7.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.7 7.5
	407305	AA715284	113.2010	gbxw35f03,r1 NCI_CGAP_Br5 Homo saplens	7.2
	434683	AW298724	Hs.202839	ESTs	7.2
45	441802	AA968536	Hs.127877	ESTs	6.9
	431242	AA987742	Hs.251278	KIAA1201 protein	6.9
	442377	AA993807	Hs.167367	ESTs	6.9
	420407	AAB14732	Hs.145010	Opopolysecceride-specific response 5-li	6.B
	428908	AW303529	Hs.144955	ESTs	6.8
50	445898	AF070623	Hs.13423	Homo sapiens clone 24458 mRNA sequence	6.7
	457673	AA551569	Hs.272034	hypothetical protein PRO2822	6.7
	458771	AW295151	Hs.163612	ESTs	8.6
	426800	AA385085	•	gb:EST98959 Thyroid Homo saplens cDNA 5'	6.6
	440504	A)948966	Hs.130017	ESTs, Wealty similar to JN0908 H+-transp	6.6
55	415025	AW207091	Hs.72307	ESTs	6.5
	438557	AW364104	Hs.143509	hypothetical protein FLI21924	6.5
	416128	AA173632	Hs.22116	CDC:4 (cell division cycle 14, S. cerevi	6.4
	457242	AA457011		gb:sa90c11.r1 Stratagene fetal retina 93	6.3
60	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	6.3
60	404793				6.2
	435563	AF210317	Hs.95497	solule carrier family 2 (facilitated glu	6.2
	415672	N53097	Hs.193579	ESTs	6.2
	455488	AA102322		gb:zi90f03.r1 Stratagene colon (937204)	6.2
65	426230	AA367019	Hs.241395	prolease, serine, 1 (trypsin 1)	6.1
OJ.	412282	BE160188	11. App.	gb:QV1-HT0413-010200-059-g05 HT0413 Homo	6.1
	431622	AW979271	Hs.2931B4	ESTs	6.1
	405523	DEACONAC	Li- America	F0-	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
70	436397	AA715013	Hs.169835	EST's	6.0
70	456476 434784	AA256753 AA649051	U- 464007	gbzs22b12.r1 NCL_CGAP_GCB1 Home sapiens	5.9
	422977	AA631498	Hs.164007	ESTS	5.9
	442849	R10099	De actions	gb:np83h04.s1 NCI_CGAP_Thy1 Horno saplens	5.9
	451519	A1800600	Hs.269805 Hs.209573	ESTs	5.9
75	412474	A)791451	10.203013	ESTS abortional of NCI CCAR Ova Harman application	5.8
, 5	457081	AA916786	Hs.180610	glxni50c09.y5 NCL_CGAP_Ov2 Homo saplens	5.8
	444827	R09764	Hs.20416	spilolog factor protine/glutamine rich (ESTs	5.8
	404822		1 13.20-1 10	T/10	5.8
	402430				5.7
80	457900	AW976692	Hs.291665	ESTs	5.7 5.7
	400292	AA250737	Hs.72472	ESTs	5.7 5.7
	410934	AW811114	1 1947 E-T4 E-	gb:MP2-ST0131-i11199-016-a04 ST0131 Homo	5.7 5.7
	440172	AAB68584	Hs.126154	ESTs	5.7 5.7
					U.1

	431374	BE258532	Hs.251871	CTP synthase	5.7
	409816	AW500954		gb:Ul-HF-BPOp-air-h-12-0-Ul.r1 NIH_MGC_5	5.6
	447613	AL041057	Hs.33363	DKFZP434N093 protein	5.6
_	417919	Al928203	Hs.86379	ESTs	5.6
5	425259	AL049280	Hs.155397	Hosno sapiens mRNA; cDNA DKFZp564K143 (fr	5.6
	439063	AF085922	Hs.113968	ESTs	5.6
	406053				5,5
	431211	M86849	Hs_323733	gap junction protein, bata 2, 26kD (conn	5.5
10	451830	H18433	Hs.21542	KIAA1035 protein	5.5
10	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.5
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	5.5
	45945B	AW270957	Hs.254577	ESTs, Weakly similar to 934087 hypotheti	5.5
	416154	Z46122		gb:HSC0VB031 normalized infant brain cDN	5.5
15	404561				5.4
15	428895	AA437124	Hs.187247	ESTs	5.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	455601	A13686B0	Hs.816	SRY (sex determining region Y)-box 2	5.4
	440925	AW511090	Hs.130419	ESTs	5.4
20	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5,4
20	448477	BE612572		gb:601452090F1 NIH_MGC_66 Homo sapiens c	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	459664				5.3
	401497				5.3
25	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.3
23	444931	AV652066	Hs.75113	general transcription factor IIIA	5.3
	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	5.3
	452542	AW812256	II. ADDEC	gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.2
	411402	BE297855	Hs.69B55	NPAS-related gene	5.2
30	404957	********	11 404000	F0.**	5.2
20	436445	AA922213	Hs.121735	ESTs	5.2
	442617	AW340093	Hs.130538	ESTa	5.2
	416045	H15990	Hs.31403	ESTs	5.2
	425178	H16097	Hs.161027	ESTs	5.2
35	441918	A1733373	Hs.128119	ESTs	5.2
55	455464	AW983901	II- coccert	gb:RC1-HN0003-220308-011-f10 HN0003 Homo	5.2
	420929	AI694143	Hs.296251	programmed cell death 4	5.2
	448844 410000	Al581519	Hs.177164	ESTs	5.2
	4306B6	NM_001942	Hs.2633	desmogleia 1	5.2
40	405229 417641	4.400c04c	N- CACCO	he will all the tennen	5.1
-70	434167	AA205015	Hs.54617	hypothetical protein FLJ20060	5.1
	450438	AA626334	Hs.116153	ESTs	5.1
	456394	A1696071	Hs.253800	ESTs	5.1
		W28506		gloc4871 Human retina cDNA randomly prime	5.0
45	455747 417420	BE074910	11-00044	gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
1.0	409545	TB5150 BE296182	Hs.268814	ESTs	5.0
	426750	AA383950	Hs.19002	hypothetical protein MGC4675	5.0
	440615	Al733055	Hs.130806	gb:EST97403 Thymus II Homo sapiens cDNA	5.0
	408959	AW890878	Hs.211610	ESTs	5.0
50	454482	BE147919	113.21 IU IU	CUG triplet repeat, RNA-binding protein	4.9
-	43650B	AW804381	Hs.121121	gb:RC3-HT0230-160200-016-e08 HT0230 Homo	4.9
	452046	AB018345	Hs.27657	ESTs, Weskly similar to S00755 pleckstri	4.9
	407415	AF073328	(15.21001	KIAA0802 protein gb:Homo sapiens tetracyline transporter-	4.9
	450090	AW448940	Hs.202259	ESTs	4.9
55	406333	*****	110.202200	DO13	4.9
	434188	Al765848	Hs.281680	peroxisomal trans 2-encyl CoA reductase;	4.9 4.8
	403344		I ASILO TOCO	by an annual trains southly contributed	4.B
	448468	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	4.8
	405455				4.8
60	411387	AW842339	Hs.130615	hypothetical protein FL121870	4.8
	426097	BE327369	Hs.112238	ESTs	4.8
	427768	T78402	Hs.174880	ESTs	4.8
	41101B	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415257	F03016	Hs.27513	ESTs	4.8
65	441107	AA917075	Hs.190520	ESTs	4.8
	419519	A1198719	Hs.176376	ESTs	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weskly similar to hypothetical pro	4.B
70	424188	AW954552	Hs_142634	zinc finger protein	4.8
70	456987	AJ557290	Hs.173536	ESTs	4.8
	405303				4.8
	414955	C15506		gb:C15506 Ciontech human aorta polyA+mR	4.8
	451620	AW449888	Hs.257224	ESTs	4.7
75	421948	L42583	Hs.334309	keratin 6A .	4.7
75	424780	U39576	Hs.15305B	butyrophilin, subfamily 1, member A1	4.7
	443271	8E568568	Hs.195704	ESTs	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	402230				4.7
QΛ	422246	AA461032	Hs.5306	hypothetical protein OKFZp586F1122 simil	4.7
80	431508	NM_012481	Hs.182979	ribosomal protein L12	4.7
	415236	R41400		95:yi94b12.s1 Scares infant brain 1NIB H	4.7
	413101	BE065215		gb:RC1-BT0314-310360-015-f01 BT0314 Homo	4.6
	444774	AW052174	Hs.196030	ESTs	4.6

	444414	AW293214	Hs.8752	transmembrane protein 4	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	436853	BE328074	Hs.148661	ESTs	4.6
5	445334	Al610081	Hs,9475	glucose transporter protein 10	4.6
3	408172	W02488 .	Hs.46039	phosphoglycerate mulase 2 (muscle)	4.6
	426985 404638	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6 4.6
	447617	Al400762	Hs.176675	ESTs	4.5
4.0	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	4.6
10	442360	Al374621	Hs.29055	EST&	4.6
	41 1738	AW859353	U= 459954	gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	444157 401365	Al 125785	Hs.153351	ESTs	4.5 4.5
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF 1 [4.5
15	436269	AA707472	Hs.190760	ESTs	4.5
	459448	AA416773	Hs.275012	EST	4.5
	452090 414899	AA022684 AW975433	Hs.124673 Hs.36288	Homo sapiens cDNA FLJ11477 ils, clone HE ESTs	4.5 4.5
	443764	F23283	NS.30200	gb:HSPD22980 HM3 Homo sapiens cDNA clone	4.5
20	444898	A1201548	Hs.30B338	ESTs	4.5
	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.5
	428528	A1004034	Ha.98638	ESTs	4.5
	405605 45 7 982	AW856093	Hs.183617	ESTS	4.5 4.5
25	427731	AA411750	Hs.20943	ESTs	4.4
	420691	AA829433	Hs.275343	ESTs	4.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	4.4
	453080 41.2147	AI423056 AW895984	Hs,23921	hypothetical protein DKFZp547A023 gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4 4.4
30	435747	A1079519	Hs.134398	ESTs	4.4
-	453824	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	4.4
	458B65	T05095	Hs. 19597	KIAA1694 protein	4.4
	459037	AW439497	Hs.290656	EST	4.4
35	403310 425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4 4.4
J J	427500	AW970017	Hs.293948	ESTs, Weakly similar to \$65657 alpha-1C-	4.4
	432020	AJ251509	Hs.272345	phosphodiesterase 11A	4.4
	453043	AW13544D	Hs.224277	ESTs	4.4
40	456293 447879	AW131715 BE503405	Hs.311561 Hs.170437	ESTs, Weakly similar to CYAT_HUMAN ADENY ESTs, Weakly similar to PRP4_HUMAN SALIV	4.4 4.4
40	428648	AA382787	Hs.122713	ESTs	4.4
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	4.4
	404898				4.4
45	435434	AA680387	Hs.187850	ESTs	4.4
40	443314 408000	AW771701 L11690	Hs.54646 Hs.620	ESTs bullous pemphigoid antigen 1 (230/240kD)	4.3 4.3
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	4.3
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	4.3
50	404767	11000150	11. 447400	For.	4.3
50	445189 452393	A1936450 H67398	Hs.147482 Hs.99858	ESTs ribosomai protein L7a	· 4.3 · 4.3
	428740	AA433B3B	125.55000	gb;zw53e12r1 Soares_total_fetus_Nb2HF8_	4.3
,	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	4.3
55	410615	AW772721	11. 545	gb:hi95c01.x1 NCL_CGAP_Thy8 Homo septens	4.3
22	445619 406073	AU076643	Hs.313	secreted phosphoprotein 1 (asteoponiin,	4.3 4.3
	405692				4.3
	436033	H75391	Hs.25574B	ESTs .	4.3
60	410733	D84284	Hs.66052	CD38 antigen (p45)	4.3
60	455587 459084	BE007829 H01699	Hs.27289	gb:QV0-BN0147-280400-213-303 BN0147 Homo CGI-125 protein	4,3 4.3
	409004 401189	I IM 1033	10.21203	GG-120 proteit	4.3 4.3
	435451	AF195420	Hs.303006	ESTs, Weekly similar to gamma-heregulin	4.3
CE	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.3
65	425733 447863	F13287 AL047611	Hs.159388 Hs.288885	Homo sapiens cione 23578 mRNA sequence	4.3
	436659	AL217900	Hs.144464	Homo saplens cDNA FLJ14246 fis, close 6V ESTs	4.3 4.3
	435463	AA682507	120177101	gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
70	455675	BE065984		gb:RC3-8T0319-120200-014-a06 BT0319 Homo	4.3
70	439481	AFC86294	Hs.125844	ESTs	4.3
	405287 405784				4.3 4.3
	436461	AW511956	Hs.293261	ESTs	4.3
75	437636	AA764781	Hs.291844		4.2
75	409629	AW449589	Hs,279724		4.2
	412999 403281	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	4.2 4.2
	427531	AA405097	Hs.97957	ESTs	4.2
QΛ	451882	A1821324	Hs.100445		4.2
80	418856	AA362B58		gb:EST72900 Ovary II Homo sapiens cDNA 5	4.2
	405494 456027	BE327387	Hs.13913	KIAA1577 protein	4.2 4.2
	414539	BE379046	1,0,100.0	gb:601236646F1 NIH_MGC_44 Homo sapiens c	4.2

	421106	AA877124	Hs.172844	ESTs	4.2
	409076	N57559	Hs.82273		
				hypothetical protein	4.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	4.2
-	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	4.1
5	416614	T83391	Hs.111849	ESTs	4.1
	454434	AA083558	Hs.261286	ESTs	4,1
	404526	Al912555	Hs.157195		4.1
				peptide YY, 2 (seminalplasmin)	
	446393	AW014174	Hs.301956	zinc finger protein	4.1
10	405302				4,1
10	432669	AL043482	Hs.267115	ESTs	4.1
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	423841				
		AW753957		gb:RC2-CT0394-080100-011-h12 CT0304 Homo	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	430484	D82880	Hs.241548	RAS p21 protein activator 2	4,1
15	403895			• • • • • • • • • • • • • • • • • • • •	4,1
-	420457	AA482280	Hs.191656	ESTs	4.1
		AAB28995	110.101000		
	438993			gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	458421	A!279978	Hs.22547	ESTs	4.1
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.1
20	411382	BE067246		gb:PM1-8T0348-151299-001-d04 BT0348 Homo	4.1
	422373	AK001843	Hs.115700		
				Homo saplens cDNA; FLJ23515 fis, clone I.	4.1
	430749	AJ242956	Hs.25960	v-myc avian myalocytomatosis viral relat	4.1
	403625				4.1
	401887				4.1
25	403667				4.1
	452744	AMETER	Hs.30504	Mana appleas Chia Chia DVC7-404C000 Ma	
		Al267652	PUGUKARN	Homo sapiens mRNA; cDNA DKFZp434E092 (fr	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4,0
	439294	AW976328	Hs.6523	chromosome 1 open reading frame 12	4.0
	432792	AA448114	Hs.278950	protocadherin beta 1	4.0
30	405443			procession our t	
-0		A1400740.40		-b-F07700000 Lb-07	4.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	4.0
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo saplens	4.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bl	4.0
	448324	A1571356	Hs.34174	ESTs, Moderately similar to ALUS_HUMAN A	4.0
35	456536	AW135986	Hs.257859		
55				ESTS	4.0
	415B11	AA450191	Hs.172963	hypothetical protein FLJ 14624	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Home	4.0
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	449327	AI638743	Hs.224672	ESTs	4.0
40	426062	N57014			
-10			Hs.75874	pregnancy-associated plasma protein A	4.0
	433485	A1493076	Hs.201967	akto-keto reductese family 1, member C2	4,0
	434849	AW292765	Hs.8053	ESTs	4.0
	400268				4.0
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	4.0
45	445414	AV653692	Hs.146105	ESTs	
10		AVULUOZ	110.140100	C015	4.0
	408470				3.9
	429809	AL162010	Hs.223603	Homo sapiers mRNA; cDNA DKFZp761D09121 (3.9
	45309B	Z25935	Hs.86379	ESTs	3.9
	402867				3.9
50	431071	AA491379		-bra-ceme at NOL COAD, COOK Name and	
20				gb:aa65f05.r1 NCI_CGAP_GCB1 Homo septens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	Al933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein t	3.9
55	428076	AW962714	113.110000		9.5
55				gb:EST374787 MAGE resequences, MAGG Homo	3.9
	443682	A1383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3,9
	430072	X13294	Hs.300592	v-myb avlan myeloblastosis virai oncogen	3.9
	413499	BE144884		gb:CMO-HT0182-041099-065-e11 HT0182 Homo	3.9
60			Ua 40004		
00	439B18	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3,9
	443323	BE560621	Hs.9222	estrogen receptor blading site associate	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	455993	BE179085	_	gb:RC0-HT0613-140300-021-d06 HT0613 Homo	3.9
	420111	AA255652		gb:zz21h11.r1 NCI_CGAP_GC81 Homo sapiens	
65			11. 70000		3.9
U.J	403956	W28077	Hs.79389	nel (chicken)-like 2	3.9
	410318	AA084050	Hs.269259	ESTs, Wealdy similar to \$23650 retroviru	3.9
	426497	AA379913		gb:EST92807 Skin tumor i Homo saciens cD	3.9
	430140	AW295771	Hs.221999	ESTs	3.8
	457042				
70		A382130	Hs.97703	ESTs	3.8
70	450236	AW16299B	Hs.24684	KIAA1376 protein	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	428692	Al372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	413071	BE064032		gb:QV3-BT0296-010300-111-b08 BT0296 Homo	
			No 204002		3.8
75	437354	AA749215	Hs.291886	ESTs	3.6
75	403381				3.8
	425798	AA3B4002		gb:EST74529 Pineal gland II Homo saptens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	428365	AA376667	Hs.10283	RNA binding motif protein 88	3.8
	430757	AI458623	- 101 1 1400		
80			21, 00	gb:tk04g09.x1 NCt_CGAP_Lu24 Home sapiens	3.8
OV	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	433887	AW204232	Hs.279522	ESTs	3.8
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.B
	404043			A seasone albumbhioto titidor titid	3.8
					3.0

	404000				
	431333	AA708488	Hs.120127	Homo sapiens cDNA: FLJ22769 fls, clone K	3.8
	451073	A1758905	Hs.206063	ESTs	3.8
	417663	R07483	Hs. 180461	ESTs	
	432363	AA534489	,		3.8
5				gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
.,	436975	AA740723	Hs.212644	ESTs	3.B
	405959				3.8
	400631	AF173937	Hs.109494	secreted protein of unknown function	
	425937	NM_013240	Hs.163846		3.7
	446158			putative N6-DNA-methyltransferese	3.7
10		AI277603	Hs.145990	ESTs, Weakly similar to 138022 hypotheti	3.7
10	450375	AA009647	`Hs.8850	a disintegrin and metalloprotelnase doma	3.7
	416548	H62953		gb:yr47f06.r1 Soeres fetal liver spicen	
	436020	AA778177	Hs.121724	ESTs	3.7
	424989				3.7
		AA985520	Hs.23575	ESTs	3.7
15	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.7
15	441416	A)990139	Hs.148609	ESTs	3.7
	456443	AW967500	Hs.133543	ESTs	
	402112	R58624	Hs.2186		3.7
	404453	100027	1005100	eukaryotic translation elongation factor	3.7
					3.7
20	451421	W16522	Hs.237689	Homo septens cDNA FL)13539 ffs, clone PL	3.7
20	421037	A1684808	Hs.197653	ESTs	
	427088	AA398085	Hs.142390	ESTs	3.7
	453375	Al990114			3.7
			Hs.240091	ESTs	3.7
	453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo	3.7
25	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
25	432291	AK001108	Hs.274274	hypothetical protein FLJ10246	
	449623	C00719	Hs.120440	EST	3.7
	419691	W03298			3.7
			Hs. 193521	ESTs	3.7
	437587	Al591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.7
20	403271				3.7
30	453123	Al953718	Hs.221849	ESTs	
	400462		1 10-15	LUIS	3.7
		ALCOHOLO			3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	443305	Al050693	Hs.133318	ESTs .	3.7
	411186	AW821257		9b:PM3-ST0307-231299-001-b11 ST0307 Homo	
35	424565	AW102723	Hs.75295		3.6
	432189	AA527941	1 10.1 0223	guanylate cyclase 1, soluble, alpha 3	3.6
		711321341		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo saplens	3.6
	403296				3.6
	41791B	AA209205	Hs.163754	hypothetical protein FLJ 12606	3.6
40	436026	A1349764	Hs.217081	ESTs	3.6
40	429864	AA460039	Hs.285	ribosomal protein L4	
	418592	X99226	Hs.2B4153	Fanconi anemia, complementation group A	3.6
	44291 D	A1365130	Hs.11307		3.6
	446304			ESTs, Weakly similar to T19326 hypotheti	3.6
		AW104432	Hs.149761	ESTs	3.6
15	441216	BE299830	Hs.192908	ESTs	3.6
45	421494	A1763322	Hs.152104	ESTs	3.6
	404476				3.6
	416327	R99822	Hs.36172	ESTs	
	414146	BE549372	Hs.317596		3.6
	417401			Homo saplens cONA FLJ12927 fls, clone NT	3.6
50		AA426026	Hs.187615	E8Ts	3.6
30	401200				3.6
	411560	AV/851186	Hs.179909	hypothetical protein FLJ22995	3.6
	426306	AA447310	Hs.164059	Homo sapiens cDNA FLJ13338 ffs, clone OV	
	437918	Al761449	Hs.121629		3.6
				ESTs	3.6
55	447917	AL046037	Hs.164588	ESTs, Moderately similar to neuronal thr	3.6
JJ	421328	BE466506	Hs.3981	ESTs	3.6
	447290	A)476732	Hs.263912	ESTs	
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403				3.6
		AL023753	Hs.158406	Human DNA sequence from clone 1198H6 on	3.6
60	403515				3.6
UU	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (fr	3.6
	435554	AF208502	Hs.185708	early B-cell factor	
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	3.6
	410500		110.002.01	The Part of the Pa	3.6
	439326	R09442	11-01-01	gb:yf26c09.r1 Soares fetal liver spleen	3.6
65		W07140	Hs.54721	ESTs	3.6
65	426296	R14454	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.6
	411311	AW836491		gb:PM3-LT0032-281299-002-f02 LT0032 Homo	
	418019	R68911	Hs.176275	ESTs	3.6
	417490	AA203335	. IO. V. CALF Q		3.6
	423035		U- 450mm	gbzx56g02.rl Soares_fetal_liver_spleen_	3.6
70		AW449679	Hs.156739	H.sapiens XG mRNA (ckne PEP11)	3.6
<i>,</i> 0	416575	W02414	Hs.38383	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	
	450350	T97817	Hs.174880	ESTs	3.5
	451704	Al755209			3.5
75	421013		Hs.205616	ESTs, Weekly similar to ALU1_HUMAN ALU S	3.5
, ,		M62397	Hs.1345	mulated in colorectal cancers	3.5
	407404	AF040257		gb:Hamo saplens TNF receptor homolog mRN	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	
	457141	AA521410	Hs.41371	ESTs	3.5
80	411772	BE170301	100-1011		3.5
			N. denne	gb:QV4-HT0536-040500-193-f05 HT0536 Homo	3.5
	440737	Al375167	Hs.132221	hypothetical protein FLJ12401	3.5
	452728	A)915676	Hs.239708	ESTa	3.5
	423266	AA323875	Hs.193574	ESTs	3.5
					4.47

	413543	AA130228	Hs.324611	ESTs, Moderately similar to ALU8_HUMAN A	3.5
	454447	BE163567	LI- 207F0	gb:QV3-HT0450-230200-101-b08 HT0450 Homa	3.5
	458067 437608	AA393603 AA761605	Hs.36752 Hs.292308	protein kinase anchoring protein GKAP42 ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5 3.5
5	415549	F11942	110.232500	ob:HSC33F061 normalized infant brain cDN	3.5
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	453211	W84B29		gbzzh53f04.r1 Soares_fetal_liver_spleen_	3.5
10	418717	AI334430	Hs.86984	ESTs	3.5
10	400641 442973	BE567665	Hs.288550	Homo sepiens cDNA: FLJ23156 fis, clone L	3.5 3.5
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
1.5	458340	AI457102	Hs.6986	Human glucose transporter pseudogene	3.5
15	412281	A1810054	Hs.14119	ESTs	3.5
	443204 416616	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.5 3.5
	44433B	H68270 A1937026	Hs.146642	gb;yr81h09.rl Soares fetal liver spleen ESTs	3.4
	436946	AW137748	Hs.125956	ESTs	3.4
20	431632	AK000992	Hs.333144	Homo saplens cDNA FLJ10130 file, clone HE	3.4
	403306	NM_005825	Hs.74368	transmembrane protein (63kD), endoplasmi	3.4
	422093	AF151852	Hs.115449	CGI-94 protein	3.4
	42881 6 442137	AA004986 AA977235	Hs.193852 Hs.128830	ATP-binding cassetta, sub-family C (CFTR ESTs, Weakly similar to Z192_HUMAN ZINC	3.4 3.4
25	405970	10 101 1 1.00	110.120000	Ed to, vidual dallies de 2 tot_ totte in 2 to	3.4
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.4
	416100	H18700	Hs.268799	ESTs	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
30	431954 440388	AK001974 Al693520	Hs.272242 Hs.223000	hypothetical protein FLJ11112 ESTs	3.4 3.4
50	421072	AI215069	Hs.89113	ESTs .	3.4
	424578	AK001973	Hs.150890	hypothetical protein	3.4
	436331	A1239495	Hs,120189	ESTs	3.4
35	444063	A)122614		gb:qe96b05.x1 Soares_fetal_heart_NbHH19W	3.4
33	444453 404196	AW379394	Hs.145126	ESTs	3.4 3.4
	421262	AA286746	Hs.9343	Homo sapisns cDNA FLJ14265 fls, clone PL	3.4
	409555	AW410788	Hs.256185	ESTs	3.4
40	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	3.4
40	416057	AJ9273B2	Ha,29857	ESTs	3.4
	425206 447738	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	3.4 3.4
	430664	A1871000 AW969834	Hs.161330 Hs.303303	ESTs ESTs	3.4
	411377	AW841462	1000000	gb:RC5-CN0014-080300-012-809 CN0014 Homo	3.4
45	415769	H94186	Hs.5912	F-box only protein 7	3.4
	429382	Al791249	Hs.278054	ESTs, Weakly similar to 138022 hypotheti	3.4
	431474	AL133990	Hs.190642	ESTS	3.4
	456908 442826	A1959671 A1018777	Hs.220994 Hs.131241	hypothetical protein FLJ14129 ESTs	3.4 3.4
50	400508	711010111	13.101240	2013	3.4
	435111	AI8030B2	Hs.157212	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	436577 412209	W84774	Hs.17643	ESTS	3.4
55	417153	AW901456 X57010	Hs.81343	gb:RCD-NN1012-270300-031-c07 NN1012 Homo collagen, type II, alpha 1 (primary osta	3.4 3.4
~~	423871	AA331906	110.01010	gb:EST35805 Embryo, 8 week I Homo saplen	3.4
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.4
	409623	AW449185		gb:UI-I3-BI3-skg-e-05-0-UI.s1 NCI_CGAP_Su	3.4
60	4161B2	NM_004354	Hs.79069	cyclin G2	3.4
w	420854 422899	AW296927 D16471	Hs.121571	gb:UI-H-BWO-ajo-o-U7-0-U1.s1 NCt_CGAP_Su Human mRNA, Xq terminal portion	3.4 3.4
	432404	AA535246	Hs.50852	ESTs	3.4
	458695	AV660159	Hs.282284	ESTs, Weakly similar to 138022 hypotheti	3.4
CE	440727	A)073991	Hs.134268	ESTs, Weakly similar to 2109250A B cell	3.9
65	428766	AA477989	Hs.98800	ESTs	3.3
	439567 456231	AI058618 H73183	Hs.134314 Hs.129885	ESTs, Weakly similar to 2004399A chromos	3.3 3.3
	454318	AW367764	Hs.7857	erythrocyte membrane protein band 4.1-li	3.3
	411956	AA099113	Hs.118609	ESTs	3.3
70	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	3.3
	437037	T63804		gb;yc21e09.r1 Stratzgene lung (937210) H	3.3
	407664 405780	AW063476	Hs.279080	ESTs	3.3 3.3
	426567	AA381579	Hs.182962	ESTs	3.3
75	400432	AX015809	Hs.287767		3.3
	403356				3.3
	404518	AI815601	Hs.79197	CDB3 antigen (activated B lymphocytes, i	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
80	429875 433785	AI091815 BE044593	Hs.112704	gb:qe58b06.s1 Soares_NhHMPu_S1 Homo sapi ESTs	3.3 3.3
	437876	AA770151	Hs.126424		3.3
	444870	AJ200621	Hs.148504	ESTs	3.3
	453324	W26592	Hs.232089	ESTs	3.3

	437963	8E396279		gb:601309785F1 NIH_MGC_44 Home sapiens c	3.3
	425361	AA355933	Hs. 132221	hypothetical protein FLJ12401	3.3
	408813	AI580090	Hs.48295	RNA helicase family	3.3
-	426692	AK001751	Hs.171835	hypothetical protein FLJ10889	3.3
5	407456	AJ237589		gb:Homo saplens mRNA for T-box transcrip	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	43616B	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	43B456	AA913381	Hs.190513	ESTs	3.3
	453242	T98327	Hs.18343	ESTs	3.3
10	415131	D61119		gb:HUM15BC11B Clontech human fetal brain	3.3
	412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogana)	3.3
	435070	AIB21270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	3.3
	444443	A1149286	Hs.55099	rab6 GTPase activating protein (GAP and	3.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinese inhibito	3.3
15	454145	AAD46872	Hs.62798	ESTs	3.3
~ ~	405264	70.040012	175.UE1UU	2013	3.3
	411849	AW964970	Hs.18851	ESTs, Moderately similar to KIAA1276 pro	3.3
	416816	T71168	Hs.119567	ESTs, Weakly similar to A47582 8-cell pr	3.3
					3.3
20	435325	A1038388	Hs.119309	ESTs	
20	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	Al369472	Hs.65407	ESTs	3.3
	429106	AA446612		gb:zw85g07.s1 Soares_total_letus_Nb2HF8_	3.3
25	405720				3.3
25	400889	Dagger -	11 56:	104 10007 1 1	3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	422094	AF129535	Hs,272027	F-box only protein 5	3.3
	425374	A1904013		gb:MR-8T041-220199-104 BT041 Homo sapien	3.3
20	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
30	42737 4	Al150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	Al336596	Hs.156294	ESTs	3,3
	457604	A1004397	Hs.334552	Homo sapiens cDNA FLJ14930 fs, clone PL	3.3
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.3
35	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	3.3
	458885	AA411303	Hs.30022	ESTs, Weakly similar to NAH6_HUMAN SODIU	3.3
	429608	U49250	Hs.210862	T-box, brain, 1	3.2
	437454	AL390159	Hs,269B12	Hamo sapiens mRNA; cDNA DKFZp761M0415 (f	3.2
	430503	AA533574	Hs.152274	ESTs	3.2
40	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	3.2
	421698	T89677	Hs.324323	ESTs	3.2
	412321	AW936913		gb:RC1-DT0029-030200-012-908 DT0029 Homo	3.2
	422219	AW978073	Hs.1010	regulator of milatic spindle assembly 1	3.2
	454962	AW847645	11011010	gb:JL3-CT0213-280100-056-A04 CT0213 Homo	3.2
45	441705	AI087052	Hs.55993	ESTs	3.2
	403619	70001002	112222200	LUIS	3.2
	435608	AW183971	Hs.250896	ESTs .	3.2
	426701	A1968103	Hs.209461	Homo sapiens cDNA FLJ12836 fls, clone NT	3.2
	401132	14200100	(10.203401	Horio appens son a restance in the late	3.2
50	407764	BE008347		ab:CMO-BN0154-080400-325-h04 BN0154 Homo	3.2
50	409425	U40462	Hs.54452	zinc finger protein, subtamily 1A, 1 (lk	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	443603	BES02601	Hs.134289	ESTs, Weakly similar to KIAA 1063 protein	3.2
	419935	AI792788	110.107203	gbxx991d05.y5 NCI_CGAP_Kid5 Homo saplens	3.2
55	455571	BE003714		gb:QV3-BN0096-200400-161-e01 BN0096 Homo	3.2
	406592	DEGWI 17		Source - Names - Charles - Letters - Charles Health	3.2
	446530	AV658909	Hs.282642	ESTs -	3.2
	454466	AA984138	Hs.155101	ATP synthase, H+ transporting, mitochond	3.2
	401449	741304130	FIB. 100 101	Vit. plunger, i.s. nerteborouh' unterneur	3,2
60	431198	AW974436	Hs.154929	ESTs	3.2
00					3.2
	422183 459458	AA431698 AA460445	Hs.112794	Human DNA sequence from clone 1068E13 on gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	3.2
	421308		U~ 400049		3.2
	427335	AA687322 AA448542	Hs.192843 Hs.251677	teucine zipper protein FKSG14 Gantigen 7B	3.2
65	455236	AW875972	115.231011	gb;CM3-PT0014-071299-051-b05 PT0014 Homo	3.2
05	425158	AA351364		gb:EST59099 Infant brain Homo saplens cD	3.2
		704001004		Anteo 192022 Harm man Louin esticate de	
	404588 4130B7	BE064655		gb:RC1-8T0313-301299-012-c09 BT0313 Homo	3.2 3.2
70	444910 426660	A1201849 NM_002719	Hs,171734	gbtqs76g04.x1 NCL_CGAP_Pr28 Homo saplens protein phosphatase 2, regulatory subunt	3.2 3.2
70					
	438315	R56795	Hs.82419	ESTs	3.2
	425523	AB007948	Hs.158244		3.2
	419340	AA236590	Hs.87530	ESTS	3.2
75	425636	AK001243	Hs.158370	hypothetical protein FLJ10381	3.2
, ,	430553	AW392821	15- 47000-	gb:CM4-ST0275-021299-053-h09 ST0275 Homo	3.2
	457030	Al301740	Hs.173381	dinydropyrimidinese-like 2	3.2
	447375	Al376660	Hs.257822		3.2
	408334	AW514652	Hs.321637		3.2
80	410085	AA428482	Hs.58589	glycogenin 2	3.2
OU	410536	N39533	N- concar	gb:yv27d04.s1 Soares fetal liver spleen	3.2
	448495	AW136516	Hs.208515	ESTs	3.2
	405634 431098	AIRIEGA ACE	Hs.249230	riborariogra I (2) El allankander data	3.2
	~0.0030	AW501465	110.245230	ribanuclease L (2',5'-oligoisoadenylate	3.2

	421581	D89331	No tocom	1. 1. 1. 1 2	_
	440633		Hs.105932	short stature homeobox	3,1
		AI140686	Hs.263320	ESTs	3.1
	453264	AA034137	Ha.271955	ESTs	3.1
5	411656	AW855576	11. 0000 00	gb::CM4-CT027B-221099-027-d01 CT0278 Нолю	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	3.1
	426591	AA431127	Hs.98685	ESTs	3.1
	446966	C01448	Hs.300611	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
10	455170	AWB60972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.1
10	41620B	AW29116B	Hs.41295	ESTs, Wealdy similar to MUC2_HUMAN MUCIN	3.1
	423657	AL045128	Hs, 1691	glucan (1,4-alpha-), branching enzyme 1	3.1
	400816				3,1
	410307	AF022913	Hs.62187	phosphaticylinositol glycan, class K	3.1
15	440046	AW402306	Hs.6877	hypothetical protein FL/10483	3.1
15	452824	W27843	Hs.73965	splicing factor, arghlne/serine-rich 2	3.1
	400315	U46120	Hs.193392	Human expressed unknown mRNA	3,1
	411965	BE467339	Hs.280115	EST\$	3.1
	416316	H58721	Hs.271628	EST _B	3.1
20	400813				3.1
20	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	3.1
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.1
	418693	A1750878	Hs,87409	thrombospondin 1	3.1
	416258	N45661	Hs.90011	adenylosuccinale synthase	3.1
25	405093				3.1
25	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	422654	AA314316	Hs.163725	ESTs	3.1
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	3.1
20	400441	M15530	Hs.99879	B-cell growth factor f (12kD)	3.1
30	402790				3.1
	438563	AA810865	Hs.134746	ESTs, Weakly similar to A46010 X-linked	3,1
	447524	D80449	Hs.45177	ESTs	3.1
	445835	BE277929	Hs.11081	UBX domain-containing 2	3.1
0.0	415979	H16427	Hs.271501	ESTs, Weakly similar to 154374 gene NF2	3.1
35	434479	AI138213	Hs.162035	olfactory receptor, family 52, subfamily	3.1
	426724	AA383623	Hs.293616	ESTs	3.1
	41B105	AW9374BB	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	3.1
	40560B			, ,	3.1
40	406508				3.1
40	421216	AV649282	Hs.102664	vesicle-associated membrana protein 4	3.1
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	3.1
	404288			, , , , , , , , , , , , , , , , , , , ,	3.1
	429878	AA460188	Hs.127263	ESTs	3,1
	439834	Al754576	Hs.124523	EST8	3.1
45	454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo	3.1
	450491	BE045604	Hs.202301	ESTs	3.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.1
	400579			•	3.1
	402953				3.1
50	404285				31
	426890	AA393167	Hs.41294	ESTs	3.1
	457770	BE065030	Hs.124179	ESTS	3.1
	435477	BE218708	Hs.117270	hypothetical protein FLJ14345	3.1
	436391	AJ227892	Hs.146274	ESTs	3.1
55	456083	U46922	Hs.77252	fragile histidine tried gene	3.1
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.1
	430101	AF110002	Hs.233363	guanylate cyclase activator 1C	3.1
	449238	AA428229	Hs,331561	muscle-specific RING-finger protein 3	3.1
<i></i>	452605	AW968557	Hs.90012	hypothetical protein FLI23441	3.1
60	456323	AW752389	Hs.87296	Homo sapiens cDNA FLJ20269 fis, clone HE	3.1
	429828	AB019494	Hs.225767	IDN3 protein	3.1
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	3.1
	452762	AW501435	Hs.278582	v-ekt murine thyrnoma viral oncogene horno	3.1
	401344				3.1
65	455511	BE144762		gb:CMO-HT0180-041099-065-b04 HT0180 Homo	3,1
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	3.1
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.1
	423600	Al633559	Hs.310359	ESTs	
~^			Hs.180171	Homo saplens cDNA FLJ10417 fis, clone NT	3.1 3.0
70	427667	AK001279			
		AK001279 AB006834	147100111	ob:Homo saciens mRNA for HRIV Fah NE.VH	
	427667			gb:Homo saplens mRNA for HRV Fab N6-VH,	3.0
	427667 407257 457041	AB006834 AA399018	Hs.250835	gb:Homo saplens mRNA for HRV Fab N6-VH, ESTs	3.0 3.0
	427667 407257 457041 421482	AB006834	Hs.250835 Hs.104715	gb:Homo saplens mRNA for HRV Fab N6-VH, ESTs Inversin	3.0 3.0 3.0
	427667 407257 457041 421482 459062	AB006B34 AA399018 AL135462 AA059246	Hs.250835 Hs.104715 Hs.110293	gb:Homo saplens mRNA for HRV Fab NG-VH, ESTs Invensin ESTs	3.0 3.0 3.0 3.0
75	427667 407257 457041 421482 459062 436475	AB006834 AA399018 AL135462 AA059246 R58808	Hs.250835 Hs.104715 Hs.110293 Hs.86149	gb:Homo saplens mRNA for HRV Fab NG-VH, ESTs Inversit ESTs phosphoinositol 3-phosphate-blading prot	3.0 3.0 3.0 3.0 3.0
75	427667 407257 457041 421482 459062 436475 411622	AB006834 AA399018 AL135462 AA059246 R58806 A1807894	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274	gb:Homo seplens mRNA for HRV Fab N6-VH, ESTs Inversit ESTs phosphoinositol 3-phosphete-binding prot Homo sepiens mRNA; cDNA DKFZp584B176 (fr	3.0 3.0 3.0 3.0 3.0 3.0
75	427667 407257 457041 421482 459062 436475 411622 417489	ABC06834 AA399018 AL135462 AA059246 R58806 A1807894 AW953341	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274 Hs.22573	gbt-flomo saplens mRNA for HRV Fab N6-VH, ESTs Inversin ESTs phosphoinositol 3-phosphete-binding prot Homo sapiens mRNA; cDNA DKFZp564B176 (fr ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0 3.0 3.0 3.0 3.0 3.0
75	427667 407257 457041 421482 459062 436475 411622 417489 418454	ABC06834 AA399018 AL135462 AA059246 R58808 AI807894 AW953341 AA315308	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274	gbtHomo saplens mRNA for HRV Fab NG-VH, ESTS Inversin ESTs phosphoinositol 3-phosphete-binding prot Homo saplens mRNA; cDNA DKF2p564B176 (fr ESTs, Wealdy similar to ALU1_HUMAN ALU S Inypothetical protein FL114991	3.0 3.0 3.0 3.0 3.0 3.0 3.0
	427667 407257 457041 421482 459062 436475 411622 417489 418454 409699	AB006B34 AA399018 AL135462 AA059246 R58308 AIB07694 AW953341 AA315308 BE154650	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274 Hs.22573 Hs.195870	gbtHomo saplens mRNA for HRV Fab NG-VH, ESTs Inversin ESTs phosphoinositol 3-phosphate-binding prot Homo saplens mRNA; cDNA DKF2p564B176 (fr ESTs, Weakly similar to ALU1_HUMAN ALU S hypothetical protein FL114991 gbtPM3-HT0344-071299-003-c08 HT0344 Homo	3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0
75 80	427667 407257 457041 421482 459062 436475 411622 417489 418454 409699 438394	AB006B34 AA399018 AL135462 AA059246 R58308 AIB07694 AW953341 AA315308 BE154650 BE379623	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274 Hs.22573 Hs.195870 Hs.27693	gbtHomo saplens mRNA for HRV Fab N6-VH, ESTs Inversin ESTs phosphoinositol 3-phosphate-binding prot Homo saplens mRNA; cDNA DKF2p5648176 (fr ESTs, Weakly similar to ALU1_HUMAN ALU S hypothetical protein FLJ14991 gbtPM3-HT0344-071299-003-c08 HT0344 Homo pspt6y/protyl isomersse (cyclophišn)-1	3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0
	427667 407257 457041 421482 459062 436475 411622 417489 418454 409699 438394 443741	AB006B34 AA399018 AL135462 AA059246 R58308 AIB07694 AW953341 AA315308 BE154650	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274 Hs.22573 Hs.195870	gbtHomo saplens mRNA for HRV Fab NG-VH, ESTs Inversin ESTs phosphoinositol 3-phosphate-binding prot Homo saplens mRNA; cDNA DKF2p564B176 (fr ESTs, Weakly similar to ALU1_HUMAN ALU S hypothetical protein FL114991 gbtPM3-HT0344-071299-003-c08 HT0344 Homo	3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0
	427667 407257 457041 421482 459062 436475 411622 417489 418454 409699 438394	AB006B34 AA399018 AL135462 AA059246 R58808 AIB07894 AW953341 AA315308 BE154650 BE379623 AW451759	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274 Hs.22573 Hs.195870 Hs.27693 Hs.145420	gbt-Homo saplens mRNA for HRV Fab N6-VH, ESTs Inversin ESTs phosphoinositol 3-phosphete-binding prot Homo saplens mRNA; cDNA DKF2p564B176 (fr ESTs, Weakly similar to ALU1_HUMAN ALU S Inypothetical protein FL144991 gbt-PM3-HT0344-071299-003-c08 HT0344 Homo peptidy/opolyl isomerase (cyclophišn)-1 ESTs	3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0
	427667 407257 457041 421482 459062 436475 411622 417489 418454 409699 438394 443741 405090	AB006B34 AA399018 AL135462 AA059246 R58308 AIB07694 AW953341 AA315308 BE154650 BE379623	Hs.250835 Hs.104715 Hs.110293 Hs.86149 Hs.47274 Hs.22573 Hs.195870 Hs.27693	gbtHomo saplens mRNA for HRV Fab N6-VH, ESTs Inversin ESTs phosphoinositol 3-phosphate-binding prot Homo saplens mRNA; cDNA DKF2p5648176 (fr ESTs, Weakly similar to ALU1_HUMAN ALU S hypothetical protein FLJ14991 gbtPM3-HT0344-071299-003-c08 HT0344 Homo pspt6y/protyl isomersse (cyclophišn)-1	3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0

	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	3.0
	406364				3.0
5	418409	AA219332	Hs.120B69	ESTs, Weakly similar to R107_HUMAN H-REV	3.0
3	427050	AA397789	Hs.161803	ESTs	3.0
	431778 448405	ALOB0276 AW207634	Hs.268562 Hs.170849	regulator of G-protein signalling 17 ESTs	3.0 3.0
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.0
	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
10	418888	AU076801	Hs.89436	cadherin 17, Li cadherin (liver-intestin	3.0
	418432	M14156	Hs.85112	Insulin-like growth factor 1 (sometomedi	3.0
	426424	BE081745	Hs.272188	Homo sapians cDNA FLJ12090 fis, clone HE	3.0
	419505	AA243560	Hs.143061	ESTs	3.0
16	403743				3.0
15	415452	F09134	Hs.12839	ESTs	3.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.0
	447046 455851	AA326187 BE146879	Hs.17170	G protein-coupled receptor 4 gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0 3.0
	400227	DC 140013		gp.qv4-n10222-201030-014-0111110222110110	3.0
20	436219	AK001695	Hs.146589	hypothetical protein FLJ10701	3.0
	439037	AF075084	((gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.0
25	403513				3.0
25	425745	U44060	Hs.14427	Homo saplens cDNA: FLJ21800 fis, clone H	3.0
	440122	A1733011	Hs.127678	ESTs	3.0
	448446 422563	AI521251 BE299342	Hs.171030 Hs.19348	ESTs	30 30
	448130	AW271635	Hs.170717	hypothetical protein FLJ13119 ESTs	3.0
30	42028B	AW071225	Hs.245556	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	436643	AA757626	Hs.10941	ESTs, Weeldy similar to IPP1_HUMAN PROTE	3.0
	448966	AW372914	Hs.86149	phosphoinesitol 3-phosphate-binding prot	3.0
25	404513				3.0
35	412074	S74683	Hs.73139	AOP-ribosyltransferase 1	3.0
	407762	AW235638	Hs.29475	ESTs	3.0
	403396 436938	AW139680	Hs.161393	ESTs	0.E
	458090	Al282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	3.0 3.0
40	400708	14202170	, KI.UVETO	LOTS, Tighty Strike B 1705_TOWN TO ONE	2.9
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.9
	444500	R41398	Hs.6996	ESTS	2.9
	403786				2.9
15	430187	AI799909	Hs.158989	ESTs	29
45	451700	A(470252	Hs.29553	EST8	2.9
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.9
	457503 446251	AW970244 AW857156	Hs.1621B3 Hs.282589	ESTs ESTs, Wealdy similar to 138022 hypotheti	2.9 2.9
	406327	7111007 100	110.202005	CO16, Weary Sittles to 100022 hypotheti	2.9
50	434671	R34758		gb:yg61g02.r1 Boares infant brain 1NIB H	29
	430175	AA468724		gbtne09a06.s1 NCI_CGAP_Co3 Homo seplens	29
	454186	BE141030		gb;MR0-HT0067-201099-002-h11 HT0067 Home	2.9
	449459	BE546846	Hs.195048	ESTs	2.9
55	435934	R19382	Hs.117869	ESTs	29
55	400325 408408	M85292	Hs.247924 Hs.44690	Homo sapians endogenous HIV-1 related se	29 29
	414514	AF070571 BE327365	Hs.280187	Homo sepiens clone 24739 mRNA sequence ESTs	29
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sepiens mRNA; cDNA DKFZp434N079 (fr	2.9
60	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	29
	424726	AK001007	Hs.138760	Homa sepiens cONA FLJ10145 fis, clone HE	2.9
	456186	W26642		gb:34b8 Human relina cDNA randomly prime	29
	412222	AA528283	Hs.292737	ESTS	2.9
65	459201 422511	AW391177 AU076442	Hs.117938	gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9 2.9
0.5	435579	Al332373	Hs.156924	collagen, type XVII, atpha 1 ESTs	29
	417027	AA192306	Hs.23926	triacin	29
	415533	174009	Hs.268738	ESTs, Weekly similar to ALU7 HUMAN ALU S	2.9
	445909	BE262656	Hs.32603	hypothetical protein MGC3279 similar to	29
70	418343	AA216372	Hs.159501	EST ₈	2.9
	459440	BE048054		gb:tz46c03.y1 NCt_CGAP_Brn52 Homo saplen	2.9
	403341	4)7700774	11- 80000	TRUE AND ALL MANAGEMENT AND ADDRESS OF THE ADDRESS	2.9
	445635 453830	A)769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	29
75	453830 455866	AA534295 BE149024	Hs.20953	ESTs gb:CM0-HT0249-291099-084-c04 HT0249 Homo	29
, ,	407676	AW064111	Hs.279823	G0:CMC-H10249-291099-084-C04 H10249 H0IIIO ESTs	2.9 2.9
	437913	A1140825	Hs.121623		2.9
	443458	R05385	Hs.143509		2.9
00	457049	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	2.9
80	400491	H25530	Hs.50868	solute cerrier family 22 (organic cation	29
	456189	H91010	Hs.44940	ESTs	2.9
	441874 416483	AA970389 H58311	Hs.128055 Hs.165077		2.9 2.9
	TIVE	1100011	19.1030/1	LUIS	2.9

	420879	N31165	Hs.238837	ESTs, Weakly similar to \$43603 RNA bindl	2.9
	446447	Al300402	Hs.202250	ESTs	29
	439953	AA918129	Hs.124638	ESTs	29
		ACC IOIZO	115.124000	Cors	
~	400643				2.9
5	436594	A)419982	Hs.156189	ESTs .	2.9
	438402	D16902	Hs.42915	ARP2 (actin-related protein 2, yeast) Ito	2.9
	451353	N21043	Hs.42932	ESTs	2.9
	419791	AI579909	Hs.105104	ESTS	29
10	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
10	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DXFZp434O1214 (f	2.9
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.9
	45277B	R71338	Hs.5921		29
				Homo saplens cDNA: FLJ21592 fis, clone C	
	457178	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	29
1.5	401526				29
15	408751	N91553	Hs.258343	ESTs	2,9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
		AA195667			
	417320		Hs.86022	ESTS	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	29
20	453901	8E065902		gb:RC2-870318-150200-011-b09 BT0318 Homo	2.9
	421847	NM_014717	Hs.108884	KIAA0390 gene product	2.8
	434424	A)81 1202	Hs.325335	Homo saplens cDNA: FLJ23523 fis, done L	2.8
	422225	BE245652	Hs.118281	zinc finger protein 266	28
~ =	403011				2.8
25	405170				2.8
	435878	R08330	Hs.20152	EST8	2.8
	436194	AKD01074	Hs.333435	Homo sepiens cDNA FLJ10212 fis, clone HE	2.8
	400394	AF040257	Hs.283818	Homo saplens TNF receptor homotog mRNA,	28
	411244	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	2.8
30	441817	AW969705	Hs.293332	ESTs	2.8
-		AA380267			
	456118		Hs.78277	DKFZP434F2021 protein	2.8
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.8
	442717	R88362	Hs.180591	ESTs, Weakly similar to 123976 hypotheti	2.8
	402131				2.8
35	428959	AF100779	Hs.194660	WNT1 Inducible signaling pathway protein	2.6
	438160	AA779332	Hs.122671	ESTS	2.8
	407594	AW057584	Hs,160581	ESTs	2.8
	417877	A1025829	Hs.86320	ESTs	28
	439235	N45513	Hs.46608	ESTs	28
40	451257	AA016255	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.8
	437113	AA744693	110001000		
			11000 /	gb:ny26c10.s1 NCI_OGAP_GCB1 Homo saplens	2.8
	430882	BE174240	Hs.79024	helerogeneous nuclear ribonucleoprolein	28
	409978	D31897	Hs.57714	double C2-like domains, alpha	28
	410572	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
45	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2,8
	417827	779366	Hs.108258	actin binding grotein; macrophin (microf	2.8
	420206				
		M91463	Hs.95958	soluje carrier family 2 (facilitated glu	28
	449676	AW380579	Hs.209657	ESTs	2.8
~^	454778	AW820199		gb:QV2-ST0296-190100-029-a07 ST0296 Homo	28
50	451203	AW070604	Hs.46517	ESTs	2.8
	4501B0	AW449644	Hs,257182	ESTs	2.8
	409432	D49372	Hs.54460		2.8
				small inducible cytokine subfamily A (Cy	
	442264	AJ278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	28
	450003	AA777809	Hs.191995	ESTs	2.8
55	401602				2.8
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.8
	436187	AK000998	Hs.297221	Homo sapiens cONA FLJ10136 is, done HE	2.8
	415652	T79213	Hs.272073	ESTs	2.8
C 0	404076				· 2.8
60	409416	AW388359	Hs.10667	E8Ts	2,8
	420814	AA721156	Hs.190440	ESTs .	28
	426960	AA393713		gb:zf71h04.r1 Sources_testis_NHT Homo sap	28
	419227	BE537383	Hs.89739		
				cholinergic receptor, nicotinic, beta po	2.8
65	448597	BE613250	Hs.98265	KIAA1877 protein	2.8
65	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	2.8
	433077	AA314262	Hs.301917	YDD19 protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.B
	447410	Al470235	Hs.172698	EST .	2.8
	414652				
70		A1620599	Hs.72068	ESTs	2.8
, ,	430454	AW469011	Hs.105635	ESTs	28
	412417	AA102268	Hs.158622	ESTs	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
	401098				2.8
75		44972750	Lla Dorge	Name and Otto to Ma \$4774	
, ,	454038	AA374756	Hs.93560	Homo saptens mRNA for KIAA1771 protein,	28
	403549				28
	414394	A1904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-101 DT0041 Homo	2.8
	433513	A1566356	Hs.171437	ESTE	28
80	446677				
		AI800311	Hs.156291	ESTs	2,8
	457756	AA126136	Hs.38125	Interferon-induced protein 75, 52kD	28
	450895	N66727	Hs.10957	ESTs	2.8
	434352	AF129505	Hs.86492	small muscle grotein, X-linked	2.8

	44D2F0	AAA04290	Lie 121420	EPT-	2.8
	449358 422816	AA001229 AA323586	Hs.131436 Hs.93235	ESTs ESTs	2.6 2.8
	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
5	446870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to 138022 hypotheti	28
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	458023	AW978161	Hs.268555	5-3 exoribonuclease 2	2,B
10	422260	AA315993	Hs.105484	regenerating gene type IV	2.8 2.8
10	429638 408936	A1916662 Al.138043	Hs.211577 Hs.293549	kinecila 1 (kinesin receptor) ESTs	2.8 2.8
	411762	AW860972	1 10-2000-001	gb:QV0-CT0387-180300-167-h07 CT0387 Homo	28
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
	455310	AW893961		gb:RC4-NN0027-050400-011-d11 NN0027 Homo	2.8
15	406992	S82472		gb:bela -pol=DNA polymerase bela (axon a	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo saplens cDNA FLI20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTS	2.7
20	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7 2.7
20	445017 411726	AL205493 AW858612	Hs.176860	ESTs gb:CM3-CTD341-190400-152-h12 CT0341 Homo	2.7
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	2.7
	416B05	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	423020	AA3B3092	Hs.1608	replication protein A3 (14kD)	2.7
25	427134	AA398409	Hs.173561	EST	2,7
	435689	AA694284		gb:zi35c02.s1 Soares_fetal_liver_spleen_	2.7
	429282	N27596	Hs.21342	ESTs	2.7
	435731	AA699581	Hs.166811	ESTS	2,7 2.7
30	426682 421274	AV660038 BE160327	Hs.2056 Hs.104572	UDP glycosyltransferase 1 family, polype ESTs	2.7
20	403776	OL 100321	113.10407 E	1016	2.7
	409526	BE298751	Hs.55014	hypothetical protein FLJ10206	2.7
	410201	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	2.7
2.5	427839	AA608823	Hs.98244	ESTs	2.7
35	447884	H29505		gb:ym60d10.r1 Soares Infant brain 1NIB H	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	422988 442772	AW673847	Hs.97321 Hs.5957	ESTS	27 27
	434890	AW503680 AF161345	Hs.283930	Homo sapiens clone 24416 mRNA sequence Homo sapiens HSPC082 mRNA, partial cds	2.7
40	412400	AW948066	112200000	gb:RC0-MT0012-290300-031-h10 MT0012 Homo	2.7
	413998	AW103807	Hs.243933	ESTs	2.7
	403677				2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
15	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo saplens	2.7
45	432591	AA543238	Hs.146144	ESTB	2.7
	446800 454938	A)341635 AW846134	Hs.156486	ESTs gb:QV0-CT0179-091199-049-d02 CT0179 Homo	2.7 2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
	445233	AV653034	Hs,297559	ESTs	2.7
50	448756	Al739241	Hs.171480	ESTs	2.7
	418379	AA218940	Hs.137516	fidgetin-like 1	2.7
	435068	H16262	Hs.31415	ESTs	2.7
	406092	4400000	13- 074004	COT- HILLS -2-1-1- THOS NOW AND THE	2.7
55	422036 441541	AA302647	Hs.271891	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.7 2.7
20	451395	AA938663 Al082419	Hs,199828 Hs,114761	ESTs ESTs	2.7
	455880	BE153208	1101	gb:PMO-HT0335-050400-007-F10 HT0335 Homo	27
	459275	AIB08913	Hs.339352	Homo septens brother of CDO (BOC) mRNA,	27
60	423949	A)014546	Hs.130912	ESTs	2.7
60	435420	Al928513	Hs.59203	ESTs	2.7
	439418	Al202149 AW820852	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH gb:RC2-ST0301-120200-011-112 ST0301 Homo	2.7 2.7
	454790 447453	AW608645	Hs.18800	hypothetical protein FLI20281	2.7
	454767	BE069199	710.10000	gb:QV3-BT0379-010300-105-g03 BT0379 Homo	2.7
65	413252	BE074910		gb:RC5-8T0580-170300-021-F12 BT0580 Homo	2.7
	402429				2.7
	403760				2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
70	435448	H17132	Hs.27085	ESTs hypothetical protein FLJ22004	2.7
,0	445706 422171	AA305620 U50529	Hs.108812 Hs.112434		2.7 2.7
	459023	AW968226	Hs.60798	ESTs	2.7
	443246	T75157	Hs.337603		2.7
	404569				27
75	4101B1	AI46B210	Hs.261285		2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	427038	NM_014633			2.7 2.7
	449880 455992	A1673006 BE179015	Hs,231948	ESTS ab:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
80	415268	R53935	Hs.287827		2.7
-	446554		Hs,301785		2.7
	452512		Hs.337636		2.7
	440728	AW086077	Hs.153272	! Homo saplens cDNA: FLI22715 fis, clone H	2.7

	419481	A1879195	Hs.90606	15 kDa selenoprotein	2.7
	454352	AW389668	LP:30000	gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.7
	422831	R02504	Hs.332943	ESTs	27
_	413645	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	2.7
5	426872	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapie	2.7
	459160 421338	A1904723 AA287443		gb:CM-BT066-120299-092 BT068 Homo saplen gb:zs52c10.r1 NCI_CGAP_GCB1 Homo saplens	2,7 2.7
	446002	Al346468	Hs.145789	ESTs	2.7
• •	454716	AW8506B4		gb:\$L3-CT0219-160200-063-D12 CT0219 Homo	2.7
10	406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	27
	453128	AW026516	Hs.31791	acylphosphalase 2, muscle type	27
	408691 454754	AW250525 AW819191		gb:2821626.5prime NIH_MGC_7 Homo sapiens gb:CM1-ST0283-071299-061-d08 ST0283 Homo	2.7 2.7
	439451	AF0B6270	Hs.278554	heterochromatin-like protein 1	2.7
15	445225	Al216555	Hs.202398	ESTs	27
	427175	H06924	Hs.23782	hypothetical protein FLJ12847	2.7
	411816 420426	AWB64609	Un 100400	gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.7 2.7
	438135 405981	Al253025	Hs.190426	ESTs	2.7
20	406005				2.7
	430762	A1343652	Hs.105667	ESTs	2,7
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	27
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.7 2.7
25	434684 445660	AA737282 AI702668	Hs.190911 Hs.201955	ESTs	2.7
	400844	74702000	120201000	2015	2.6
	415725	BE219771	Hs.237146	hypothetical protein FLJ12752	26
	420159	Al572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fls, clone C	2.6
30	408812	BE397160	Hs.254763	ESTs, Wealdy similar to A42442 integrin Alg5, S, cerevisiae, homolog of	2.6 2.6
20	430052 440310	AF102850 AA878939	Hs.227933 Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	26
	417252	AA195014	Hs.85971	ESTs	2.6
35	427167	AI239607	Hs.99196	hypothetical protein MGC11324	2.6
33	431613 414546	AA018515 BE379492	Hs.264482	Homo sepiens mRNA; cDNA DKFZp761AD411 (f gb:801236215F1 NIH_MGC_44 Homo sepiens c	2.6 2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.6
40	442240	A1791883	Hs.292719	ESTs	2.6
40	452821	AW471181	Hs.160874	ESTs	2,6
	410238 419236	N94320 AA330447	Hs.144225 Hs.135159	EST8 Homo sapiens cDNA FLJ\$1481 fis, clone HE	2.6 2.6
	440801	AA906366	Hs.190535	ESTs	2.6
	440274	R24595	Hs.7122	scraple responsive protein 1	2.6
45	411597	AW852925		gb:PM0-CT0248-131099-001-110 CT0248 Homo	2.6
	417956 420621	AA210704 AA278808	Hs.190465	ESTs gb:zs79c09.r1 NCL_CGAP_GCB1 Homo sapiens	2.6 2.6
	425176	AW015844	Hs.155005	TEA domain family member 1 (SV40 transcr	26
50	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	2.6
50	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	426098	NM_014906	Hs.166351	KIAA1072 protein	· 26
	435113 438188	AA665469 AA779975	Hs.117136 Hs.128859	ESTs ESTs	2.6
	445550	A1242754	Hs.137306	ESTs	2.6
55	458804	Al.157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.6
	436407 425195	T88803 AA352026	Hs.271507 Hs.94319	ESTs, Weekly similar to TIM_HUMAN PROBAB VPS10 domain receptor protein	2.6 2.6
	418282	AA215535	Hs.98133	ESTs	2.6
60	442757	Al739528	Hs.28345	ESTa	2.6
	413470	N20934	11 05400	gb:yx54c11.s1 Soares melanocyte 2NbHM Ho	26
	428527 441209	Al902398 AA922939	Hs.34492 Hs.135742	Cyt19 protein ESTs	2.6 2.6
	458679	AW975460	Hs.143563		2.6
65	442279	AW867006	Hs.159970		2.6
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	26
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Home saplens	2,6
	404845 411693	AW857271		gb:CMO-CT0307-210100-158-g09 CT0307 Homo	2.6 2.6
70	438298	H23542	Hs.181788		2.6
	444517	eeeeela	Hs.146883		2.6
	455870	AW452631	Hs.313803		2.6
	457630 424D15	AI580803 N95696	Hs.112627 Hs.166361		2.6 2.6
75	417563	AA203701		gbzx52a10.r1 Soares_fetal_liver_splean_	2.6
	413174	AA723564	Hs.191343	ESTs	2.6
	438875	AA827640	Hs. 189059		2.6
	440700 423257	AW952281 AW161039	Hs.296184 Hs.125876		2.6 2.6
80	431086	Al829692	Hs.211581		2.6
_	409337	H71289	Hs.220535	ESIS	2.6
	442818	AK001741	Ha.8739	hypothetical protein FLJ10879	2.6
	410004	A1296027	Hs.5057	carboxypeptidase D	2.6

	455935	BE150687		gb:CM0-HT0395-280100-169-b09 HT0395 Homo	26
	403273		11- 450400	Internal the state of the state	2.6
	445955 425626	AA332209 A1537536	Hs.158196 Hs.173519	transcriptional adaptor 3 (ADA3, yeast it ESTs	2.6 2.6
5	451531	AA018311	Hs.114762	ESTs	2.6
-	428085	AA421081	Hs.12388	ESTs	2.6
	429761	A12767B0	Hs.135173	ESTs	26
	437958 442666	BE139550 W74633	Hs.121668 Hs.303720	ESTs, Moderately similar to PC4259 femi	2.6 2.6
10	4130B8	BE064962	1 13.5051 20	gb:RC1-BT0313-130400-016-c02 BT0313 Hemo	2.6
	419107	AW085152	Hs.292987	ESTs	2.6
	435766	R11673	Hs.186498	ESTs	26
	452879 440400	AW905328 AA994364	Hs.180842 Hs.125594	ribosomat protein 1.13 ESTs, Wealdy similar to T25472 hypotheti	2.6 2.6
15	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	424146	AA705092	Hs.202368	ESTs	2.6
	439950	AW937417	Hs.293561	ESTs	2.6
	410366 417485	Al267589 AA203304	Hs.302689 Hs.32826	hypothetical protein CGI-130 protein	2.6 2.6
20	412566	AW962574	ISIOEUEU	gb:EST374647 MAGE resequences, MAGG Homo	2.6
	416498	U33632	Hs.79351	potassium channel, sublamily K, member 1	2.6
	440397	AA884448	Hs.157239	ESTS	2.6 2.6
	451236 411819	A1767406 AVV947884	Hs.207026	ESTs, Weakly similar to B56205 transcrip gb:PM1-MT0010-200300-001-g08 MT0010 Homo	26
25	430357	AW976789	Hs.165607	ESTs	2.6
	432889	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	2.6
	427506 401614	AK000134	Hs.179100	hypothetical protein FLJ20127	26 26
	404531	Z25884	Hs.121483	chloride channel 1 , skeletal muscle (Th	2.6
30	426698	AA394104	Hs.97489	ESTs	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160 419323	Al467915 Al092379	Hs.36053 Hs.135275	ESTs ESTs	2,6 2.5
	442813	Al018435	Hs.270970	ESTS	25
35	436196	AK001084	Hs.333498	Homo saplens cDNA FLJ10222 fis, clone HE	2.5
	433561 434059	BE540937	Hs.20104 Hs.235456	hypothetical protein FLJ00052	2.5
	454B36	AA649162 AWB33711	HS.230430	ESTs qb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5 2.5
40	458589	AV654623	Hs.288141	hypothetical protein MGC3166	2.5
40	459716	D 450 12	11 04000	rov.	2.5
	436340 428020	R42246 L19058	Hs.21606 Hs.181581	ESTs glutamate receptor, ionotropic, kainate	2.5 2.5
	416951	AA190926	Hs.190785	ESTs, Moderately similar to \$65657 alpha	25
15	401078				2.5
45	410644	AW902125		gb:QV0-NN1022-120500-220-li12 NN1022 Forno	2.5 2.5
	411660 425201	AW855718 AA352111		gb;RC3-CT0279-070100-021-e03 CT0279 Homo gb;EST60061 Activated T-cells XX Homo sa	25
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
50	439096	AA830185	Hs.269680	ESTs	2.5
50	442627 457 7 99	AI027990 AF22018B	Hs.132303 Hs.236510	ESTs uncharacterized hypothalamus protein HTM	2.5 2.5
	428799	Al478619	Hs.104677	ESTs	2,5
	450402	BE218027	Hs.89969	ESTs	25
55	411156 431673	AW819939 AW971302	Hs.273629	ESTS ESTs	2.5 2.5
55	415706	8E182587	Hs.293233 Hs.57485	ESTs	2.5
	412BB2	BE006919	Hs.134106	ESTs	2.5
	441300	R35063	Hs.181536	EST&	2.5
60	413257 434662	BE075035 AA641957		gb:PM3-BT0584-260300-002-g05-BT0584 Homo gb:ns18d08.r1 NCL_CGAP_GCB1 Homo sapiens	2.5 2.5
- •	455255	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.5
	417137	U46265	Hs.81281	mitochondrial ribosomal protein S21	25
	417909 458043	R35614 AW979009	Hs.326108	gbcyg66e08.r1 Soares infant brain 1NIB H ESTs	2.5 2.5
65	417006	AW67360B	Hs.80758	aspartyl-iRNA synthetese	2.5
	442006	AW975183	Ha.292663	ESTs, Weakly similar to S72482 hypotheti	25
	455756 454032	BE079307	11-404202	gb:RC1-BT0823-120200-011-g09 BT0623 Homo	2.5 2.5
	444983	W31790 A1916973	Hs.194293 Hs.213603		2.5
70	443526	AW792804	Hs.134002		2.5
	454532	AA344685	Hs.58831	regulator of Fas-induced apoptosis	2.5
	428832 442003	AA578229 AW297497	Hs.324239 Hs.201891		2.5 2.5
	452768	AW069459	Hs.61539	ESTs	2.5
75	411355	AW838479	Hs.22692	ESTs	2.5
	458890 400074	AW865523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.5 2.5
	405241				2.5 2.5
00	413096	BE065209		gb:RC1-BY0314-310300-015-b12 BT0314 Homo	2.5
80	414349	BE512968	U_ 400FA	gb:801172296F1 NiH_MGC_15 Home sapises c	2.5 2.5
	422884 429515	AW860975 AL031228	Hs.13256 Hs.204370	ESTs DNA segment on chromosome 6 (unique, pse	2.5 2.5
	431925	AK000890		gb:Homo sepiens cDNA FLJ10028 fis, clone	2.5
				439	
				- 1 52	

	442653	BE269247		gb:601185486F1 NIH_MGC_8 Homo saplens cD	2.5
	401882	1140254	11- 004040	FOT. M. Maria Parta C1904C when his	2.5
	458257 405336	U48351	Hs.201219	ESTs, Weakly similar to \$18945 ultra hig	2.5 2.5
5	439492	AF086310	Hs.103159	ESTs	2.5
	459390	BE385725		gb:501276347F1 NIH_MGC_20 Homo sepiens c	25
	436359	Z83806		gb:H.saplens mRNA for axonemal dynein he	2.5
	429322	D86984	Hs.199243	KIAA0231 protein	2.5
10	431699 437107	NM_001173 AA745598	Hs.267831 Hs.291840	Rho GTPase activating protein 5 ESTs, Weakly similar to 178885 serine/th	2.5 2.5
LV	441953	H11695	Hs.322901	disrupter of silencing 10	2.5
	442777	AW341541	Hs.271153	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
15	455275	AW977806		gb:EST399810 MAGE resequences, MAGO Homo	2.5
15	457824 428550	R84938 AW297880	Hs.98661	gb;yt65f04.r1 Soares retina N2b4HR Homo ESTs	2.5 2.5
	445900	AF070526	Hs.13429	Homo sepiens done 24787 mRNA sequence	2.5 2.5
	456359	AI967991	Hs.93574	homea box D3	2.5
20	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sepiens c	2.5
20	452528	AA742457	Hs_291479	ESTs	2.5
	408444 440327	AW661839 R12581	Hs.253204 Hs.191146	ESTs ESTs	2.5 2.5
	410406	A1969703	Hs.1466	glycerol kinase	2.5 2.5
	457021	AW968934	Hs.173108	Homo seplens cDNA: FLJ21897 fls, clone H	2.5
25	418948	AJ217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	2.5
	435427	AA682573	Hs.188982	ESTs, Weakly similar to organic anton tr	2.5
	427791 403509	AA412446 AF231919	Hs.98138 Hs.18759	ESTs KIAA0539 gene product	2.5 2.5
	436590	A)393115	Hs.127655	ESTs	2.5 2.5
30	455556	AW995423	12.12.1000	gb:QV0-BN0042-010400-183-g08 BN0042 Hamo	2.5
	405869				2.5
	408274	R17315		gb:yg12g11.r1 Soares infant brein 1NIB H	2.5
	448015 454190	AI458065	Hs.23196	ESTS	2.5 · 2.5
35	436154	AW177821 AA764950	Hs.119898	gb:1L3-HT0059-180899-007-C05 HT0059 Homa ESTs	25 25
	406377	121104220	12.710000	2010	2.5
	437030	AA742577	Hs.303781	EST	2.5
	420815	AA280684	Hs.270584	ESTs	25
40	418421 423638	R58620	Hs.85050	phospholamban	2.5
70	415425	A1003521 F08365	Hs.130310	Homo saptens mRNA for cyclin 83 Isoform gb:HSCZSA121 normalized infant brain cDN	2.5 2.5
	404577			Source of the Hollowers August 4211	2.5
	403568				2.5
45	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.5
40	449899 451078	A1610700 A1927694	Hs.103280 Hs.204470	ESTS ESTS	2.5 2.5
	453343	AA905353	Hs.121622	ESTs	2.5
	428728	NM_016625	Hs.191381	hypothetical protein	2.5
50	409642	AW450809	Hs.257347	ESTs	25
50	428235	A1631964	Hs.34447	ESTS	25
	452043 401992	H86231		gb:yt03f02.r1 Soares retina N2b5HR Homo	2.5 2.5
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
55	444575	Al264847	Hs.22545	Homo saplens cDNA FLJ 12935 fis, clone NT	25
	449311 454566	AV657014 AW807605		gb:ti49a12.x1 NCL_CGAP_GC6 Homo saplens	25
	454597	AW809648		gb:MR4-ST0098-120100-001-b06 ST0098 Homo gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5 2.5
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.4
60	421583	AA293333		gb:zl53c09.r1 Soares ovary lumor NbHOT H	2.4
	426237	AK001104	Hs.168241	hypothelical protein FLJ10242	24
	454437 419187	A1248173 AA234852	Hs.191460 Hs.44693	hypothetical protein MGC12936 ESTs	2.4 2.4
	444493	R59410	Hs.282094	ESTs, Moderately similar to 138022 hypot	2.4
65	405547				2.4
	454086	AW885909	Hs,6975	PRO1073 protein	2.4
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	2.4
	416277 420976	W78765 A1924940	Hs.180145 Hs.108082	HSPC030 protein ESTs, Wealdy similar to T31636 hypotheti	24 24
			113.100002	Coro, from ballian to forest (ipposite	2.4
70	406468				
70	406468 408617	R61736	Hs.124128	ESTs	2.4
70	406468 408617 418994	AA296520	Hs.124128 Hs.69546	selectin E (endothelial adhesion molecu)	24
70	406468 408617 418994 445432	AA296520 AV653771	Hs.69546	selectin E (endothelial adhesion molecul gicAV653771 GLC Homo saplens cDNA clone	24 24
	406468 408617 418994 445432 454137	AA296520 AV653771 AW500340		selectin E (endothelial adhesion molecu) gb:AV653771 GLC Homo saptens cDNA clone ESTs, Weakly similar to 138022 hypotheti	24 24 24
70 75	406468 408617 418994 445432	AA296520 AV653771	Hs.69546	selectin E (endothelial adhesion molecul gb:AV653771 GLC Homo saplens cDNA clone ESTs, Weakly similar to 138022 hypotheti gb:PM1-NN0047-040400-001-d09 NN0047 Homo sulfotransferase, estrogen-preferring	24 24
	406468 408617 418994 445432 454137 455328 409500 434138	AA296520 AV653771 AW500340 AW895438 U08098 AA625804	Hs.89546 Hs.313876 Hs.54576	selectin E (endothalial adhesion molecul gb:AV553771 GLC Homo saplens cDNA clone ESTs, Weakly climiar to 138022 hypotheti gb:PM1-NN0047-040400-001-d09 NN0047 Homo sulfotransferase, estrogen-preferring gb:zu86h01.s1 Soares_lestis_NHT Homo sap	24 24 24 24 24 24
	406468 408617 418994 445432 454137 455328 409500 434138 419511	AA296520 AV653771 AW500340 AW895438 U08098 AA625804 AA429750	Hs.89546 Hs.313876 Hs.54576 Hs.75113	selectin E (endothelial adhesion molecul gb:AV553771 GLC Homo saplens cONA clone ESTS, Weakly slmilar ib 186025 Hypotheti gb:PM1-NN0047-040400-001-d09 NN0047 Homo sulfotransferase, estrogen-prataring gb:zu85h01.s1 Soares	24 24 24 24 24 24 24
75	406468 408617 418994 445432 454137 455328 409500 434138 419511 437980	AA296520 AV653771 AW500340 AW895438 U08098 AA625804 AA429750 R50393	Hs.89546 Hs.313876 Hs.54576 Hs.75113 Hs.278436	selectin E (endothelial adhesion molecul) gbzAV553771 GLC Homo saplens cDNA clone ESTs, Weakly similar to 138022 hypotheli gb:PM1-NN0047-040400-001-d09 NN0047 Homo sulfotrarsferase, estrogen-preferring gbzzu85801.15 Soares_lestis_NHT Homo sap general transcription factor IIIA KIAA1474 protein	24 24 24 24 24 24 24
	406468 408617 418994 445432 454137 455328 409500 434138 419511	AA296520 AV653771 AW500340 AW895438 U08098 AA625804 AA429750	Hs.89546 Hs.313876 Hs.54576 Hs.75113	selectin E (endothelial adhesion molecul gb:AV553771 GLC Homo saplens cONA clone ESTS, Weakly slmilar ib 186025 Hypotheti gb:PM1-NN0047-040400-001-d09 NN0047 Homo sulfotransferase, estrogen-prataring gb:zu85h01.s1 Soares	24 24 24 24 24 24 24 24
75	406468 408617 418994 445432 454137 455328 409500 434138 419511 437980 439999	AA296520 AV653771 AW500340 AW895438 U08098 AA625804 AA429750 R50393	Hs.89546 Hs.313876 Hs.54576 Hs.75113 Hs.278436	selectin E (endothelial adhesion molecul) gbzAV653771 GLC Homo saplens cDNA clone ESTs, Weakly similar to 138022 hypotheti gb:PM1-NN0047-040400-001-d09 NN0047 Homo sulfotransferase, estrogen-preferring gb:zu86h01.s1 Soares_lestis_NHT Homo sap general transcription factor IIIA KIAA1474 protein ras homolog gene family, member E	24 24 24 24 24 24 24

	410845	AW807182 AW901879	Hs.314453	gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4 2.4
	411836 412879	BE092219	ns.a 14458	ESTs qb: L2-BT0734-240400-071-B04 BT0734 Homo	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to 138022 hypotheti	24
5	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	428945	AW192803	Hs.98974	ESTs, Weakly sknilar to \$65824 reverse t	2.4
	434627	AI221694	Hs.39311	EST8	2.4
10	435256	AF193766	Hs.13872	cylokine-like protein C17	2.4
10	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.4
	458239	BE439877	Hs.283389	ESTs	2.4
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	2.4 2.4
	441262 402076	AI809130	Hs.176906	ESTB	2.4
15	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.4
1.5	400587	17/340302	IBATO	Obligion in lives femore 1	24
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	24
	411203	AW872430	Hs.273743	ESTs	24
	447849	Al538147	Hs.164277	ESTS	2,4
20	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	424131	AA335714	Hs.199665	ESTs	2.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	2.4
	440385	AA884283	Hs.192136	ESTs	2.4
25	417976	BE565892	Hs.63077	interleukin 18 (Interferon-gamma-Inducin	2.4
23	447179	AW015633	Hs.157299	ESTs ESTs	2.4 2.4
	412977 436958	AA125910 AA740322	Hs.191461 Hs.293539	Homo saplens mRNA for KIAA1758 protein,	2.4
	401361	UNI-HODZZ	1 13.233203	I mile septens that at the report to proceed	24
	403891				24
30	408419	AW250092	Hs.305953	zinc linger protein 83 (HPF1)	24
- •	417002	179613	Hs.14613	ESTs	2.4
	439446	Al927629	Hs.57873	ESTs	2.4
	458570	AW971698	Hs.12627	TJ6 protein	2.4
0.0	458624	Al362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
35	459344	AW499533	Hs.257976	ESTs	2,4
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.4
	412114	100ECGWA	Hs.240833	ESTs, Wealdy similar to 138022 hypotheti	2.4
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	2.4 2.4
40	419983	W55958	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	24
70	42826B 450947	AA424957 A1745400	Hs.294132 Hs.204662	ESTs ESTs	2.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.4
	438142	T90309	Hs.269651	ESTs	2.4
	409239	AA740875	Hs.44307	ESTs, Moderately similar to 138022 hypot	24
45	424235	NM_003181	Hs.143507	T brachyury (mouse) homelog	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	433868	AA612960	Hs.337300	EŞŢs	2.4
	401645				2.4
50	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.4
50	453393	AWB56392	Hs.110376	ESTs	2.4
	436054	A1076262	Hs.119813	ESTs	2.4
	425433 417712	AA357471 AA205569	N. 104102	gb:EST66274 LNCAP cells I Home sepiens c	2.4 2.4
	420639	A1683116	Hs.194193 Hs.25328	ESTs, Moderately similar to ALU1_HUMAN A ESTs, Moderately similar to ALU7_HUMAN A	2.4
55	453369	BE551550	Hs.232630	ESTS	2.4
-	405017	02501000	THOILUCUS	2010	2,4
	405385				2.4
	435633	Al248152	Hs.270047	ESTs .	2.4
~~	457128	A1932995	Hs.183475	Homo sapiens cione 25061 mRNA sequence	2.4
60	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	2.4
	434544	C05875	Hs.91575	ESTs	2.4
	449432	AW451381	Hs.196529	ESTs	2.4
	455219	AW879403	He decrees	gb:PMO-OT0019-150300-002-d01 OT0019 Homo ESTs	2.4
65	458734	A1554946	Hs.158794	====	2.4 2.4
05	442179 444313	AA983842 A1140494	He.333555 Hs.197955		24
	440448	AAB85428	Hs.125646		2.4
	441498	Al379248	Hs.58742	ESTs	2.4
	438205	AA780385	Hs.122161		2,4
70	402615		1101122101		2.4
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	24
	422306	8E044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.4
	413697	AA131315	Hs,47144	DNFZP586N0819 protein	2.4
75	421755	AW169454	Hs.207422		2.4
75	449007	A1620433	Hs.193201		2.4
	449916	T60525	Hs.299221		2.4
	416857 422486	D10216	Hs.89394	POU domain, class 1, transcription facto	24 24
	458914	BE514492 BE327698	Hs.117487 Hs.280922		2.4
80	435061	Al651474	Hs.163944		2.4
	41645B	AA180511		gbzp53f03.r1 Stratagene NT2 neuronal pr	2.4
	453785	Al368236	Hs.283732		2.4
	421515	Y11339	Hs. 105352		2.4

	403003				2.4
	405347				2.4
	406091				2.4
_	428402	AW237531	Hs.326876	Homo sapiens SOX6 mRNA, complete cds	2.4
5	438762	AW844412	Hs.65450	reticulon 4	2.4
	4557B0	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397545	Hs.119151	ESTs	2.4
	404249				2.4
10	443921	Al091310	Hs.134848	ESTs	2.4
10	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.4
	417154	Al574701	Hs.21388	ESTs	2.4
	419720	AA249131	Hs.337778	hypothetical protein FLJ 11068	2.4
	405230			•	2.4
1.5	405935				2.4
15	436998	AA745625	Hs.291414	ESTs, Wealdy similar to ALU8_HUMAN ALU 8	2.4
	445748	U80766	Hs.13252	Human EST done 22453 mariner transposon	2.4
	419233	AA458873	Hs.178306	ESTs	2.3
	414277	BE269910		gb:601186291F1 NIH_MGC_8 Homo septens cD	2.3
00	452092	BE245374	Hs.27842	hypothetical protein FLI11210	2.3
20	453736	AL118674	Hs.34871	zinc finger homeobox 1B	2.3
	410688	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.3
	434239	AF119910	Hs.283047	hypothetical protein PRO2964	2.3
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapl	2.3
25	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.3
25	445688	Al248205	Hs.153244	ESTs	2.3
	451656	BE3270B8	Hs.212752	ESTs	2.3
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,	2.3
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo	2.3
20	436149	Al75430B	Hs.159452	ESTs	2.3
30	405629				2.3
	432702	AW973953	Hs.293744	ESTs	2.3
	433377	Al752713	Hs.43845	ESTs	2.3
	444711	AI188739	Hs.148488	ESTs	2.3
35	445621	AI733818	Hs.145549	ESTs	2.3
33	456432	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	2.3
	449236	AJ403126	Hs.26373	Homo saplens cDNA: FLJ23449 fis, clone H	23
	459024	AA020799	Hs.262869	plasminogen-like	2.3
	441037	AA913360	Hs.12646B	E8Ts	23
40	431577	T34523	Hs.302040	Homo sapiens DNA sequence from PAC 43401	2.3
40	438782	AA82B380	Hs.126733	ESTs	23
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2,3
	429044	Al261490	Hs.145527	ESTs	23
45	431655	AW971119	11. 450007	gb:EST383206 MAGE resequences, MAGL Homo	2.3
73	439642	W81441	Hs.153967	ESTs	2.3
	441721 443482	AI288259	Ha.127652	ESTs	2.3
		AW188093	Hs.250385	ESTS	2.3
	403416 416443	AI744626	Hs.151385	KIAA0564 protein	2.3
50	419714	N69469	Hs.194225	ESTs	2.3
50	415511	AA758751 AI732617	Hs.98216	EST's	2.3
	412344		Hs.182362	ESTs	2.3
	449264	AW938384 Al637649	Hs.264190	vacuolar profein sorting 35 (yeast home)	2.3
	451664	AA889081	Hs.196105 Hs.153952	ESTs	2.3
55	441269	AW015206		5 nucleotidase (CD73) ESTs	2.3
-	402333	A11013200	Hs.178784	E018	2.3
	453649	Y07494	Hs.34114	ATOres No. 46: Improvelies eleks 2.(.)	2.3
	430880	AW138724	Hs.168974	ATPase, Na+K+ transporting, alpha 2 (+)	2.3
	404357	111100124	110.100077	ESTs, Highly similar to ALU7_HUMAN ALU S	2.3
60	403696				2.3
••	441622	AW450957	Hs.224864	ESTs	2,3
	411004	AWB13242	*********	gb:MR3-ST0191-020200-207-g10 ST0191 Homo	2.3
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	23
	428548	AA430058	Hs ₂ 98649	EST	23 23
65	404059	,-112202	· spoots	201	23 23
	446861	Al696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	23 23
	413640	BE158118		gb:MR2-HT0378-240200-205-d09 HT0378 Homo	23
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	
	435338	AA678071	Ha_194300	ESTs, Weakly similar to 138022 hypotheti	23 23
70	442710	AI015631	Hs.23210	ESTs	
	444206	AW301017	Hs.146492	ESTs	2.3 2.3
	451250	AA491275	Hs.236940	hypothetical protein FLJ12542	23 23
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	23
	458455	AV648310	Hs.2134B8	ESTs	23 23
75	458521	Al651039	Hs.148559	ESTs	2.3
	407938	AA905097	Hs.85050	phospholamban	23
	439546	AF088056		gb:Homo sapiens full length insert cDNA	23
	441274	AW593781	Hs.131357	ESTs	2.3
0.0	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.3
80	409660	AW452065	Hs.258905	ESTs	2.3
	428532	AF157326	Hs.184786	TBP-interacting protein	2.3
	411384	AW842115		gb:RC0-CN0026-090200-031-e11 CN0026 Homo	2.3
	453687	755674	Hs.283108	hemoglobia, gamma G	2.3

	410140	AL134435	Hs.22269	neurexin 3	
	422443	NM_014707	Hs.116753	histone deacetylase 78	2.3
	409071	AW316932	Hs.181982	ESTs	2.3
	421253	Al188102	Hs.31028		2.3
5	441398	AA932398	Hs.292036	ESTs	2.3
•	448458	AW614367		ESTs, Weakly similar to B34087 hypotheti	23
	457225	AW820035	Hs.171054	ESTs	23
	443718	A1083580	Hs.278679	a disintegrin and metalloproteinase doma	23
	445568	H00918	Hs.221373	ESTs	23
10		HOUS 19	Hs.268744	KIAA1796 protein	23
10	400582	*******			2.3
	411262	AVV834480		gb:MR2-TT0014-151199-011-b07 TT0014 Homo	2.3
	401145				2.3
	407440	AF227135		gb:Homo sapiens candidate taste receptor	2,3
15	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Home	2.3
15	459077	N20370	Hs_235883	ESTs	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	453331	A1240665	Hs.8895	ESTs	2.3
	443751	A1285839	Hs.153324	EST	2,3
	402038				
20	402176				2.3
	456605	A1B27786	Hs.259044	ESTs	2,3
	432479	ALD42844	Hs.275675		2.3
	402527	110012077	112.21 0070	katanin p80 (WD40-containing) subunit B	2.3
	449272	AW137656	Hs.197645	ECT-	2.3
25	411024	BE062590	115.15(045	ESTS	2.3
	455608			gb:QV1-BT0260-281099-023-f05 BT0260 Homo	23
	458818	BE011437	11- 03000	gb:CM4-BN0220-080500-170-f03 BN0220 Homo	23
		A1523857	Hs.232257	ESTs	2.3
	419875	AA853410	Hs.93557	proenkephalin	23
30	405521				23
20	436517	BE080932	Hs.135225	EST ₃	23
	456801	AW961886	Hs.13B263	Homo sapiens cione 24528 mRNA sequence	23
	430444	AW296421	Hs.121035	ESTs	23
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLI14890 ffs, cione PL	23
25	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	23
35	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	23
	419337	AW291112	Hs.209978	ESTs	23
	419699	AA248998	Hs.173044	ESTs, Weakly similar to 138022 hypotheti	23
	454456	AWB50984		gb:lL3-CT0220-150200-068-H08 CT0220 Homo	
	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	23
40	457028	AW449838	Hs.97582	ESTs	23
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	23
	428336	AA503115	Hs.183752	microseminoprotein, bela-	23
	430850	BE144152	113.100) UK		23
	408622	AA056060	Un ONGETT	gb:MR0-HT0165-060200-006-e02 HT0165 Homo	23
45	421227	R78581	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	2.3
	426902		Hs.266309	mosaic serine protease	23
	430789	Ai125334	Hs.97408	ESTs	23
	447475	AA632577	Hs.310235	ESTs, Weakly similar to 178885 serine/th	23
		At380797	Hs.158992	ESTS	23
50	45214B	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	23
50	430712	AW044647	Hs.1962B4	ESTs	23
	458103	AW780192	Hs.267596	ESTs	2,3
	420959	AA282119	Hs.68975	ESTs	2.3
	44409B	AV647969	Hs.109694	KIAA1451 protein	2.3
55	445641	A1245987	Hs.149442	ESTS	2,3
JJ	449276	AW241510	Hs.252713	E8Ts	2.3
	452294	AI871925	Hs.117995	ESTs, Moderately similar to A47582 B-cel	2.3
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	459497	AA825742	Hs.87517	E8Ts	2.3
60	412852	8E004117	Hs.37415	ESTs, Weekly similar to ALU1_HUMAN ALU S	23
60	437539	AA974673	Hs.121419	ESTs	2.3
	421813	BE048255		gb:tz49b05.y1 NCt CGAP Bm52 Homo sapien	2.3
	411994	R67298	Hs.109087	Homo sepiens cDNA: FLJ22845 fis, clone K	2.3
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCO1_HUMAN HYPOT	2.3
	452463	R36452	Hs.300817	ESTs	2.3
65	404936				2.3
	442833	AA328153	Hs.B8201	ESTs, Weakly similar to A Chain A, Cryst	
	440836	AW370882	Hs.222080	ESTs	2.3
	405120			2013	2.3
	400238				2.3
70	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW935336	. WIL TTIVU		2.3
	420478	AA521259	Hs.193796	gb:QV4-DT0021-281293-070-g11 DT0021 Homo E8Ts	2.3
	441417	Al733297	Hs.144474		2.3
	445117	A1733257 A1208754		ESTS	2.3
75	431182	AW971180	Hs.147369	ESTs	23
, ,	437036		LL 422000	gb:EST383268 MAGE resequences, MAGL Homo	2.2
		Al571514	Hs.133022	ESTs	2.2
	455849	BE146866	11-00-10	gb:QV4-HT0222-211099-014-f06 HT0222 Homu	2.2
	447624	A1640326	Hs.62713	ESTs	2.2
80	439780	AL109688		gb:Horno sapiens mRNA full length insert	2.2
~0	405706	A1760000	11- 40	FOR	2.2
	447732	A1758398	Hs.16131B	ESTa	2.2
	440625	BE539853	Hs.22452	Homo sepiens mRNA for KIAA1737 protein,	2.2
	404257				2,2

				·	
	437722	AW292947	Hs.122872	ESTs, Wealdy similar to JU0033 hypotheti	2.2
	449133	AI631655	Hs.197919	ESTs	2.2
	456555	AW592167	Hs.293299	ESTs	2.2
_	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodlesta	2.2
5	428192	AA424051	Hs.304742	ESTs	22
	435634	TB2384		gb:yc14f05.r1 Stratagene lung (937210) H	2,2
	43801B	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446096	A)276454		gb:ql71a12,x1 Soeres_NhHMPu_S1 Homo sapi	22
• •	448106	A1800470	Hs.171941	EŞTS	2.2
10	450232	8E300815	Hs.201326	ESTs	2.2
	436134	AK000618	Hs.123784	ESTs	2.2
	448466	Al522109	Hs.171066	ESTs	2.2
	420678	AW593288	Hs.3530	TLS-associated serine-arginine protein 2	2.2
	430692	X80240		gb:HLsapiens endogenous retrovirus HERV-	2.2
15	446453	AV658469	Hs.186646	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	423611	AB011163	Hs.129908	KIAA0591 protein	2.2
	444050	AW138295	Hs.135024	ESTs	2.2
	431532	AI537B17	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	422669	H12402	Hs.119122	ribosomal protein L13a	2.2
20	403388	1112702	1101110111	noodina proun 2122	2.2
20	403780				2.2
	419423	D26488	Hs.90315	KIAA0007 protein	22
	424719	H90452	115.50315	gbyv01c03.r1 Spares fetal liver spisen	2.2
					2.2
25	431453	AW753917	11- 202020	gb:RC0-CT0299-291199-031-F02 CT0299 Homo	22
23	442078	AW268583	Hs.262629	ESTS	2.2
	452975	M85521	Hs.244482	Homo sepiens, cione IMAGE:3611719, mRNA,	2.2
	426197	AA004410	Hs.100009	acyl-Coenzyme A cyldase 1, palmitoyl	
	427119	AW880562	Hs.114574	ESTs	2.2
20	400486				2.2
30	448482	AW294070	Hs.171092	ESTs	2.2
	402621				2.2
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	2.2
	424584	H10692	Hs,13310	ESTs	2.2
2.5	445061	A)253094	Hs.145227	ESTs	2.2
35	431065	AA491286	Hs.128792	ESTs	2.2
	411908	L27943	Hs.72924	cytidine deaminase	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2,2
	446901	Al347274		gb:tc05d02x1 NCI_CGAP_Co16 Homo saptens	2.2
40	422677	AL046388	Hs.208206	hypothetical protein FL321162	2.2
40	455534	AW991925		gt::PM3-BN0011-130100-002-b07 BN0011 Homo	2.2
	400163				2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	409206	AW364844		gb;QV3-DT0044-221299-045-c03 DT0044 Homo	2.2
	410556	R32158		gb:yh67a07.s1 Soares piscenta Nb2HP Homo	2.2
45	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	2.2
	439482	W70045	Hs.58089	ESTs	2.2
	447877	A)495184	Hs.164252	ESTs	2.2
	418297	R91254	7100101-0-0	gb:yp94e12.s1 Soares fetal liver spleen	2,2
	403534			4-77	2.2
50	410594	AW770778	Hs.281238	ESTs	2.2
	414000	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.2
	432762	NM_014099	Hs.278924	PRO1768 protein	2.2
	437608	AA761594	Hs.122440	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
55	439626	N22415	Hs.189080	ESTs	2.2
	444540	A1693927	Hs.265165	ESTs	2,2
	450024	AA005129		gb:zh90h08.rl Soares_fetal_liver_spicen_	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	22
	435138	BE314734	1,2,1,00,110	gb:601152976F1 NIH_MGC_19 Horno sapiens c	2.2
60	412887	BE007420		gb:PM3-BN0t42-200300-001-c04 BN0142 Homs	2.2
~~	454204	AW816498		gb;QV0-ST0236-171299-075-b02 ST0236 Homo	2.2
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.2
	432887	Al926047	Hs.162859	ESTs	22
	448063	AJ459108	Hs.159818		2.2
65	416171	H23896	Hs.125790		2.2
-	433098	AW190593	Hs_151143		2.2
	409781	AW812266	Hs.15220	zinc finger protein 196	2.2
	423441	R68649	Hs.278359		2.2
	423646	H02364	1 13.21 03.23	gbyj35d08.r1 Soares placenta Nb2HP Homo	2.2
70	436572	AA723274	Hs.279596		2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	22
	448828	Al580296	Hs.174782		22
	444585	AW170015	Hs.6594	ESTs	2.2
	437334	AL353947	Hs.283780		2.2
75	437334	D16181	Hs.2868	peripheral myalin protein 2	2.2
, ,	400843	PIOIDI	112.2000	herbitanistikani luotan v	22
	45568B	BE067238	•		22
			U. 47004	gb:PM1-BT0348-151299-001-p12 BT0348 Homo ESTs, Moderately similar to ALU1_HUMAN A	22
	449560	AA001767 M585B3	Hs.17924	cerebellin 1 precursor	2.2
80	408940		Hs.662	gb:PM1-MT0010-200300-901-g08 MT0010 Homo	2.2
30	455201	AW947884	We WOLAT		2.2 2.2
	413617 459495		Hs.279518	amyloid beta (A4) precursor-like protein gb:601076707F1 NIH_MGC_12 Homo saplens c	22
	433225		Un 47254		2.2 2.2
	***************************************	AW816515	Hs.173540	t the god ness stake inn	

	444547	AV650207	Hs.282437	ESTs, Weakly similar to 138022 hypotheti	2.2
	417156	N49476	Hs.166563	replication factor C (activator 1) 1 (14	2.2
	416761	HB5422	Rs.108556	ESTs	2.2
_	408867	AA437199	Hs.656	call division cycle 25C	2.2
5	406748	AW339106	Hs.217493	annexin A2	2.2
	427443	AA402713	Hs.97872	ESTs	2.2
	452843	A1796769	Hs.208320	ESTs	2.2
	427473	AW274439	Hs.252709	ESTs	2.2
	433919	AA746311		gb:oa56d12.r1 NCL_CGAP_GCB1 Homo saptens	2.2
10	431058	AW968865		gb:EST380941 MAGE resequences, MAGJ Homo	22
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sep	
	415250	F02614	Hs.27319		2.2
	440253			ESTs	2.2
		Al651329	Hs. 160289	ESTs	2.2
15	434470	AA634B18	Hs.298138	ESTs	2.2
1.5	41B849	AW474547	Hs.53565	Homo saplens PIG-M mRNA for mannosyltren	2.2
	432463	AA548518	Hs. 186733	ESTs	2.2
	400861				2.2
	407287	Al678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens	2.2
20	414817	AW902892	Hs.23782	hypothetical protein FLJ12847	2.2
20	416143	A1955650	Hs.79033	glutaminy)-peptide cyclotransferase (glu	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	22
	442952	A1743261	Hs.131860	ESTs	2.2
	425187	AW014486	Hs.22509	ESTs	2.2
25	408221	AA912183	Hs.47447	ESTs	22
	411480	AW848022		gb:lL3-CT0214-231299-053-A09 CT0214 Homo	2.2
	459681			g	22
	414784	NM_600344	Hs.288986	survival of motor neuron 1, telemente	2.2
	442726	AW136066	Hs.19145	ESTs	
30	450433				2.2
20		AW44453B	Hs.231863	ESTs	2.2
	437642	AL079309		gb:Homo saplens mRNA full length insert	22
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
25	433266	A1863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
35	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	446534	A1307356	Hs.175225	ESTs	2.2
	4037 6 4				22
40	442735	R91949		gb:yq06h06.s1 Soares fetal liver spleen	2.2
40	455221	AW867751		gb:MR0-SN0038-290300-001-e03 SN0038 Homo	2.2
	405965				22
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.2
	441679	BE502267	Hs.65996	ESTs	2.2
	432781	NM_014133	Hs.278940	PRO0618 protein	2.2
45	448470	AW028226	Hs.309479	ESTs	
•••	419637	W27493	1 18.303473		2.2
	443180	R15875	LL DEGETO	gb:31h10 Human retina cDNA randomly prim	22
	422213		Hs.258576	claudin 12	2.2
		AA308385	Hs.133160	ESTs .	2.2
50	423119	AA322201	Hs.131976	ESTs	2.2
50	450192	AA263143	Hs.24596	RAD51-interacting protein	2.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	2.2
	400734				22
	430499	AW969408	Hs.231991	ESTs	2.2
55	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.2
55	401694	,			2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2,2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
CC	436840	AA724411	Hs.156065	ESTs .	2.2
60	436802	N3448B	Hs.170504	ESTs	22
	443994	A1094805	Hs.135522	ESTs, Weakly similar to \$38038 hypotheti	22
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	446412	AW135313	Hs.150098	ESTs	22
	448390	AL035414	Hs.21068	hypothetical protein	2.2
65	449939	T86420	Hs.272139	ESTs	
	412700	BE222433	Hs.201262	ESTs, Weakly similar to 138022 hypotheti	2.2 2.2
	453125	AW779544	Hs.115497		
	422757	At909995	Hs.65551	hypothetical protein FLJ22655 Homo sapiens, Similar to DNA segment, Ch	22
	452864			Fund Sapiens, Sinner to DNA Segment, Cit	2.2
70	452441	AAD33714	Hs.287629	hypothetical protein FLJ14260	2.2
, ,	402395	BE22207B	Hs.113069	E8Ts	22
	459659				22
		ASSAUG APPRO	11 00000-	managaridasa al-ba ata 81t0	22
	4281B6	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.2
75	438432	AW444990	Hs.258B00	ESTs, Weakly similar to 138022 hypotheti	2.2
13	409446	· A)561173	Hs.6768B	ESTs	2.2
	408764	BE087164	Hs.302415	ESTs	2.2
	408908	BE296227	Hs.250822	serine/threonine kinese 15	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
90	436992	AA741074	Hs.120750	ESTs	2.2
80	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	444199	Al128931	Hs.260681	ESTs, Moderately similar to ALUF_HUMAN!	2.2
	446009	A1989885	Hs.231926	ESTs	2.2
	435510	BE143837		gb:MR0-HTD164-151299-012-b08 HT0164 Homo	2.1
				445	

	403691				2.1
	458333	AJ000792	Hs.108209	EST ₆	2.1
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	2.1
_	439343	AF086161	Hs.114611	hypothetical protein FL3t1806	21
5	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protei	2.1
	406941	X58140		(NONE)	2.1
	445712	AI458246	Hs.167451	ESTs	2.1
10	451270	AW341392	Hs.235795 Hs.40919	ESTS	2.1
10	451403 437073	AA885569 Al885608	Hs.94122	Homo saplens cDNA FLJ14511 fis, clone NT ESTs	2.1 2.1
	4347B9	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	21
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.1
	445944	H06336	Hs.13480	Homo sepiens done 24875 mRNA sequence	2.1
15	405233		,,,,,,		2.1
	446512	H30351	Hs.207982	ESTs	2.1
	403188				2.1
	404443				2,1
00	433645	AI821746	Hs.190258	ESTs, Moderately similar to ALU6_HUMAN A	2.1
20	414456	H74314		gb:yu56e10.r1 Soares felal liver spleen	2.1
	433479	AW511459	Hs.249972	ESTs	2.1
	455482	AW948353	U- 4 2040	gb:RC0-MT0015-130400-031-d07 MT0015 Homo	2.1
	446364	AB006624	Hs.14912	KIAA0286 protein	2.1 2.1
25	452004 405059	A)827815	Hs.277359	ESTs	21
24	425457	AW964212		gb:EST376285 MAGE resequences, MAGH Homo	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	413B01	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
30	432774	AA564946	Hs.156280	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	21
	445532	BE138944	Hs.146200	ESTs	21
	456313	AA225741		gb:nc17b10.s1 NC1_CGAP_Pr1 Homo saplens	21
25	412818	NM_003337	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 h	2.1
35	450271	A1693900	Hs.200920	ESTs	2.1
	401521	1 dobout 1		1.91	2.1
	422880	AF228704	Hs.121524	glutathione reductase	2.1
	448871	BE616709	Hs.159265 Hs.196511	kruppel-related zinc finger protein hcKr	2.1 2.1
40	449233 408217	BE048401 AI433201	Hs.279860	ESTs tumor protein, translationally-controlle	2.1
70	457003	S78234	Hs.172405	cell division cycle 27	21
	41744B	AA203135	Hs.130186	ESTs	21
	402103	, , , , , , , , , , , , , , , , , , , ,	10.100100		21
	450579	AW136774	Hs.48614	ESTs	21
45	429597	NM_003816	Hs.2442	a disinlegrin and metalloproteinase doma	21
	456596	AA291834	Hs.78950	branched chaîn keto acid dehydrogenese E	2.1
	415333	H24415	Hs.13273	KIAA0692 protein	2.1
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	2,1
50	434985	AA658229	Hs.291228	ESTE	21
50	414729	BE466928	Hs.281901	ESTs .	2.1
	400510	1.4.50,550		1 100 PO 41101 POLD TI 411	21
	420844 427434	AA595522	ti- 201722	gb:nh22c09.s1 NCL_CGAP_Pr1 Homo sapiens	2.1 2.1
	432188	BE53B374 Al362952	Hs.301732 Hs.2928	hypothetical protein MGC5306 solute carter family 7 (catlonic amino	21
55	446296	AA985662	Hs.63131	Homo sepiens cDNA FLI13155 fis, clone NT	21
	453853	ALO4060D	Hs.188083	ESTs	21
	459108	AW084176	Hs.223296	ESTs, Weakly similar to 138022 hypotheti	2,1
	430118	Al377255	Hs.183287	ESTs	2.1
	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.1
60	437981	AA774445	Hs.192095	ESTs, Weakly similar to KIAA1397 protein	2.1
	439957	A1453164	Hs.66357	ESTs	21
	423734	H02217		gb:yj3Bd11.r1 Soares placenta Nb2HP Homo	2.1
	450721	Al732271	Hs.25567	ESTs	2.1
65	429392	AL109712	Hs.296506	Homo seplens mRNA full length insert cDN	2.1
OJ	429986	AF092047	Hs.227277	sine coulis homeobox (Drosophila) homolo	2.1
	432919 434791	AL079B0D AA649235	Hs.116457	gb:DKFZp434O2330_r1 434 (syrronym: hiss3)	2.1 2.1
	445273	Al218441	Hs.153845		21
	400514	LXT (044 1	1 10.100040	101/10	2.1
70	412798	AW998657	Hs.119120	E3 ubiquifin ligase SMURF1	2.1
- -	416085	H18072	Hs.92576	ESTs	21
	437846	AA773866	Hs,244569		21
	439391	AW975638	Hs.293490		2.1
	428414	AL049980	Hs.184216		2.1
75	429430	Al381837	Hs.155335	ESTs	2.1
	449689	AF228421	Hs.23889	DKFZP564A032 protein	2.1
	430909	AF034632	Hs.248126		2.1
	453116	Al276680	Hs.146086		21
80	416312	W02640	Hs.16247	ESTs, Wealdy similar to 2004399A chromos	2.1 2.1
30	423019 414007	A1640185 A1733895	Hs.283626		2.1
	459535	AV654907	Hs.103B13	gb:AV654907 GLC Homo sapiens cDNA clone	2.1
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	21
					-•

	421279	AW664878	Hs.106645	ESTs	2.1
	443167	Al202009	Hs.132087	ESTs	2.1
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1 ESTs, Highly similar to A53933 myosin t	2.1 2.1
5	448078 436858	A1460117 BE545498	Hs.170464	gb:601070344F1 NIH_MGC_12 Homo saplens c	2.1
•	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.1
	431089	BE041395	Hs.283576	ESTs, Weakly similar to unknown protein	2.1
	407401	AF029325		gb:Homo saplens leminin beta-4 chain pre nb:EST88135 HSC172 cells II Homo saplens	2.1 2.1
10	426338 451124	AA375802 AJ185203	Hs.31432	go:Es red tos risc riz ceas il Homo sapieris cardiac ankyrin repeat protehi	2.1
••	425541	AA359119	10.01702	gb:EST68172 Fetal lung II Homo sapiens c	2.1
	406504				2.1
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo saplens c	21
15	415186 416175	AA160945 H24230	Hs.14479 Hs.271498	Homo sepiens cDNA FLJ14199 fis, clone NT ESTs, Moderately similar to ALU1_HUMAN A	2.1 2.1
1.5	436820	A)684535	Hs.200811	ESTS MODERATELY SHIMAN TO ALCO I DISNAMA	2.1
	442095	Al733162	Hs.128470	ESTs	2.1
	451878	AI821027	Hs.8429	ESTs	21
20	449178 427307	A1633748	Hs.197597	ESTs	2.1 2.1
20	427307 415857	AF117947 AA866115	Hs.174795 Hs.127797	PDZ domain-containing guarine nucleotide Homo saptens cDNA FLJ11381 ffs, clone HE	2.1
	425154	NM_001851	Hs.154850	collegen, type IX, alpha 1	2.1
•	449746	A1668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	2.1
25	441543	A1733014	Hs.269715	ESTs	2.1
23	403065 428811	AA436052	Hs.99487	ESTs	2.1 2.1
	451803	BE541174	Hs.25205B	ESTs, Moderately similar to PC4259 femi	2.1
	442906	AW2968BB	Hs.170939	ESTs	2.1
20	409171	R17126		gb:yg09c11.r1 Soares intent brain 1NIB H	21
30	414175	AI308876	Hs.103949	hypothetical protein OKFZp761D112	2.1
	450785 412039	AAB52713 AW887384	Hs.25459	Homo saplens, alpha-1 (VI) collagen gb:RC0-070089-130300-021-d07 070089 Homo	2.1 2.1
	453055	AW291436	Hs.31917	Homo sepiens, clone MGC:9658, mRNA, comp	21
	443268	AJ800271	Hs.129445	hypothetical protein FLJ12496	2.1
35	455022	AW850845		gb:lL3-CT0220-111199-028-D11 CT0220 Homo	2.1
	447972	AL137275 AF054839	Hs.20137	hypothetical protein DKFZp434P0118	2.1 2.1
	422942 400451	N-034639	Hs.122540	letraspan 2	2.1
40	406668	T62745	Hs.184411	elbumin	21
40	450159	A)702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	404834	DEC44003	the southern	VIA A4000	2.1
	448732 423453	BE614063 AW450737	Hs.334689 Hs.128791	KIAA1838 protein CGI-09 protein	2.1 2.1
- C-2	421447	AB005216	Hs.104481	Nck, Ash and phospholipase C binding pro	21
45	408774	AW270899	Hs.254569	ESTs, Wealtly similar to B34087 hypotheti	2.1
	419986	Al345455	Hs.78915	GA-binding protein transcription factor,	2.1
	405732 417846	AA206581	Hs.39457	ESTs, Weakly similar to JC5314 CDC28/cdc	2.1 2.1
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	21
50	420344	BE463721	Hs.97101		2.1
	455778	BE088746		gb:CM2-BT0593-210300-123-d09 BT0693 Homo	2.1
	426953	A1769281	Hs.97439 Hs.129990	ESTS	2.1 2.1
	440454 493917	A1733037 A1809325	Hs.122814	ESTs Human DNA sequence from clone RP5-1028D1	21
55	424872	AA347923	10.144017	gb:EST54302 Fetal heart II Homo saplens	21
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	441963	A7733307	Hs.128002	ESTs	2.1
	439498 468224	AA908731 AW292905	Hs.58297 Hs.128770	CLLL8 protein ESTs	2.1 2.1
6 0	413525	BE145899	110.1201/0	gb:MR0-HT0208-221299-204-b10 HT0208 Homo	21
* *	444702	Al220122	Hs.326560	hypothetical protein MGC2780	2.1
	417787	R14948	Hs.23883	ESTs	2.1
	400612	AW809201	Nº 244230	ECTo Machinemilar to 67124 Dillama st 110	21
65	410878 414494	AA768491	Hs.314248 Hs.6783	ESTs, Weakly similar to ALU4_HUMAN ALU 8 hypothetical protein FLJ22724	21 21
•••	427027	Al924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	451067	BE172186		gb:MRO-HT0559-110300-005-h11 HT0559 Homo	2.1
	455032	A1830890	Hs.192422		2.1
70	417945	R29072	Hs.293502	gb:F1-101D 22 week old human fetal liver	2.1
70	438268 424754	AA782163 R09692	rus, <i>C</i> gaaVZ	ESTs gb:yf23b12.r1 Soares fetal liver spleen	2.1 2.1
	404599			Barbara im i adoleo lami etal phanii	2.1
	459655			•	21
75	402455	41ama 20-4)), 484m4	Manager Palace P	21
13	459278 421987	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H CGI-101 protein	2.1 2.1
	400339	Al133161 X57131	Hs.286131 Hs.248209		2.1
	438206	AA780385	Hs.187885		2.1
oΛ	458451	AW297181	Hs.195922	ESIs	2.1
80	447534	AW953935	Hs.30837	ESTS	2.1
	417687 41 <i>2</i> 717	A1828596 W00973	Hs.250691 Hs.334728		21 21
	405759		110204720	- 	21

	406413				21
	442081	AA401863	Hs.22380	ESTs	2,1
	45793B	AI373638	Hs.133900	ESTS Horra contona «DNA EL 112/27 for closes PI	2.1 2.1
5	420687 428822	AA279392 W28418	Hs.88605 Hs.30715	Homo sapiens cDNA FLJ13427 fis, clone PL potassium vollage-gated channel, lsk-rel	2.1
-	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2,1
	411421	BE272110	Hs.21177	ESTs	21
	437825 437083	AA769123 AW082597	Hs.291947 Hs.244862	ESTs ESTs	2.1 2.1
10	409466	AA436207	Hs.226666	ESTs, Moderately similar to 154374 gene	2,1
	433523	H29882	Hs.162514	EST8	2.1
	446868	AV660737	Hs.135100	ESTs	21
	445882 438005	A1948717 BE151746	Hs.225155	ESTs, Wealthy similar to A46302 PTB-assoc gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1 2.1
15	406817	Al936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo saplens	2.1
	410486	AW235094	Hs.69233	zinc finger protein	21
	411940 412446	AW876686 Al768015	Hs.92127	gb:CM4-PT0031-180200-507-e05 PT0031 Homo ESTs	2.1 2.1
	457289	AW573204	Hs.137078	ESTs	2.1
20	400335	Y13187	Hs.246067	Homo sapiens dmd gene, intron 11	2.0
	435959	AW296243	Hs.118375	ESTS	2.0
	448188 418339	AW001835 AA639902	Hs.13323 Hs.104215	hypothetical protein FLJ22059 ESTs, Moderately similar to SPCN_HUMAN S	2.0 2.0
	420430	AI703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	2.0
25	445717	AW664658	Hs.149332	ESTs .	2.0
	451862 459686	H09260	Hs.32333	ESTs	2.0 2.0
	441998	BE349537	Hs.38383	ESTs	20
20	412194	AW900282	Hs.115412	hypothetical protein FLJ13881	20
30	444229	AV648613	Hs.282397	ESTs Straight and CORCOO homestern	2.0 2.0
	441635 421387	A1908538 AF059566	Hs.133000 Hs.103983	ESTs, Weakly similar to 826689 hypotheti solute carrier family 5 (sodium lodide s	2.0
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.0
25	428209	AA424197	Hs.98947	ESTs, Wealdy similar to S33496 trypsin [20
35	443520 409248	W90022 AB033035	Hs.186809 Hs.51965	ESTs, Highly similar to LCT2_HUMAN LEUKO KIAA1209 protein	2.0 2.0
	444518	Al160278	Hs.146884	ESTs	2.0
	422237	M13149	Hs.1498	histidine-rich glycoprotein	2.0
40	409316	U28251	Hs.53237	ESTs, Highly similar to 2169_HUMAN ZINC	2.0 2.0
40	402725 413783	AA314337	Hs.301547	ribosomal protein \$7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo saplen	2.0
	42500B	AW675764	Hs.174248	ESTS	2.0
45	427271 444102	AW195922 AV647953	Hs.188758 Hs.83077	connexin 59 Interleukin 18 (interferon-gamma-inducin	2.0 2.0
	445829	A1452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical prolein FLJ20457	2.0
	457652 429540	AF116656 M85776	Hs.273809	Homo saplens PRO1167 mRNA, complete cds gb:EST02297 Fetal brain, Stratagene (cal	20 20
50	459456	AA4B6036	Hs.190124	ESTs	2.0
	409840	AW502122		gb:Ut-HF-BR0p-ajr-c-08-0-Ut.r1 NIH_MGC_5	2.0
	441025 457802	AA913880 T78013	Hs.176379 Hs.167279	ESTS EVVE finance contribution Point effective pers	20 20
_0	445627	AW818475	Hs.7363	FYVE-finger-containing Rab5 effector pro ESTs	2.0
55	440299	Al871778	Hs.250112	ESTs	2.0
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	429998 455135	N90822 AW857989	Hs.48969	ESTs cb:PM2-CT0328-281299-003-e04 CT0328 Homo	20
<i>c</i> 0	411537	BE073250		gb:MR0-BT0551-050300-102-e05 BT0551 Homo	2.0
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	454197 445297	BE140966 BE544163	Hs.87128	gb:MRO-HT0065-081199-002-b06 HT0065 Homo hypothetical protein FLJ23309	20
	403977	DED4-14B	1 12.01 12.0	agposition protein a service	20
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03	418663 411479	AK001100 AW848047	Hs.41690	desmocollin 3 gb:ll:3-CT0214-291299-052-A12 CT0214 Homo	2.0 2.0
	426536	A1949749	Hs.44441	ESTs	20
	442765	BE567353	Hs.99480	ESTa	2.0
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	415258	AW752247	Hs.293853	ESTS	2.0
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75	416184 437733	R48481 A1792574	Hs.269177 Hs.122876		2.0 2.0
	453118	AW195849	Hs.252757		20
	457039	H29990	Hs.101937	' sine oculis homeobox (Drosophila) homoto	2.0
	444292 431360	Al139794 NM_000427	Hs.146569 Hs.251680		2.0 2.0
80	407644	D16815	Hs.37288	nuclear receptor subtamily 1, group O, m	2.0
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	457040 436464	N77624 Al046176	Hs.173717 Hs.269783	phosphatidic acid phosphatase type 2B ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
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•	408733	AW264812	Hs.254290	ESTs	20
	408767	AAD57279	Hs.211928	ESTs	2.0
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10	404604	DC499009	No. 246072	ESTB	2.0
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15	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	20
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	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0 2.0
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	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pl	2.0
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65	437620	AW976930	Hs.128760	ESTs qb:H.sapiens mRNA HTPCRX16 for olfactory	20 20
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75	435373		Hs.117689		2.0
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Table 318

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                        Indicates DNA strand from which exons were predicted.
           Nt_position: Indicates nucleotide positions of predicted exons.
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	403696	3135242	Minus	143467-143634
	403743	7652003	Minus	136463-136646
40	403760	7712202	Minus	45910-46260,47563-47824
	403764	7717105	Minus	118692-118853
	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Phra	93160-93409
45	403786	8083636	Minus	73028-73217
43	403891	7331467	Minus	191508-193220
	403895	7381715	Minus	3502-4002,4070-4308
	403977 404043	7657840 9558573	Minus Plus	115573-115820 29042-29135,46597-46699
	404059	3548785	Plus	104326-10678B
50	404076	9931752	Minus	3B48-3967
	404196	3805917	Minus	67928-88109
	404249	8655533	Plus	64270-64633
	404257	9367215	Plus	15262-16227
EE	404285	2326514	Plus	32282-32416
55	404288	2769644	Pkus	3512-3691
	404367	9965011	Minus	114391-114628
	404443 404453	7579073 7657714	Minus Plus	87198-87441 27768-29179
	404476	8080699	Pius	101841-102043
60	404513	B151941	Minus	112837-113339
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404577	4020145	Plus	17991-18420
65	404588	6456726	Minus	40059-40210
65	404599	8705107	Plus	110443-110733
	404604	9212537	Minus	72019-72509
	404638 404767	9796751 7882827	Minus Minus	99433-99528,100035-100161 23244-23759
	404793	7232206	Mimas	61087-61590
70	404822	3810614	Plus	7541-8132
• -	404834	6911603	Minus	37948-38226
	404845	7958980	Minus	47174-47326,52928-53146,53312-53602
	404898	7331420	Minus	177015-177328
75	404936	6850774	Plus	191519-191664
75	404957	7407927	Plus	147512-148011
	405017	8532084	Plus Plus	35551-35690 340-833
	405059 406000	7656683 8072525	Minus	349-822 38652-39202
	405090 405093	8072575	Plus	95878-96020
80	405120	B099940	Plus	140178-140340
	405170	9966524	Plus	37047-37198
	405229	7249019	Plus	51081-51701
	405230	7249032	Minus	97493-97682

	40.00.0	7040040		0.000 4.0000
	405233	7249045	Plus	9568-10065
	405241	7249178 7329374	Minus Plus	69927-70526
	405264			28556-28684
5	405287	3928029	Plus	69802-89999 404598 464848
,	405302	2078453	Minus	121688-121840
	405303	2078453	Minus	130607-130802
	405336	6094635	Plus	33267-33563
	405347	2979602	Minus	977-1116
10	4053B5	6552772	Plus	48332-48454
IV	405443	7408143	Plus	90716-90887,101420-101577
	405455 405494	7656675 8050952	Plus Minus	134112-134571 70284-70518
		9454643	Phys	
	405521 405523	9454643	Plus	65096-65247,77509-77637,81242-81364,84246-84395 114550-114668,117265-117407,119490-119599,123237-123395,131140-131217
15	405547	1054740	Plus	
15	405605	5836195	rius Minus	124361-124520,124914-125050
	405608	5B15499	Minus	117070-117270 66822-66925
	405629	4508116	Minus	101678-101866
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
20	405654	4895155	Minus	53624-53759
20	405692	4314424	Plus	61379-62562
	405706	4165003	Plus	44307-44431,49619-49802
	405720	9797144	Pius	13409-13861
	405732	7534017	Phos	146981-147316
25	405759	3288022	Minus	18283-18399
	405780	7248203	Minus	48204-48371
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
	405869	6758731	Minus	89867-90358
30	405935	6758795	Minus	163112-163652
	405959	6758815	Plus	1-642
	405965	8247786	Minus	179930-180373
	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
35	405981	8247790	Plus	4771-5338
-	406005	8247801	Minus	39912-40220
	406053	6758997	Pkis	30921-31532
	406073	9119150	Plus	60495-60610
	405091	9123919	Minus	197370-197935
40	406092	9123919	Plus	251370-251797,252168-252882
	406298	5686278	Minus	30084-30770
	406327	9212407	Plus	168241-168492
	406333	9213235	Plus	64689- 6479 8
4.5	406364	9256114	Minus	50715-50833
45	406377	9256135	Plus	126826-126979,129755-129942
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406470	9795562	Minus	15532-15697
50	406504	7711360	Minus	10706B-107277
50	406506	7711374	Minus	6843-8077F
	406592	4567182	Plus	352560-352963

55

Table 32A lists about 969 genes upregulated in lung florosis relative to normal body tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstital pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

60

Table 33A lists about 800 genes upregulated in lung fibrusts relative to normal lung. Types of pulmonary fibrosis samples included in this enalysis were kilopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (IHP), and non-specific intensitial pneumonitis (INSIP). These genes were selected from 59690 probesets on the Eos/Affymetrix Hu03 Genechtip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (Al), a normalized value reflecting the relative levels of mRNA expression.

65

Table 34A lists about 703 genes upregulated in idiopathic pulmonary fibrosis (IPF) relative to hypersensitivity pneumonitis (IHF) or non-specific intensitial pneumonitis (INSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (A1), a normalized value reflecting the relative levels of mRNA expression.

70

Table 35A lists about 323 genes upregulated in hypersensitivity pneumonitis (HP) relative to trilopathic pulmonary fibrosis (IPF) or non-specific intersitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Ecol/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (Al), a normalized value reflecting the relative levels of mRNA expression.

75

Table 36A lists about 52 genes upregulated in non-specific Interstitial pneumonitis (NSIP) relative to hypersensitivity pneumonitis (HP) or idiopathic pulmonary fibrosis (IPF). These genes were selected from 59690 protesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

80

Table 37A lists about 206 genes downregulated in lung fibrosts relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopatitic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstital pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 38A fists about 207 genes upregulated in lung fibrosis relative to normal fissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific intenstital pneumonitis (NSIP). These genes were selected from 59680 probasets on the Eos/Affymethx Hu03 Genechip array. Gene expression data for each probaset obtained from this analysis was expressed as average intensity (Al), a normalized value reflecting the relative levels of mRNA expression.

TABLE 32A: About 969 genes upregulated in lung fibrosis relative to normal body tissues

Pkey:

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number ExAcon:

10 UnigenelO: Unigene number

5

15

Unigene Title: Unigene filter
Unigene Title: Unigene filte
Unigene Title: Unigene filte
Unigene filte
Unigene filte
Unigene filte
Unigene filte
Unigene filte
90th percentile of lung fibrosis Als divided by 90th percentile of normal fissue Als, where the normal filter
90th percentile of lung fibrosis Als divided by 90th percentile of normal fissue Als, where the 15th percentile of normal fissue Als was subtracted from both the
normal first Unigene filte
90th percentile of lung fibrosis Als divided by 90th percentile of normal fissue Als, where the 15th percentile of normal fissue Als was subtracted from both the
normal fiscue Als was subtracted from both the

	Pkey	ЕхАссп	Unigenel D	Unigene Title	RI	R2
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	22,45	28.63
20	406964	M21305		FGENES predicted novel secreted protein.	16.10	7.65
20	431723	AW058350	Hs.16762	Homo saplens mRNA; cDNA DKFZp564B2062 (f	15.83	14,86
	442275	AW449467	Hs.54795	ESTs	15.74	21.96
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	13.83	34.53
	444342 431089	NM_014398	Hs.10887	similar to lysosome-associated membrane	12.40	7.38
25	421110	BE041395 AJ250717	Hs.1355	ESTs, Weakly similar to unknown protein	12.3B	6.05
20	457200	U33749	Hs.197764	cathepsin E	11.86	6.49
	425211	M18667	Hs.1867	thyroid transcription factor 1 progastricsin (pepsinogen C)	11.38	9.79
	443709	A1082692	Hs.134662	ESTs	10.89	15.94
	431164	AA493650	Hs.94367	Homo sepiens cDNA; FLJ23494 fis, clone L	10.84 10.06	8,27
30	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.96	8.92 5.43
	432519	Al221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	9.90	7.87
	421798	N74880		N-acylsphingosine amidohydrolase (acid c	9.38	8.35
	400259			Eos Control	9,03	6.48
25	444325	AW152618	Hs.16757	ESTs	8.31	6.76
35	416402	NM_000715	Hs.1012	complement component 4-binding protein.	8.14	5.51
	413048	M93221	Hs.75182	mannose receptor, C type 1	7.70	4.09
	432985	T92363	Hs.178703	ESTs	7.56	7.83
	443324	R44013	Hs.164225	ESTs	7.06	4.47
40	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	6.90	2.89
70	408562 449523	AM36323	Hs.31141	roundabout (axon guidence receptor, Dros	6.88	4.00
	449525 421952	NM_D00579 AA300900	Hs.54443 Hs.98849	chemokine (C-C motif) receptor 5	6.56	4.25
	427383	NM_005411	Hs.177582	dynein light chair. 28 (DNLC28)	6.48	4.47
	409203	AA780473	Hs.587	surfactant, pulmonary-associated protein cytochronie P450, subfamily IVB, polypept	6.30	13,57
45	441835	AB036432	Hs. 184	advanced glycosylation and product-speci	6.28	3.38
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.99 5.88	13,26
	415323	BE269352	Hs.949	neutrophil cytosofic factor 2 (65kD, chr	5.88	4,10 3.35
	442652	AI005163	Ha_201378	ESTs, Weakly similar to T12545 hypotheti	5.87	5.69
50	414812	X72755	Hs.77367	monoldne induced by gamma interferon	5.84	3.34
50	416007	M13509	Hs.83169	metrix metalloproteinase 1 (interstital	5.72	5,90
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	5.69	6.89
	436954	AA740151	Hs.130425	ESTs	5.58	4.72
	446998	N99013	Hs.18762	Homo sapians mRNA; cDNA DKFZp564B2062 (f	5.48	5.33
55	421340	F07783	Hs.1369	decay accelerating factor for complement	5.48	269
33	420556	AA279098	Hs.187636	ESTs	5.45	3.99
	432441 408380	AW292425	Hs.163484	Intron of hepatocyte nuclear factor-3 at	5.3B	3.65
	414998	AF123050 NM_002543	Hs.44532 Hs.77729	diubiquitin	15.37	3.11
	446921	AB012113	Hs.16530	oxidised low density lipoprotein (lectin small inducible cytokine subfamily A (Cy	5.30	3.99
60	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.29	4.0D
	442832	AW206560	Hs.253569	ESTs	5.2B 5.20	2.48 3.78
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	5.20 5.11	3.15 3.81
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	5.11	2.88
C 5	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.07	3.46
65	428043	T92248	Hs.2240	uteroglobin .	5.06	9.46
	431745	AW972448	Hs.163425	ESTs	5.04	4.16
	444527	NM_005408	Hs.11383	small Inducible cytokine subfamily A (Cy	5.04	3.68
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	5.02	4.26
70	419231	AL046294	He,136245	ESTs, Weakly similar to T17227 hypotheti	4.97	3.35
70	428927 432222	AA441837	Hs.90250	ESTs	4.92	3.15
	442994	Al204995 Al026718	11- 10004	gb:an03c03.x1 Stratagene schizo brain S1	4.79	3.05
	416030	H15261	Hs.16954 Hs.21948	ESTs ESTs	4.76	2.65
	438873	Al302471	Hs. 124292	Homo sapiens cDNA: FLJ23123 fis, clone 1.	4.76	4.26
75	453142	AA033848	Hs.7473	ESTs	4.73 4.66	3.24
	424917	A163620B	Hs.96901	hypothetical protein FLJ23049	4.64	2.92
	439750	AL359053	Hs_57664	Homo saplens mRNA full length insert cDN	4.60	4.88 2.60
	432810	AA863400		ESTs	4.54	2.42
90	418259	AA215404		ESTs	4.54	2.54
80	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	4.48	4.86
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.46	3.62
	423575	C18863	Hs.163443	intron of periostin(OSF-2os)	4.44	3.41
	428667	Al375550	Hs.346868	nucleolar protein p40; homolog of yeast	4.42	3.41

		-1440000				
	429228 432435	Al553633 BE218886	Hs.282070	ESTs ESTs	4.32 4.30	2.98
	446932	AA961459	Hs.125644	ESTs	4.30	2.26 2.81
_	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30	2.39
5	409435	AIB10721	Hs.95424	ESTs	4.30	2.60
	419490 452561	NM_006144 Al692181	Hs.90708 Hs.49169	granzyme A (granzyme 1, cytoloxic T-lymp KIAA1634 protein	4.29 4.23	2.48 2.26
	427698	AW972594	Hs.335499	ESTs	4.22	3.49
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	4,22	13.34
10	446608 428227	N75217	Hs.257846	ESTS	4.20	3.62
	459702	AA321649 AJ2D4995	Hs.2248	small inducible cytokine subfamily B (Cy gb:an03c03.x1 Stratagene schizo brain S1	4.18 4.16	3.14 2.64
	445885	Al734009	Hs.127699	KIAA1603 protein	4.16	3.99.
15	430280	AA36125B	Hs.237868	interlaukin 7 receptor	4.13	2.79
13	425259 427019	AL049280 AAD01732	Hs.155397 Hs.173233	Homo sapiens mRNA; cDNA DKFZp564K143 (fr hypothetical protein FLJ10970	4.12	2.19
	420556	AA278300	Hs.124292	Homo saplens cDNA: FLJ23123 fis, clone L	4.12 4.08	3.02 3.13
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.0B	3.48
20	432731	R31178	Hs.287820	fibronectin 1	4.06	2.66
20	439398 409153	AA284267 W03754	Hs.221504 Hs.50813	ESTs hypothetical protein FtJ20022	4.06 4.05	2,86 3.51
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04	2.44
	436120	A)248193	Hs.119860	ESTs	4.04	3.11
25	407910 421462	AA650274	Hs.41296	fibronectin teucine rich transmembrane p	4.03	2.69
2,3	443257	AF016495 Al334040	Hs.104624 Hs.11614	aquapodo 9 HSPC065 protein	4.00 4.00	2.51 2.61
	421659	NM_014459	Hs.106511	protocadherin 17	4.00	3.00
	424273	W40460	Ha.144442	phospholipase A2, group X	3.98	2.30
30	415457 450656	AW081710 AA010539	Hs.7369 Hs.18912	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs	3.97	3.36
20	429784	MB9796	Hs.30	membrane-spanning 4-domains, subfamily A	3.96 3.94	4.37 2.44
	424527	AW13855B	Hs.334873	ESTs, Weakly similar to 154374 gene NF2	3.93	3.08
	413385	M34455	Hs.840	Indolaamine-pyrrole 2,3 dioxygenasa	3.92	3.53
35	452416 428434	AA026115 AW363590	Hs.114777 Hs.65551	ESTs Home sapiens, Similar to DNA segment, Ch	3.92 3.90	2.90
00	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, done PL	3.90	5.06 2.00
	453204	R10799	Hs.191990	ESTs	3.90	2.22
	450896 422173	A1654223 BE385828	Hs.16026 Hs.250619	hypothetical protein FLJ23191	3.81	3.82
40	425638	NM_012337	Hs.158450	phorbolin-like protein MDS019(CEM15) nasopharyngeal epithelium specific prote	3.80 3.76	2.23 2.86
	406672	M26041	Hs.198253	mejor histocompatibility complex, class	3.78	3.70
	457411	AW085961	Hs.130093	Iroquals-class homeobox protein IRX2	3.76	2.56
	432606 436260	NM_002104 BE172762	Hs.3066 Hs.292710	granzyme K (serine protease, granzyme 3; ESTs, Weakly similar to ALU5_HUMAN ALU S	3.76 3.74	2.76 2.83
45	414821	M63835	Hs.77424	Fo fregment of IgG, high affinity la, re	3.74	2.55
	428820	AA435187	Hs.172631	Integrin, alpha M (complement component	3.71	2.25
	458079 419556	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.70	2.26
	417412	U29615 X16896	Hs.91093 Hs.82112	chitinase 1 (chitotriosidase) interieuldin 1 receptor, type i	3.69 3.68	7.71 2.17
50	426174	AA547959	Hs.115838	EST ₈	3.65	2,93
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	3.64	2.62
	435990 427621	Al015862 BE621182	Hs.131793 Hs.179882	ESTs hypothetical protein FLJ12443	3.62 3.62	2.27
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L.	3.61	3.48 3.18
55	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.60	3.05
	426116 419235	AAB68729 AW470411	Hs.144694	ESTs neurohimin	3.60	2,80
	424054	1154EEAA	Hs.288433 Hs.26638	membrane-spanning 4-domains, subtamily A	3.58 3.56	2.88 2.58
<i>c</i> o	422667	H25642		E\$Ts	3.55	244
60	406673	M34996	Hs.198253	major histocompatibility complex, class	3.54	3.98
	414142 428330	AW368397 L22524	Hs.334485 Hs.2256	hemicentin(fibulin 6) matriyaln,	3.54 3.54	3.30 3.11
	430832	A1073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	3.53	2.38
65	417318	AW953937	Hs.240845	ESTs	3.52	2.02
03	456034 415992	AW450979 C05837	Ue 1/EPA7	gb:UI-H-BI3-sta-s-12-0-UI.s1 NCI_CGAP_Su hypothetical protein FLJ13593	9.50	3.21
	430709	R34356	Hs.145807	gb:yh85d01.s1 Sozres placenta Nb2HP Homo	3.48 3.48	2.35 2.13
	440273	A1805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3,47	2.93
70	424711	NN_005795	Hs.152175	calcitorin receptor-like	3.47	2.69
70	418832 416847	X04011 1.43821	Hs.86974 Hs.80261	cytochrome b-245, beta polypeptide (chro enhancer of filamentation 1 (cas-like do	3.46 2.46	231
	448019	AW947164	Hs.195641	ESTs, Moderately similar to 136022 hypot	3.46 3.45	2.37 2.07
	447183	Al554733	Hs.173182	ESTs	3.42	201
75	435299	AI745458 AI 157466	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40	3.49
, 5	425922 413714	AL157466 Al580944	Hs.162751 Hs.71428	Homo saplens mRNA; cDNA DKFZp761E2423 (f ESTs	3.40 3.38	2.42 2.52
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.36	2.13
	436043	AW963838	Hs.168830	Homo sapiena cDNA FLJ12136 fis, clone MA	3.36	2.41
80	450330 407756	AW500775 AA116021	Hs.24817 Hs.38250	hypothetical protein FLJ20136 ubiquitin specific protesse 18	3,36 3.35	2.06
	410606	AW418779	Hs.114889	ESTs	3.35	2.42 2.39
	450726	AW204600	_	refinolo acid receptor, alpha	3.34	6.35
	430573	AA7445 5 0	Hs.136345	ESTs	3.33	1.94
				450		

	424F0F	1105696	Lie anania	-homeline (C.C. melifi mannier like 2)	3.32	2.75
	421585 433658	U95626 L03678	Hs.302043 Hs.156110	chemokine (C-C molif) receptor-like 2(Immunoglobulin keppa constant	3.31	2.22
	454076	AW204712	Hs.61957	ESTs	3.31	1.95
_	452039	A192298B	Hs.172510	ESTs	3.30	2.95
5	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30 3.30	2.37 2.48
	430414 41795B	AW365665 AA767382	Hs.120388 Hs.193417	ESTs	3.30	2.04
	423001	AA320014	Hs.208603	ESTs	3.29	2.62
••	443774	AL117428	Hs.9740	DKFZP434A236 prolein	3.28	2.35
10	424084	AJ940675	Hs.20914	hypothetical protein FLJ23056	3.28	2.05
	424238	AA337401	Hs.137635	ESTS Home analoge multiple annia OVEZnA34D301 (fr	3.28 3.27	2.45 2.63
	429819 446859	Al.133011 Al792798	Hs.225108 Hs.12496	Homo saplens mRNA; cDNA DKFZp434P201 (fr ESTs, Weakly similar to ALU4_HUMAN ALU S	3.26	2.67 .
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.26	2.04
15	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22	2.36
	440452	A!925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22 3.20	3.87 2.79
	422109 430378	S73265 Z29572	Hs.1473 Hs.2556	gastrin-releasing peptide turnor necrosis factor receptor superfami	3.20	2.30
	413802	AW96449D	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18	2.42
20	408761	AA057264	Hs.238936	ESTs, Weakly similar to (deffine not ava	3,18	2.12
	438568	R98865	Hs.11135	major histocompatibility complex, class	3.18	3.86
	451497 444034	H83294 AL161957	Hs.284122 Hs.10177	Whi inhibitory factor-1 plackstrin homology domain interacting p	3.18 3.17	2.99 2.02
	446094	AK001760	Hs.13801	KIAA1685 protein	3.17	2.42
25	442048	AA974603		gb:op34f05.s1 Soares_NF1_T_GBC_S1 Home s	3.17	2.27
	4066B5	M18728	11 000044	gb:Human nonspecific crossreading antig	3.17	2.80
	430253 424943	AK001514 AU077260	Hs.236844 Hs.153924	hypothetical protein FLJ10652 death-associated protein Kinase 1	3.16 3.16	1,95 2,18
	436805	AA731533	Hs.270751	ESTs	3,16	1.95
30	412610	X90908	Hs.74126	tatty acid binding protein 6, iteal (gas	3.15	3.63
	409799	D11928	Hs.76845	phosphoserine phospholase-like	3.14	1.74
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.13 3.12	3.35 2.09
	420729 419839	AW964897 U24577	Hs.290825 Hs.93304	ESTs phospholipase A2, group VII (platelet-ac	3.12	2.06
35	4165B0	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12	2.58
	451B20	AW058357	Hs.199248	ESTs	3.10	2.26
	440028	AVV473675	11- 00-000	ESTs, Wealdy similar to T17227 hypotheti	3.10	3.01 2.32
	448030 437866	N30714 AA156781	Hs.325960	membrane-spanning 4-domains, subfamilly A metallotidonein 1E (functional)	3.10 3.10	1.80
40	428513	BE220806	Hs. 164697	plexin C1	3.10	2.11
	438607	AW080237	Hs.252884	ESTs	3.10	2.20
	445034	AW293376	Hs.143659	ESTs	3.08	281
	458332 415063	A1000341 A1632683	Hs.27179	ESTs Homo sapiens cDNA FLJ12933 fis, clone NT	3.08 3.08	1.87 1.87
45	407930	AA045847	Ha.188361	Homo saplens CDNA FL312807 fis, done NT	3.08	1.94
	407192	AA609200		gb:af12e02.s1 Soares_lestis_NHT Homo sap	3.07	212
	452960	AK001335	Hs.31137	protein tyrosine phosphalase, receptor t	3.07	2.16
	425509	AFU79363	Hs.158213	sperm associated antigen 6 ESTs	3.06 3.05	2.75 2.41
50	431087 452235	H12723 AL039743	Hs.290791 Hs.28514	lestes development-related NYD-SP21	3.06	2.64
	449328	A1962493	7.0.2001	ESTs	3,06	2.78
	422900	AA641201	Hs.222051	ESTs	3.05	1.87
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7 chloride Intracellular channel 5	3.05 3.05	1.99 2.49
55	430250 437527	NM_016929 A)241019	Hs.283021 Hs.145644		3.04	217
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo saptens	3.04	1.78
	420495	Al338247	Hs.98314	Homo saplens mRNA; cDNA DKFZp586L0120 (f	3.02	2.43
	445495 411252	BE622641 AB018549	Hs.38489 Hs.69328	ESTs, Weakly similar to 138022 hypotheti MD-2 protein	3.02 3.02	1.77 1.95
60	439581	Al348408	Hs.124675		3.02	2.24
	420683	AA830168	Hs.271305	ESTs	3.01	2.14
	412095	A)624707	Hs.6921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00	2.13
	410434 436396	AF051152 Al6B3487	Hs.63668 Hs.152213	tol/-like receptor 2 wingless-type MATV Integration site fami	3.00 3.80	2.60 1.94
65	434194	AF119847	110.102210	Homo saplens PRO1550 mRNA, partial cds	3.00	1.81
	435800	A1248285	Hs.118348	ESTs .	3.00	1.89
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	3.00	2.08
	449057	AB037784 AA127382	Hs.22941 Hs.22404	KIAA1363 protein proteese, serine, 12 (neurotrypsin, moto	3.00 2.99	2.18 2.46
70	413195 436198	AK001125	TIS,2291/4	Homo sapiens cDNA FLJ10263 fis, clone HE	2.99	2,76
• •	411492		Hs.70337	immunoglobulin superfamily, member 4	2.99	2.16
	444020	R92962	Hs.35052		2.98	221
	427785		Hs.180828		2.98 2.98	2.08 2.40
75	432583 457675		Hs.162283 Hs.306574		2.96	2.03
. –	414846		Hs.901	CD48 antigen (B-cell membrane protein)	296	1.74
	429950	AW08160B	Hs.10505	3 ESTs	2.96	2.40
	420394		Hs.97403	KIAAD944 protein	2.95 2.95	245 413
80	406698 419038		Hs.73931 Hs.19032		2.94 2.94	4.13 1.72
	449768		Hs.20683		2.94	2.93
	418293	A1224483	Hs.16063	hypothetical protein FLJ21877	2.94	1.94
	400880			NM_000611*:Homo sepiens CO59 entigen p18	2,94	1.74
				459		
				_		

	100000		11 pagenn	more state to the connection.	224	0.40
	430382 419034	AA477908	Hs.282267 Hs.89565	ESTs, Moderately similar to I38022 hypot hemopoletic cell kinase	2.94 2.93	2.12 2.25
	439335	NM_002110 AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobin, fa	2.55 2.93	3,72
_	429597	NM 003816	Hs.2442	a disintegrin and metalloprotelnase doma	2.92	1.91
5	419981	AA897581	Hs.128773	ESTs	2.92	2.18
	400419	AF084545		Target	2.92	1.83
	435176	AA744875	Hs.189413	ESTs .	2.91	2.15
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	2.90	2,25
10	444339 429272	T96555 W25140	Hs.31562 Hs.110867	ESTs ESTs	2.90 2.90	3.16 2.43
10	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.90	2.29
	435080	A)831760	Hs.155111	hypothetical protein FLJ14428	2.90	2.40
	402474			NM_004079:Homo saplens cathepsin S (CTSS	2.88	247 _
1.5	421554	AW137676	Hs.97775	ESTs	2.88	3.37
15	422770	AL117544	Hs.120021	DKFZP4341092 protein	2.88	2.00
	434658	AI624436	Hs.310286	ESTS	2.88	2.06 2.24
	440248 442006	AA876138 AW975183		ESTs ESTs, Weakly similar to S72482 hypotheti	2.86 2.86	4.32
	430515	AA746503	Hs.283313	ESTs	2.86	2.96
20	446063	Al720140	Hs.151079	ESTs	2.86	2.47
	438177	BE327015		ESTs .	2.86	1.70
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.85	2.06
	417105	X60992	Hs.81226	CD6 antigen	2.85	3.00
25	433230 438676	AW136134	Hs.220277 Hs.123446	ESTs ESTs	2.84 2.84	1.97 2.62
25	435575	AA813745 AF213457	Hs.44234	triggering receptor expressed on myeloid	2.82	4,33
	420252	AW270404	Hs.193161	ESTs	2.82	3.22
	415788	AW628686	Ha.78851	KIAA0217 protein	2.82	1.78
20	428065	A1634046	Hs.157313	ESTs	2.81	2.47
30	434340	AJ193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.81	2.67
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1 ESTs	2.78	3.39
	435517 439883	AA928626 AL359652	Hs.130177 Hs.171096	Homo sapiens EST from ctone DKFZp434A041	2.78 2.78	2.36 1.82
	434158	T86534	Hs.14372	ESTs	2.78	1.96
35	428923	BE047698	Hs.188785	ESTs	2.78	2.07
	413786	AW613780	Hs.13500	ESTs	2.78	1.97
	406387			Target Exon	2.77	4.22
	421168	AF182277	Hs.330780	cylochrome P450, subfamily IIB (phenobar	2.76	3.24
40	444561 427484	NM_004459 N32859	Hs.11392 Hs.37288	c-fos induced growth factor (vascular en nuclear receptor subfamily 1, group D, m	2.78 2.76	2.11 1.94
. 40	417728	AW138437	Hs.24790	KIAA1573 protein	2.76	1.78
	435154	AA668764	11022-160	ESTs	2.76	2.10
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.76	2.21
45	423387	AJ012074		vascactive intestinal peptide receptor 1	2.76	2.36
45	432060	AW971364	Hs.324775	ESTs .	2.75	2.02
	434164	AW207019	Hs.148135	serine/threonine kinase 33	2.74 2.74	2.48 1.93
	423706 442703	U95218 Alo44949	Hs.131924 Hs.116298	G protein-coupled receptor 65 ESTs	2.74	1.89
	450247	AF123303	Hs,24713	hypothetical protein	2.74	1.73
50	43099B	AF128B47	Hs.204038	indolethylamine N-methyltransferase	2.74	2.85
	426535	AU077012	Hs.288582	ESTs, Weakly similar to abiquitous TPR m	2.74	1.88
	409196	NM_001874	Hs.334873	сельохурервазе M	2.73	1.88
	422389	AF240635	Hs.115897	protocatherin 12	2.72	2.26
55	444324 417831	A1301330 H16423	Hs.143838 Hs.82685	ESTs CD47 antigen (Rh-related antigen, integr	2.72 2.72	1.74 2.40
22	428769	AW207175	Hs.106771	ESTs	2.72	219
	404277			NM_019111*:Homo sepiens major histocompa	2.72	3.12
	409653	AW451693	Hs.220826	ESTs	2.72	2.62
60	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.72	2,25
60	430299	W28673	Hs.105747	serine carboxypepildase 1 precursor prot	272	2.09
	4443B1 44 3 547	BE387335 AW271273	Hs.283713	hypothetical protein BC014245 hypothetical protein FLJ12666	2.71 2.71	2.26 1.74
	408741	M73720	Hs.646	carboxypepiidase A3 (masi celi)	2.70	2.39
	402674	***************************************	12,0,0	Target Exon	2.70	1.95
65	438068	AJ927209	Hs.308210		2.70	2.23
	415075	L27479	Hs.77689	Friedreich ataxta region gene X123	2,69	211
	444314	Al140497		gb:ow/fb09.s1 Soares_felal_liver_spleert_	2.69	2.28
	428656	AB037798	Hs.188790		2.6B	1.91
70	418883 443951	BE387036 F13272	Hs.1211	acid phosphatase 5, tertrale resistant ferrilin, light polypeptide	2.68 2.68	3,95 2.66
10	427581	NM_014788	Hs.179703		2.68	1.74
	432639	AW973785	113.170700	gb:EST385886 MAGE resequences, MAGM Homo	2.68	1.78
	446423	AW139655	Hs.150120		2.68	2.29
75	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.67	2.07
75	431779	AW971178	Ha.268571		2.67	3.00
	458124	AW005548	Hs.124590		2.67	3.78
	432882 445745		Hs.279696 Hs.13245	serum/glucocorticoid regulated kinase-li KIAA0455 gene product	2.56 2.66	1.64 1.64
_	425188	AK002052	Hs.155071		265	1,92
80	432231		Hs.274127		2.64	4.23
	442200	AW590572	Hs.235768	ESTs	2.64	2.46
	426828				2.64	2.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.63	3.23

	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.63	2.48
	411213	AA676939	Hs.69285	neuropiin 1	2.62	1.73
	439737	A)751438	Hs.41271	Homo sapiens mRNA full length Insert cDN	2.62	2,69
5	446570	AV659177	Hs.127160	EST's	2,61	2.44
,	411020 434792	NM_006770 AA649253	Hs.67726 Hs.132458	macrophage receptor with collagenous str ESTs	2.60 2.60	3.39 1.74
	426782	R14614	Hs.33846	ESTs ·	2.60	2.36
	425371	D49441	Hs.155981	mesothelin	2.60	6.97
10	447720	AL038765	Hs.161304	ESTs	2.59	3.06
10	444623 433376	Al183829 Al249361	Hs.202111 Hs.74122	ESTs caspase 4, apoptosis-related cystelne pr	2.59 2.58	2.77 2.01
	444542	Al161293	Hs.280380	aminopepidase	2.58	2.31
	439549	AW937885	Hs.137314	ESTs	2.58	2.37 .
15	4313B5	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.5B	2.56
15	417015 433308	M83772 AA582718	Hs.80876 Hs.291650	flavin containing monocxygenase 3 ESTs	2.56 2.56	2.47 2.01
	443885	H91806	Hs.15284	ESTs	2.55	1.71
	408170	AW204516	Hs.31B35	ESTS	2.55	1.59
20	456844	A)264155	Hs.152981	COP-diacylglycerol synthase (phosphatida	2.54	1.63
LU	412104 428791	AW205197 AA435661	Hs.240951 Hs.264750	Homo saplens, Similar to RIKEN cDNA 2210 ESTs	2,54 2.53	2.98 2.29
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.53	3.91
	447357	AI375922	Hs.159367	ESTs	2.52	2.83
25	431393 424105	AW971493 Al142336	Hs.134269 Hs.43977	ESTs, Highly similar to cytokine recepto Human DNA sequence from clone RP11-196N1	2.52 2.52	1.90 3.45
23	408308	AL033377	Hs.44197	hypothatical protein DKFZp564D0462	2.52	1.98
	438698	AW297855		ESTs, Weakly similar to 138022 hypotheti	2.52	1.98
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FL300111 protein,	2.52	241
30	424049 438543	AB014524 AA810141	Hs.138380 Hs.192182	KIAA0624 protein ESTs	2.51 2.51	2.19 2.06
50	414061	NM_000699	Hs.335493	anytase, alpha 2A; pancreatic	251	2.14
	424806	AA382523	Hs.105689	MSTP031 protein	2.51	2.11
	438580	AAB11262	Hs.299202	ESTs	2.50	1.83
35	434445 444001	Al349306 Al095087	Hs.11782 Hs.152299	ESTs ESTs, Moderately similar to S65657 alpha	2.50 2.50	3.13 1.76
55	413638	H71252	113.100.003	gb:ys12h12.s1 Soares fetal liver splean	2.50	2.00
	421281	Al299139	Hs.17517	ESTs	. 2.50	2.40
	441384	AA447849	Hs.288660	retinoic acid induced 3	2.50	2.75
40	435772 433102	AW975688 Al343966	Hs.158528	metallothioneln 1E (functional) ESTs	2.49 2.49	1.80 2.25
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.48	209
	445612	N94126	Hs.12969	hypothetical protein	2.48	2.28
	445261 433854	179759 AA610649	Hs.250651 Hs.333239	ESTa, Waakly similar to 138022 hypotheti	2.48 2.48	1.87
45	447997	H00656	Hs.29792	ESTs ESTs, Weakly similar to 138022 hypotheti	2.48	2.09 2.75
-	411069	AL193092	Hs.68055	hypothetical protein DKFZp434I0428	2.48	2.01
	440594	AW445167	Hs.126036	ESTs	2.48	1.57
	450295 431316	A1786732 AA502663	Hs.210628 Hs.145037	ESTs ESTs	2.48 2.48	1.99 1.80
50	438564	AA381553	Hs.198253	major histocompatibility complex, class	2,48	2.80
	439593	BE073597	Hs.124863	ESTs	2.48	1.89
	422355	AW403724	Hs.300697	coaguiation factor VII (serum prothrombi	2.47	3.74
	453134 417169	AA032211 R13550	Hs.118493 Hs.21388	ESTS ESTS	2.46 2.46	2.72 1.88
55	434411	AA632649	Hs.201372	ESTS	2.46	1.95
	440381	AA917808	Hs.190495	ESTs	2.46	2.09
	448782 404240	AL050295		KIAA0758 protein	2.46 2.45	2.69
	450843	AJ741483	Hs.205383	NM_018950:Homo sapiens major histocompat ESTs	2.44	2.83 2.25
60	434137	AA907734	Hs.124895	ESTs	2.44	2.55
	438315	R56795	Hs.82419	ESTs	2.44	1.94
	420B02 439402	U22376 W02753	Hs.1334 Hs.103002	v-myb avian myeloblastosis vixal oncogen ESTs	2.44 2.44	1.61 1.90
	445903	Al347487	Hs.132781	class I cytokine receptor	2,44	2.32
65	437323	AA371145	Hs.194397	teptin receptor	2.44	1.70
	433923	A)823453	Hs.146625 Hs.208726	ESTs	2.44	1.58
	442201 437982	AW516704 N93466	Hs.121764	ESTs ESTs, Weakly similar to testicular tekti	2.43 2.43	1.68 3.22
	452698	NM_001295	Hs.301921	chemokina (C-C motif) receptor 1	2.43	2.21
70	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	2.43	2.13
	486973 428055	M34996 AA420564	Hs.198253 Hs.101760	major histocompatibility complex, class ESTs	2.43 2.42	2.68 2.05
	428970	BE276891	Hs.194691	retinoic acid Induced 3 (RAIG1); metabo	2.42	2.79
me	433138	AB029498	Hs.59729	seméphoda sem2	2.42	1.6B
75	415757	AA830854	Hs.187810		2.42	2.02
	438507 450811	AA809052 A1739486	Hs.245497	ESTs	2,42 2.42	2.08 1.97
	424027	AW337575	Hs.201591	ESTs	2.42	2.76
ρΛ	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.41	3,15
80	435978 426291	AF272899 U58913	Hs.135118 Hs.169191	Homo saplens PR-domain zinc finger prote small inducible cytokine subfamily A (Cy	2.41 2.40	2.08 1.76
	416370	N90470	Hs.203697		2.40 2.40	1.76
	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	2.40	1.63

	445633	AI453386	Hs.17287	ESTs, Weakly similar to \$26689 hypotheti	2.39	1.99
	431300	AA502346	110.11 251	gb:ne26b03.s1 NCI_CGAP_Co3 Home sapiens	2.39	1.79
	407690	R47799	Hs.266957	hypothetical protein FL114281	2.39	1.84
5	418113	Al272141	Hs.83484	SRY (sex determining region Y)-box 4	2.39	2.21
3	425235 451406	AA353113 Al694320	Hs.112497 Hs.6295	Homo saplens cDNA: FLJ22743 fis, clone H ESTs, Weakly similar to T17248 hypotheti	2.38 2.3B	2.09
	437479	R61866	Hs.101277	ESTs	2.3B 2.3B	1.78 3.00
	445784	Al253155	Hs.146065	ESTs	2.38	1.61
10	418300	A1433074	Hs.86682	Homo saplens cDNA: FLJ21578 fis, clone C	2.38	2.25
IV	413753 418945	U17760	Hs.75517	taminin, beta 3 (nicela (125kD), kalinin	2.37	1.55
	416140	BE246762 Al918035	Hs.89499 Hs.30119B	arachidonate 5-lipoxygenase roundabout (axon guidance receptor, Dros	2.37 2.37	2,41
	418262	Z38958	1102041100	ESTs	2.37	1.61 2.05 -
1.0	420943	A1718702	Hs.279930	major histocompatibility complex, class	2.37	2.00
15	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.37	2.05
	429747 420460	M87507 AA262331	Hs.2490 Hs.48376	caspase 1, apoptosis-related cysteine pr	2.37	1.67
	420137	AA306478	Hs.95327	Homo sepiens clone HB-2 mRNA sequence CD3D antigen, delta polypeptide (TiT3 co	2.36 2.36	1.88 2.61
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	2.36	2.84
20	427250	R35941	Hs.25418	ESTa	2.36	2.15
	452194	A)694413	11. 0-010	olfactory receptor, family 2, subfamily	2.36	3.41
	411027 407242	AF072099 M18728	Hs.67846	leukocyte immunoglobulin-like receptor, gb:Human nonspecific crossreading antig	2.36 2.35	3.05
	418875	W19971	Hs.233459	ESTs	2.35 2.35	2.34 1.95
25	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.35	1.85
	432608	A1492660	Hs.170935	ESTs	2.35	2.06
	40804B 415189	NM_007203 L34657	Hs.42322 Hs.78146	A kinase (PRKA) anchor protein 2 platelet/endothelial cell adhesion molec	2.35	1.91
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	2.35 2.35	2.34 2.13
30	410577	X91911	Hs.64639	glioma pathogenesis-related protein	2.34	1.73
	422099	AA156022	Hs.111518	hypothetical protein	2.34	1.80
	427337 427541	Z46223	Hs.176663 Hs.82921	Fe tragment of IgG, low affinity (lib, r	2,34	2.24
	420899	A1798983 NM_001629	Hs.100194	solute carrier family 35 (CMP-static aci arachidonate 5-lipoxygenese-activating p	2.33 2.32	2.62
35	431848	Al378857	Hs.271605	ESTs, Highly similar to AF175263 1 zinc	2.32	2.52 2.50
	446354	AW449650		ESTs	2.32	2.21
	423354	AB011130	Hs.127436	caldum channel, voltage-dependent, alph	2.32	4.34
	423961 410798	D13666 BE178622	Hs.136348 Hs.16291	perioetin(OSF-20s) gb:PM3-HT0605-270200-001-a02 HT0605 Homa	231 231	2.19 2.34
40	457250	AA811987	Hs.125779	ESTs	2,31	1.66
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	2.31	2.96
	426839 422746	M74782 NM_004484	Hs.172689 Hs.119651	interleukin 3 receptor, alpha (low affin glypican 3	2.30 2.30	2,12 2,16
	439920	H05430	Hs.288433	neurotrimin	2.30	4.08
45	414942	C14898	Hs.192986	ESTs	2.30	2.02
	419092 424878	J05581 H57111	Hs.89603 Hs.221132	mucin 1, transmembrane ESTs	2.29	3.CB
	406687	M31126	143.22.11.02	matrix metalloproteinase 11 (stromelysin	2.29 2.29	1.84 2.76
EA	411605	AW006831		ESTs	2.29	1.58
50	416965	N26223	Hs.160436	ESTS	2.29	4.71
	428713 435106	AA432067 AA100847	Hs.5976	ESTs, Moderately similar to CYA4 RAT ADE ESTs, Highly similar to AF174600 1 F-box	2.29	1.73
	420380	AA640891	Hs.102406	ESTs	2.28 2.28	1.90 2.82
EE	407137	T97307		gb;ye53h05.s1 Soares fetal liver spleen	2.28	1.52
55	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-	2.28	2.09
	447160 421114	AA330310 AW975051	Hs.24181 Hs.293156	ESTs ESTs, Weakly similar to 178885 section/lb	2.28	1.71
	453686	AL110326	Ha,304679	ESTS, Moderately similar to Z195_HUMAN Z	2.27 2.27	1.9B 1.91
60	452114	N22687	Hs.8236	ESTs	2.27	1.68
60	417355	D13168	Hs.82002	endothelin receptor type B	2.26	1.63
	434927 442262	H46612 BE170651	Hs.293815 Hs.8700	Homo saptens HSPC285 mRNA, partial cds deleted in liver cancer 1	2.2 6	1,84
	426216	N77630	Hs.13895	Homo sepiens cDNA FL311654 fis, clone HE	2.26 2.28	1.86 1.72
15	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26	1.70
65	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.26	1.56
	414221 435272	AW450979 AA906415	Hs.110041	gb:UJ-H-BI3-ala-a-12-0-UL:s1 NCI_CGAP_Su ESTs	2.26	212
	414991	C17898	113.114041	gb:C17898 Human placenta cDNA (TFujiwara	2.25 2.24	2.15 3.58
70	424623	AW963062	Hs.270737	ESTs	2.24	1.87
70	424665	AW368576	Hs.139851	caveolin 2	2.24	2.15
	422426 413829	W79117 NM_001872	Hs.58559 Hs.75572	ESTs	2.22	3.33
	427535	R29543	Hs.2164	carboxypeptidase 82 (plasma) pro-platelet basic protein (includes pla	2,22 2.22	2.39 3.28
	447197	R36075		gbtyh88b01.s1 Soares placenta Nb2HP Homo	2.22	1.59
75	446142	A1754693	Hs.145968	ESTs	2.22	1.68
	410503 435523	AW975746 T62849	Hs.188652 Hs.11090	KIAA1702 protein	2.22	1.56
	437629	AW574774	Hs.121692	membrane-spanning 4-domains, subfamily A ESTs	2.22 2.22	2.49
00	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	2.21	1.70 1.64
80	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20	2.73
	447033 429496	A1357412 AA453800	Hs.157601 Hs.192793	Predicted gene: Eos cloned; secreted w/V ESTs	2.20	2.58
	425516	BE000707	Hs.29567	ESTs	2.20 2.20	2.97 1.58
					-1-5	

	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.19	1.92
	423526	AB011086	Hs.129739	KIAA0514 gene product	2.19	2.85
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.19 2.19	2.01 2.53
5	426251 443441	M24283 AW291196	Hs.1683B3 Hs.92195	intercellular adhesion molecule 1 (CD54) ESTs	2.18	1.73
•	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesteroi es	2.18	2.53
	408705	AA312135	Hs.46967	HSPC034 protein	2.18	1.54
	419150 430915	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous qb;aa55e05,1 NCL CGAP_GCB1 Homo sapiens	2.18 2.18	1.93 1.57
10	418791	AA488953 AA935633	Hs. 194628	ESTs	2,17	2.05
	432620	AA777749	Hs.5978	LIM domain only 7	2.17	1.75
	424321	W7404B	Hs.1765	lymphocyte-specific protein tyrosine kin	2.17	2.01
	406646	M33600	Hs.308026	mejor histocompatibility complex, class	2.17	3.12 4.14
15	424450 426410	AL137526 BE298446	Hs.305890	dynein Intermediate chain 2 BCL2-like 1	2.17 2.16	2.19
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.16	1.70
	421077	AK000061	Hs.101590	hypothetical protein	2.16	1.60
	424563	AA446932	Hs.151428	ret finger protein 2	2.16	1.B3
20	405102 452436	BE077546	Hs.31447	C15001220":gi]4469558 gb]AAD21311.1) (AF ESTs, Moderately similar to A46010 X-lin	2.16 2.15	1.78 1.87
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	2.15	1.65
	418067	Al127958	Hs.83393	cystatin E/M	2.15	2.40
	436372	AW972301	Hs.310286	ESTs	2.15 2.14	2.35 2.58
25	418728 450400	AW970937 A1694722	Hs.293B43 Hs.279744	ESTs ESTs	2.14	2.05
20	409031	AA376836	TIVIAL OF THE	ESTs	2.14	2.14
	435143	R12375	Hs.194600	EST ₈	2.14	1.69
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas choline/ethanolaminephosphotransferase	2.14 2.14	2.03 1.57
30	453927 418304	AA082465 AA215702	Hs.125031	gbzr97g10,r1 NCI_CGAP_GCB1 Homo saplens	2.14	1.68
20	418299	AA279530	Hs.83968	inlegrin, beta 2 (antigen CD18 (p95), ly	2.14	2.04
	408996	AI979168	ls.344096	glycoprolein (transmembrane) nmb	2.13	1.72
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2,13 2.13	1.68 2,47
35	41 <i>8</i> 741 452353	H83265 C18825	Hs.8881 Hs.29191	ESTs, Weakly similar to S41044 chromosom epithelial membrane protein 2	2.12	2.31
55	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	2.76
	424006	AF054815	Hs.13754B	CD84 antigen (laukocyte antigen)	2.12	211
	437581	N59284	Hs.288010 Hs.25092	ESTS	2.12 2.12	2.85 2.04
40	410976 429716	R36207 R25685	Hs.211933	typothetical protein MGC10744 collagen, type XIII, alpha 1	2.12	2.00
	423069	W15813	Hs.1613	adenosine A2a receptor	2.12	1.72
	43286D	AW974077	Hs.203349	ESTs	2.12	1.75
	449509 456062	AA001615 A)866286	Hs.84561 Hs.71962	ESTs, Weakly similar to B36298 profine-r	2.12 2.11	1.84 4.42
45	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.11	1.65
	459680	H96982	Hs.42321	ESTs	2.11	2.20
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_splean_	2.10	212
	443071 443021	AL080021 AA358546	Hs.8986 Hs.8904	complement component 1, q subcomponent, Ig superfemily protein	2.10 2.10	2.48 2.42
50	437838	Al307229	1 10,000	ESTs	2.10	1,67
	429421	AL031658		Human DNA sequence from clone RP1-310013	2.10	1.91
	407202	N58172	Hs.109370 Hs.134587	ESTs ESTs	2.10 2.10	1.68 1.64
	443569 411990	A1140462 AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	2,10	1.71
55	408410	AA447438	Hs.44697	ATPese, Class V, type 10C	2.10	2.05
	436293	A1601188	Hs.120910	ESTs	2.10	201
	410730 427876	AW368860 Al494291		DnaJ (Hsp40) homolog, subtamily B, membe ESTs	2.10 2.10	1.66 2.48
	456672	AKU02016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.09	3.11
60	434967	AW975114		ESTa	2.09	1.69
	433735	AA608955	Hs.109653		2.09	1.78
	433226 425787	AW503733 AA363867	Hs.9414 Hs.155029	KIAA1488 protein ESTs	2.09 2.09	1.62 1.85
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.08	3.41
65	442369	A1565071		ESTS	2.08	1.60
	430478	NM_014349			2.08 2.08	2.39
	434421 415138	AI915927 C18366	Hs.34771 Hs.295944	ESTs Tissue factor pathway Inhibitor 2	2.08	1.68 1.72
	431728	NM_007351			2.08	1.51
70	444929		Hs.161354		2.08	3.14
	408873		D. 1554F	calmodulin 2 (phesphorylase kinase, delt	2.08 2.08	2.09 1.66
	437634 400277	MVESSUMO	Hs.255158	ESTS Eos Control	2.0B	1.46
	443601	AJ078554	Hs.4265B	ESTs	2.08	1.87
75	432212			ESTS	2.08	2.84
	410763		Hs.8966	hypothetical protein FLJ21776 Target Exon	2.07 2.06	1.4B 2.75
	406122 430665		Hs.157367		2.06	1.66
00	408788	AL134947	Hs.21395	Homo sepiens BAC clone RP11-10205 from Y	2.06	1.70
80	421057		Lin dozen	Homo sapiens cDNA: FLJ22063 fis, clone H	2.06	1.78
	413936 431924		Hs.29768 Hs.27220		2.06 2.05	2.30 2.31
	449444			solute carrier family 16 (monocarboxylic	2.06	1.41
				463		
				405		

	421464	AA291553	Hs.190086	ESTs	2.06	2.61
	424831	H61453		ESTS	2.06 2.06	2.12 1.44
	434542	AA769310	Ut- 4462	hypothetical protein FLJ13164	2.05	2.61
5	418323 418836	NM_002118 A)855499	Hs.1162 Hs.161712	major histocompatibility complex, class ESTs	2.05	1.73
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FL322765 fis, clone K	2.05	1.99
	400750	THE STEEL	110.100000	Target Exon	2.05	1.75
	406851	AA609764		major histocompatibility complex, class	2.05	3.94
	414936	C14774		gb:C14774 Clontech human aorta polyA mRN	2.05	2.41
10	453459	BE047032	Hs.257789	ESTs	2.04	1.86
	443450	N66045	Hs.133529	ESTs	2.04	2.46
	430015	AW768399		ESTs	2.04	1.63
	429399	AA452244	Hs.16727	ESTs	2.04	1.51 -
15	411653	AF070578	Hs.71168	Horno sepiens clone 24674 mRNA sequence	2.04	1.73
15	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-stalic act	2.04	1.46
	421757	Z20897	Hs.296259	paraoxonase 3	2.04	213
	441942	AF182645	Hs.8024	IK cytokine, down-regulator of HLA II	2.04	1.B2
	431843	AA516420	Us 272220	ESTs, Weakly similar to 138022 hypotheti	2.04 2.04	1.67 3.23
20	432006 414154	AL137382 AW205314	Hs.272320 Hs.323060	Homo saplens mRNA; cDNA DKFZp434L1226 (f ESTs	2.03	2.95
20	449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1.59
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.03	2.01
	406645	M57466	Hs.814	major histocompatibility complex, class	2.03	2.49
	414516	Al307802		ESTs, Weakly similar to T43458 hypotheti	2.02	1.56
25	417032	AA192489	Hs.271838	ESTs	2.02	1.48
	414875	H42679	Hs.77522	major histocompatibility complex, class	2.02	2,79
	414522	AW518944	Hs.76325	Immunoglobulin J chain	2.02	1.84
	410511	AA743475	Hs.285655	ESTs	2.02	1.87
20	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.02	2,26
30	437259	Al377755	Hs.120695	ESTs	2.02	2.34
	426298	AW965058	Hs.111583	ESTs, Weakly similar to 138022 hypotheti	2.02	1.86
	426722	U53823	Hs.171952	occludin	2.02	1.57
	421229 410491	A1056590 AA465131	Hs.7086 Hs.64001	hypothetical protein MGC12435	2.02 2.02	1.79 1.97
35	447232	AW499834	Hs.327	Homo saplens clone 25218 mRNA sequence interleukin 10 receptor, alpha	2.02	2.09
55	449317	AW293413	Hs,132906	19A24 protein	2.02	1.B4
	439556	Al623752	Hs.163603	ESTs	2.02	1.62
	443031	AW134696	Hs.49418	ESTs	2.01	1.58
	444838	AV651880	Hs.208558	ESTs	2.01	1.69
40	453108	Al311457	Hs.99472	ESTs	2.01	1.64
	432967	AA572949	Hs.207566	ESTs	201	1.83
	441390	A1692560	Hs.131175	ESTS	201	1.63
	448076	AJ133123	Hs.20196	adenylate cyclese 9	2.01	1.80
15	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	201	2.32
45	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.01	1.90
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.01	1.90
	415443	T07353	Hs.7948	ESTs	2.00	1.54
	424925 404394	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant ENSP00000241075:TRRAP PROTEIN.	2.00 2.00	2.74 2.99
50	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	2.00	1.89
20	437204	AL110216		ESTs, Weakly similar to 155214 salivary	2.00	1.46
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALUS_HUMAN A	2.00	1.37
	440567	BE076969	Hs.7337	hypothetical protein FLJ10936	2.00	1.51
	431193	AW749505	Hs.296770	KIAA1719 protekt	1.99	201
55	432485	N90856	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	1.99	2.11
	450293	N36764	Hs,171118	hypothetical protein FLJ00026	1.98	1.79
	417072	BE243915	Hs.81178	leukohiene A4 hydrofase	1.98	2.47
	429073	AA446187	Hs.47385	ESTs	1.98	1.92
60	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.98	2.94
60	420838	AW118210	Hs.42321	EST8	1.98	1.67
	435252	AI539519 U56979	Hs.120969	Home sapiens cDNA FLI11562 fis, clone HE	1.97 1.97	2.10 1.84
	430702 456804	A1421645	Hs.278568 Hs.139851	H factor 1 (complement) caveolin 2	1.97	1.58
	439195	H89360	LIST 19900 I	gb:yw28d08.s1 Morton Fetal Cochlea Homo	1.97	1.93
65	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	1.97	2.28
0,5	413836	W92003	Hs.70614	ESTs	1.97	1.80
	400417	X72475	113.70014	Target	1.97	1.75
	427814	W2B383	Hs.180900	Williams-Beuran syndrome chromosome regi	1.96	1.46
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.96	2,18
70	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	1,95	2.06
	455615	BE045344	Hs.274923		1.96	2.21
	414572	AU077174	Hs.28B181		1.96	2,65
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	1.95	1.71
75	417370	T28651	Hs.82030	tryptophanyl-IRNA synthetase	1.95	2.88
13	451609	AL046019	Hs.209276		1.94	3.26
	447131	NM_004585		retinolo acid receptor responder (tazaro	1.94	2.94
	430887 414700	10833N	Hs.260287 Hs.38163		1.54	1.62
	417874	H63202 BE616160	Hs.82829	ESTs protein tyrosine phosphatase, non-recept	1.94 1.94	1.72 1.56
80	443907	AU078484	Hs.9963	TYRO protein tyrosine kinase binding pro	1.93	2.22
	425252		1 10,000	catalicula	1,92	2.14
	428758	AA433988	Hs.98502	CA125 anligen; much 16	1.92	219
	425810		Hs.31903	ESTs	1.92	1.76

	400000	1.1700000		FOT	4.00	4.04
	43361B 424517	AA602539 Al539443	Hs.345494	ESTs Homo sapiens cDNA FLJ12169 fis, clone MA	1.92 1.92	1.84 2. 2 7
	418036	Z37976	Hs.137447 Hs.83337	latent transforming growth factor beta b	1.92	1.76
_	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	1.92	1.72
5	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	1.91	1.83
	426780	BE242284	Hs.172199	adenylate cyclase 7	1.91	1.67
	452386	R12499	Hs.20468	ESTs	1.91	264
	438670 414359	A§275803 M62194	Hs.123428 Hs.75929	ESTs cadherin 11, type 2, O8-cadherin (osteob	1.91 1.91	3.12 1.82
10	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.90	2.06
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.90	1.85
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	1.9 0	1.65
	428165	AA423849	Hs.79530	M5-14 protein	1.90	1.70
15	426721 449271	AA383588 AW338067	Hs.131816 Hs.7869	ESTs, Weakly similar to T29012 hypotheti	1.89 1.88	3.22 2.07
13	438576	ANSSESSIS	Hs.77542	Homo saplens cDNA FLJ11946 fis, clone HE ESTs	1.88	2.25
	437751	AA767373	110.000	ESTs, Moderately similar to ALU1_HUMAN A	1.88	2.41
	449518	A1076459	Hs.15978	KIAA1272 protein	1.88	1.63
20	430634	AI860851	Hs.26685	catcyphosine	1.88	3.01
20	440563	AW452976	Hs,247112	hypothetical protein FLJ10902	1.88	1.65
	440099 414662	ALDBOOSB ALDBOOSB	Hs.6909	DKFZP564G202 protein	1,58 1,68	1.78 2.37
	444051	AL036058 N48373	Hs.76807 Hs.10247	major histocompatibility complex, class activated leucocyte cell adhesion molecu	1.87	2.07
	414464	Al870175	Hs.13957	ESTs	1,87	2.68
25	427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	1.87	2.25
	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity lib, re	1.87	2.05
	430027	AB023197	Hs.227743	KIAA0980 protein	1.87	1.70
	425771 412443	BE561776 AW951103	Hs.159494 Hs.130767	Bruton agammagiobulinemia tyrosine kinas Homo sepiens cDNA: FLJ23553 fls. clone L	1.87 1.86	2.18 2.27
30	408771	AW732573	Hs.47584	potassium voltage-galed channel, delayed	1.86	231
-	420361	N92054	Hs.194718	zinc finger protein 265	1.86	1.63
	413869	NM_000978	Hs.75596	interleukin 2 receptor, beta	1.86	2.13
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.85	1,77
35	442434	AA995787	Hs.129583	ESTs	1.85	2.15
33	422735 444083	AA169685 AI123195	Hs.119529	Niemann-Pick disease, type C2 gene gbooo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.85 1.84	2.77 1.73
	449679	A1823951	Hs.129700	toiloid-like 1	1.84	1.57
	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.84	2.02
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.84	1.72
40	414803	X03100	Hs.914	Human mRNA for SB classil histocompatibi	1,84	2.47
	408669 455608	Al493591 AW976165	Hs.78146	plateletiendothelial cell adhesion molec gbcEST388274 MAGE resequences, MAGN Homo	1.84 1.84	2.29 1.69
	455508 410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	1.83	2.12
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1,83	1.59
45	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	1.83	1.57
	417086	AA194446		ESTs, Weakly similar to \$55024 nebulin,	1.83	1.45
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	1.83	2.18
	429952 438596	AF080158 AA829427	Hs.226573 Hs.243081	Inhibitor of kappa light polypeptida gen ESTs	1.83 1.83	1.75 2.83
50	436486	AA742221	Hs.120633	ESTs	1.82	2.14
	433365	AF026944	Hs.293797	ESTs	1.82	2.50
	449943	AF104266	Hs.24212	letrophilin	1.82	2.08
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.82	2.37
55	421563 449161	NM_006433 N53431	Hs.105806 Hs.47647	granulysin ESTs, Weakly similar to T00057 hypotheti	1.82 1.81	2.48 2.81
<i>J</i>	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.81	2.65
	418371	M13580	Hs.84298	CD74 antigen (Invariant polypeptide of m	· 1.B1	2.50
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.81	2.05
60	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DXFZp434A119 (fr	1.80	3,13
60	428877 409485	A1857119 S80990	Hs.120036 Hs.252136		1.80 1.80	2.94 2.28
	423081	AF262992	Hs.123159		1.80	1,56
	425458	H89317	Hs.182889		1.80	2.21
~~	425390	A1092634	Hs.156114		1.80	1.41
65	409208	Y00093		integrin, elpha X (antigen CD11C (p150),	1.80	2.20
	430570	AI417881	Hs.292464		1.80	1.62
	439425 408688	AF086244 Al634522	Hs.114659 Hs.152925		1.80 1.80	2.37 2.13
	440875	AW005054	Hs.279788		1.80	1.60
70	423590	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	1.79	1,57
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.79	2.18
	431958	XB3629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.79	1.68
	403421 430423	A1400E49	Lb- 449470	NM_016369*:Homo saplens claudin 18 (CLDN	1.79 1.79	2.47 2.92
75	416384	A(190548 A)(076903	Hs.143479 Hs.79283	ESTs, Weakly similar to hypothetical pro selectin P ligand	1.79	1.87
	440638	Al376551	: 44.1 3244	gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	1.78	1.69
	422003	AA361760	Hs.296326	ESTs	1.78	205
	412288	NM_003005		selectin P (granule membrane protein 140	1.77	1.82
80	432987	AI864771	Hs.27964	CD86 antigen (CD28 antigen ligand 2, B7-	1.77	203
3V	441602 458194	AI655043 AW383818	Hs.133456	ESTs Hoderately similar to ALU2_HUMAN A	1.77 1.78	2.01 2.35
	432565	AA553477	Hs.152428		1.76	2.63
	421071	AJ311238	Hs.104478		1.75	2.59

					4	4.00
	408989	AW361666	Hs.49500	KIAA0746 protein	1.75 1.75	1.66 1.54
	414807 403903	A1738616	Hs.77348	hydroxygrastaglandin dehydrogenase 15-{N C5001632*:gi]10645308 gb]AAG21430.1]AC00	1.75	3.20
	421461	AW291023		ESTs, Weakly shriler to A46010 X-linked	1.74	2.67
5	430850	DE144152		gb:MR0-HT0165-080200-006-e02 HT0165 Homo	1.74	2.52
	424377	AF081675	Hs.146322	killar cell lectin-like receptor subfami	1.74	215
	443884	N20617	Hs.194397	leptin receptor	1.74	1.51
	423057	AW961597	Hs.130816	ESTs, Moderately similar to 138022 hypot	1.74 1.73	1.63 2.57
10	448262 431890	AW880830 X17033	Hs.186273 Hs.271986	ESTs integrin, alpha 2 (CD49B, alpha 2 subuni	1.73	1.87
10	431630	NM_002204	Hs.285829	Integrin, alpha 3 (antigen CD49C, alpha	1.73	221
	412896	AW804157	Hs.308026	major histocompatibility complex, class	1.72	2.37
	407366	AF028942	Hs.17518	gb:Homo sapiens cig33 mRNA, partlal sequ	1.72	2.16 _
15	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	1.72	1.52
13	442117 438606	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447 KIAA0672 gene product	1.71 1.71	1.55 1.57
	434795	NM_014859 BE620794	Hs.6336 Hs _r 4147	Insustrating chain-associating membrane	1.71	2.21
	426490	NM_001621	Hs.170087	anyl hydrocarbon receptor	1.71	1,46
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	1.71	2.49
20	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	1.71	1.57
	423857	N48902	Hs.1334B1	Homo saptens mRNA; cONA DKFZp564O0862 (f	1.71	1.55
	408393	AW015318	Hs.23165	ESTs	1.70 1.70	1.43 1.54
	432409 440817	AAB06538 Al341423	Hs.130732 Hs.288433	KIAA1575 protein neurolúmin	1.70	217
25	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1,69	254
	453691	H12235	Hs.226505	ESTs	1.69	2.07
	42227B	AF072B73	Hs.114218	fritzzled (Drosophila) homolog 6	1.68	1,54
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.6B	2.29
20	434951	AF161442	Hs.191591	Homo saplens HSPC324 mRNA, partial cds	1.68	2.24
30	444301 407775	AK000136 NM_004914	Hs.38772	asportn (LRR class 1) RAB36, mamber RAS encogene family	1.68 1.68	1.44 2.03
	437119	Al379921	Hs.177043	ESTs	1.68	4.21
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1,68	2.28
~ ~	453498	BE18\$412	Hs.23245	hypothetical protein FLJ11767	1.68	2.76
35	428289	M26301	Hs.2253	complement component 2	1.67	240
	404854	43004746	LI- aced	Target Exon	1.67	1.76
	450954 410048	A1904740 W76467	Hs.25691 Hs.343874	receptor (calcitonin) activity modifying proline oxidase homolog	1.67 1.67	2.32 3.03
	407857	A1928445	Hs.92254	synaplotagmin-like 2	1.66	1.51
40	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.66	2.01
	417193	A1922189	Hs.288390	hypothetical protein FL122795	1.66	2.05
	421237	U25029	Hs.102761	Human glucocorticold receptor alpha mRNA	1.66	2.20
	433350	BE563152	Hs.10352	Homo seplens cDNA: FLJ20944 fis, clone A	1.66	2.11
45	417451 443791	AW007280	Hs.115537 Hs.143345	pulative dipeptidase ESTs	1.65 1.65	2.11 2.11
45	440475	N64458 A1807671	Hs.24040	potassium channel, subfamily K, member 3	1.65	2.04
	431743	AW972642	Hs.293055	ESTs	1.64	2.64
	400328	X87344		transporter 2, ATP-binding cassette, sub	1.64	2.43
60	451876	T63141		gb:yb99a12.s1 Stratagene lung (937210) H	1.64	2.02
50	417321	N68722	Hs.191368	ESTs	1.64	2.53
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64 1.63	2.01 2.17
	418707 432176	U97502 AW090386	Hs.87497 Hs.112278	butyrophiin, subfamily 3, member A2 arrestin, beta 1	1.63	2.04
	450708	AA376654	10.112210	eukaryolic translation initiation factor	1.62	2.05
55	429570	BE242256	Hs.2441	KIAA0022 gene product	1.62	1.39
	448406	AW772298	Hs.21103	Homo saplens mRNA; cDNA DKFZp564B076 (fr	1.62	1.57
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	1.62	1.44
	452424	AI964028	Hs.48353	ESTS	1.62 1.62	2.53 1.38
60	423161 416316	AL049227 H58721	Hs.124776 Hs.271628	downstream of cadherin 6 (by 3.3kb) ESTs	1.62	1.39
UU	431806	AF186114	Hs.270737	furnor necrosis factor (ligand) superfami	1.62	2.67
	452203	X57522	1,4,4,	transporter 1, ATP-binding cassette, sub	1.82	2.45
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.62	1.51
65	438089	W05391	** *****	nuclear receptor subfamily 1, group L m	1.61	1.45
65	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.61 1.61	1.52 2.40
	433417 444009	AA587773 Al380792	Hs.8859 Hs.135104	Homo sepiens, Similar to RIKEN cDNA 5830 ESTs	1.60	2.15
	436057	AJ004832	Hs.5038	neuropathy target esterase	1.60	2.60
	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.60	2.57
70	433614	W07475	Hs.277101	cylochrome c oxidese aubunit IV isoform	1.60	3.30
	410494	M36564	Hs.54016	protein 8 (alpha)	1.59	1.42
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypaptide	1.59	2.02
	446616	R65964 X80700	Hs.334873	ESTs, Weakly similar to ALUS_HUMAN ALU S pre-B-cell leukemia transcription factor	1.59 1.59	2.52 2.04
75	419918 428141	D50402	Hs.93728 Hs.182611		1.59	1.98
. •	434308		Hs.47282	ESTs	1.58	2.29
	447341	AF106941	Hs.18142	arrestin, bela 2	1.58	2.09
	454315		Hs.251928		1,58	2.10
80	423281	AJ271684	Hs.126355		1.57	1.75
30	433671 412869		Hs.132906 Hs.82407	i 19A24 protein CXC chemokine ligand 16	1.57 1.57	2.05 2.71
	436906		Hs.181244		1.57	2.24
	417771		Hs.82547	retinole acid receptor responder (tazaro	1.57	1.43
			**			

	100000		11 01000	COTA college (investor) - hora - Ede of so	1.87	2.37
	406825 406868	AJ9B2529 AA505445	Hs.84296 Hs.300697	CD74 autigen (invariant polypeptide of m immunoglobulin heavy constant gamma 3 (G	1.56	1.61
	423329	AF054910	Hs.127111	tektin 2 (testicular)	1.56	2.51
_	424909	S78187	Hs.153752	cell division cycle 25B	1.55	2.00
5	431921	N46466	Hs.58879	ESTs	1.54	3.04
	437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	1.54 1.54	1.44 3.04
	426274 415078	D38122 AA311223	Hs.2007 Hs.283091	tumor necrosis factor (ligand) superfami found in inflammatory zone 3	1.53	2,61
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.53	218
10	401854			Target Exon	1.53	2.08
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.52	1.52
	433815	A1696602	Hs.112757	ESTs	1.52 1.52	2.57 1.36 .
	431130 453870	NM_006103 AW385001	Hs.2719 Hs.8042	HE4; epididymis-specific, whey-ecidic pr Horno sepiens cDNA: FLJ23173 fis, clone L	1.51	1.43
15	414763	U97276	Hs.77268	quiescin Q6	1.50	2.07
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	1.50	1.46
	412870	N22788	Hs.82407	CXC chemokine ligand 16	1.50	2.B3
	407601	AC002300	Hs.37129 Hs.279772	sodium channel, nonvoltage-galed 1, beta brain specific protein	1.50 1.50	2.04 2.25
20	432894 457941	AW167668 AJ004525	Hs.14587	ESTs, Weakly similar to AF151859 1 CGI-1	1.49	2.22
	442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_HUMAN MUCIN	1.49	2.09
	419542	AA366037	Hs.90911	solute carrier family 16 (monocarboxylic	1.49	2.40
	433124	U51712	Hs.13775	hypothetical protein SMAP31	1.49 1.49	1.39 1.39
25	422487 429610	AJ010901 AB024937	Hs.198267 Hs.211092	mucin 4, tracheobronchial LUNX protein; PUUNC (palate lung and nas	1.48	1.76
23	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.48	1.41
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	1.48	1.44
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.47	1.31
30	427872	AA835058	H- SANA	Human DNA sequence from clone RP1-261G23 potassium channel, subfamily K, member 3	\$.47 1.47	2.50 2.21
30	449853 431369	AF006823 BE184455	Hs.24040 Hs.251754	secretory leukocyte protesse inhibitor (1.47	1.50
	415149	X12451	Hs.78056	cathepsit L	1.46	1,84
	447217	BE465754	Hs.17778	neuroplin 2	1.46	1.40
35	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.46 1.46	2.18 2.01
33	445672 432210	A1907438 A1567421	Hs.282862 Hs.273330	ESTs Homo sapiens, clone IMAGE:3544662, mRNA,	1.46	210
	458208	Al380016	100,51000	ESTs, Weakly similar to T4S4_HUMAN TRANS	1.46	1,60
	452518	AA280722	Hs.24758	ESTs, Weakly similar to 138022 hypotheti	1.45	1.40
40	419577	1.36531	Hs.91296	Integrin, elphá 8	1.45 1.45	1.40 1.57
40	439620 423804	AAB38727 AW40344B	Hs.124405 Hs.16725	ESTs, Wealdy similar to A46010 X-linked Interferon-stimutated transcription fact	1.45	2.10
	42465B	NM_002406	Hs.151513	mannosyl (alpha-1,3-)-glycoprotein beta-	1.44	2.00
	42B494	AA233439	Hs.184634	hypothetical protein FLJ20005	1.44	1.45
45	431573	AW971070	Hs.291160	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.44 1.43	1.40 2.01
47	409524 406787	AW402151 AW090702	Hs.54673 Hs.240615	tumor necrosis factor (ligand) superfami Tubulin alpha 1	1.42	1.86
	419452	U33635	Hs,90572	PTK7 protein tyrosine kinase 7	1.42	1.95
	406422			Target Exon	1.41	2.02
50	421341 421195	AJ243212	Hs.133017	deleted in malignant brain tumors 1 ESTs	1.41 1.41	1.47 2.42
20	425998	BE464560 AU076629	Hs. 165950	fibroblast growth factor receptor 4	1,41	2.05
	426125	X87241	Hs.186994	FAT tumor suppressor (Drosophila) homolo	1.41	1.34
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	1.40	2.10
55	409238	AL049990	Hs.61515	Homo saptens mRNA; cDNA DKFZp564G112 (fr gb:hm30f03.x1 NCL_CGAP_Thy4 Homo saptens	1,40 1,40	3.64 3.24
23	411880 432133	AW872477 AB033088	Hs.272567	KIAA1282 protein	1.40	2.78
	428833	Al928355	110272207	ESTs	1.40	2.02
	455797	BE091633		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.39	1.55
60	415765	NM_005424		tyrosine kinase with immuroglobulin and secretin receptor	1.39 1.38	2.09 2.44
OO	427732 449746	NM_002980 Al668594	Hs.176588		1.38	1.85
	407568	AA740964	Hs.62699	ESTs	1.38	3.13
	422573	AW297985	Hs.295726		1.38	1.38
65	42713B	N77624	Hs.173717		1.37 1.36	1.12 2.01
0.5	457918 423696	AL359590 Z92546	Hs.162604 Hs.131819		1.35	254
	416700	AW498958	Hs.343476		1.36	2.04
	407244	M10014		fibrinogen, gernma polypeptide	1.36	1.29
70	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.35	1.34
70	406654 407603	M90686 AW955705	Hs.73885 Hs.62604	HLA-G histocompatibility antigan, class Homo sapiens, clone IMAGE:4299322, mRNA,	1.35 1.34	2.47 1.68
	445417		Hs.12680	a disintegrin-like and metalloprolease w	1.34	1.92
	436982		Hs.5378	spondin t, (f-spondin) extracellular met	1.34	1.86
75	427507		Hs.17915		1.34	2.11
75	446967 436553		Hs.156781 Hs.8997	l ESTs immunoglobulin tambda locus	1.34 1.34	3.75 2.18
	436533 456637				1.33	1.78
	422129		Hs.1478	serine (or cysteine) proteinase Inhibito	1.33	1.95
οΛ	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.32	205
80	414849 436986		Hs.29162 Hs.21079		1.32 1.32	2.08 2.06
	410598		Hs,9195	Homo sepiens cDNA FLJ13698 fis, done PL	1.32	2.08
	424247		Hs.23473		1.31	1.29

	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolectin)	1.30	1.25
	413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 ffs, clone HE	1.30	1.92
	406659	AA663985	Hs.277477	major histocompatibility complex, class	1.30 1.30	2.22 2.12
5	451049 436494	AA013353 AA720997	Hs.128295	gb:ze28h10.s1 Soares retina N2b4HR Homo ESTs	1.29	2.12 2.30
	438374	AA321866	Hs.6193	hypothetical protein FLJ14590	1.28	2.34
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	1.2B	2.39
	425883 428458	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.28 1.27	1.69 2.00
10	443180	AA428B20 R15875	Hs.251399 Hs.258576	neurogranin (protein kinase C substrate, claudin 12	1.26	1.25
	421764	Al681535	Hs.148135	serina/threcorina kinasa 33	1.26	2.01
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.26	1.21
	433283 426759	BE041135 Al590401	Hs.175622 Hs.21213	ESTs ESTs	1.24 1,23	3.05 ₋ 1.20
15	436446	AW016809	Hs.119021	ESTs	1.23	1.20
	421467	AA291590	Hs.97252	ESTs	1.22	1.54
	431353	AA828032	11-053430	ESTs	1.22	3.00
	427403 453037	AA402107 AA045175	Hs.257146 Hs.17914	ESTs, Moderately similar to 138022 hypot ESTs	1.22 1.22	1.91 2.40
20	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.22	2.26
	439941	A1392640	Hs.18272	amino acid transporter system A1	1.22	1.22
	451385	AA017656		gbze39h01.r1 Scares relins N2b4HR Homo	1.21	1.49
	400496 409432	D49372	Hs.54460	ENSP00000224716*:GTP-binding protein SAR small inducible cytokine subfamily A (Cy	1.20 1.20	1.25 1.44
25	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.19	2.06
	426486	BE178285	Hs.170056	Home septens mRNA; cDNA DKFZp586B0220 (f	1.18	2.02
	445033	AV652402	Hs.72901 Hs.6727	cyclin-dependent kinase inhibitor 28 (p1	1.17 1.14	1.14
	439866 440555	AA280717 D31292	Hs.6853	Ras-GTPase activating protein SH3 domain hypothetical protein FLJ22167	1.14	1.16 2.19
30	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.13	1.12
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.12	2.43
	432798	AA565309	Hs.194015	ESTs	1.10 1.10	2.23
•	411274 438856	NM_002776 N40027	Hs.69423 Hs.7473	kalikrain 10 ESTs	1.09	1.09 1.52
35	421552	AF026692	Hs.105700	secreted trizzled-related protein 4	1.09	1.07
	448253	H25899	Hs.201591	ESTs	1.08	210
	409718 409798	D88640 AA248587	Hs.56045 Hs.30237	src homology (bree (SH3) and cystefine ri ESTs, Weakly similar to ALUB_HUMAN !!!!	1,08 1.06	2.0B 1.5B
	449321	AA001150	Hs.132937	ESTs	1.03	2.06
40	418693	AI75087B	Hs.87409	thrombospondin 1	1,06	1,02
	402333	146050	11. 400000	Target Exon	1.03	1.03
	421814 425664	L12350 AJ006276	Hs.108623 Hs.159003	thrombospondin 2 translent receptor potential channel 6	1.02 1.00	1.02 2.36
	458158	AW296778	Hs.144734	Human DNA sequence from clone RP3-416F21	1,00	2.73
45	.406517			nel (chicken)-like 2	1.00	2.07
	442526	AW277221		ESTS	1.00	2.21 2.52
	446164 449122	AW273539 Al631310	Hs.196955	hypothetical protein FLJ23577 ESTs	1.00 1.00	2.23
	438038	Al732629	1.0.100000	ESTs, Wealdy similar to TA2R HUMAN, BETA	1.00	2.04
50	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	1.00	2.02
	453672 436187	U73531 AKD00998	Hs.34526 Hs.297221	G protein-coupled receptor Homo sapiens cDNA FLJ10136 fis, clone HE	1.00 1.00	2.57 2.64
	438909	AF085839	118.2231221	gb:Homo septens full length Insert cDNA	1.00	2.23
	423609	AA328348	Hs.218289	ESTs	1.00	219
55	419261	X07876	Hs.89791	wingless-type MMTV integration site famil	1.00	2.28
	436284 440932	AA708016 AI801509	Hs.190389 Hs.182080	ESTS ESTS	1.00 1.00	2,22 1.66
	403420	74001000	1 104 104 105	Target Exon	1.00	1.86
CO	431169	AW971240		gh:EST383329 MAGE resequences, MAGL Horno	1.00	2.02
60	425916		. Hs.162200	urotensin 2 aquaporin 4	1.00 1.00	2.11 2.26
	419721 421761	NM_001650 AL120297	Hs.108043		1.00	1.86
	4257B1	AF001622	Hs.159523	class-I MHC-restricted T cell associated	1.00	1.96
65	415094	D59513	Hs.330778		1.00	2.32
05	434088 420727	AF116677 H75701	Hs.249270 Hs.99886	hypothetical protein PRO1966 complement component 4-binding protein.	1.00 1.00	2.26 1,84
	430049		Hs.99619	EST's	1.00	1.87
	446868	AV660737		ESTs	1.00	1.79
70	418786		Hs.203594		1.00	1.44
70	436391 413059	AJ227892 BE151498	Hs.146274	ESTs gb:RCO-HT0295-291199-031-E11 HT0295 Homo	1.00 1.00	/ 1.30 1.42
	427739		Hs.98105	NYD-SP14 protein	1.00	2.41
	452788	AW294571	Hs.136040	ESTs	1.00	2.23
75	TABLE	32B.				
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	Pkey:			nüller number		
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	Pkey	CAT Numi	ber Access	sion		
	431089	125941_2	110071) 189 AW063469 AA715980 BF001091 BF880066 AA666102 AA621946 AA45	1826	
	701003	122341_2	וויינים	, 103 / 111000-100 / ATT 12300 EX 90 103 (DECOUVO AMOUNTA AMAZ 1340 MAS	1.020	

	421798	3042_4	BC017829 AW278646 A1984209 AA663933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329 T60644
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	400209	2726_1	BG482911 AA617793 AJ807697 AW205576 T944Z7 AA467101 T94513 B1819407 B1822450 B1820618 B1824619 BG542624 BG537862
5			BOACCELL WARELLING WIDGLOST WASTERN FRANCE IN 194219 DIOLEMAN PROSTADIO DIOCOGLIO DIOCAGNA DIOCAGNA
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	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	432810	101919_1	BG292389 C05094 A1668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 A1810530 BF092924 AA334151 AA334725
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5	,,,,,,,,,		AA193115 AA086469 F20375 F32370 AA6 AA670099 BF475559	5 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 53078 BF574897 724852 F00172 T30560 AW449825 A1620346 BG986374 BE706521 C02691 AL596834 F31902 F26078 5 F30818 F37524 AJ346558 F28050 F17933 F31637 C03413 A1092152 AA180743 AA085730 F21998 F20854 F18944 F31180 93162 Z17344 AA192546
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10	440638 458194 421461 430850	371165_1 506272_1 128918_1 296806_1	BG009500 Al376551 Al692525 AW005303 AA291529 Al629027	
15	400328 451876	2328579 1	T63141 AI821021 FI	F370092 BF370127 BF370060 T62998
,	45070B	12745_1	AK055196 AW95203 AW197042 Al36708 H22794 Z43122 H10	31 A694545 AI742A03 AW874431 AW204731 AI887383 BE220997 AA011287 AA115112 AI306385 AW571707 8F433009 6 H23002 H11743 R37085 Z39208 AI002267 H10206 T23948 W74801 R51633 R37677 R59986 H10833 BG012000 R13817 D257 BG984543 H10875 BG984542 AA318232 BF849799 W76367 AA376654 R18795 AA114979 AA303838 AW139819 W94102 R67170 H11820 BG015023
20	452203	2630_1	BC014081 NM_0009 BI770023 AL554969 BG742981 AA27968 AA487429 BE85823	W99102 R671V0 P11020 B0210023 953 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL566882 AL541576 AL550654 B1823519 1 B1489906 A3304593 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 15 AA847441 AA319737 BF172639 BF897216 BF914190 BF903647 S70277 A1559694 AW073296 A1361433 AA564644 12 AA838610 A1539114 A1719375 A1829129 BG057675 A1423422 AU158860 BE300655 AW170777 AA5869556 AL571889 4 AL582800 B1266544 BF342301 BG675594 AA054458 AA353161 A1940434 BE816522 AL577636 A1479550 AW150377
25			AU154395 AW9512 BE271141 AL68193 AI433367 T78652 A AA487637 AA03184	71 Algg22221 Aib19778 Ai346733 AW771150 AW512525 Ai249904 AA279809 Ai352549 AW512517 BG056280 AA521222 12 Al541575 Bib19184 AV660190 Al556475 Ai620020 AW089888 AW079179 Z21518 AA687601 F04651 Ai783961 T57198 1.554968 AA365648 Al682819 Be874601 BF804669 Al574458 BM145502 Al556514 AI538823 A475626 AA948210 AA684054 14 AA535221 AW794256 AW381447 BE788505 Ai682892 AA639089 AA682356 AA6633084 BM009154 AA135727 H05927 9997 AW366665 AW366601 AA678742 Al556474 AA135770 BE774050 BF914200 H88457 AA627746 Bi550216 Bi753586
30	438089	22448_4	BM475665 BE6449	17 AW770789 AW952971 N64863 BM263259 A1224545 A1184866 N69114 AW518902 A1440169 AA809472 AV654440 30 AW337382 A1872923 A1537113 N73882 T83378 H63731 BF671764 AW897824 A1811204 AA344646 BE009112 BG899664
	427872	4983_5	BIB26340 BI868674	R12515 AW897767 BF439409 AI424995 BG059893 AA417003 AI220270 AA418740 AI190974 Z39070 AA742556 AA835058 AA418795 BG460307 BI560147
35	45820B 421341	45807_4 1407_1	AI990640 AI380016 NM_007329 AF159	; BM273298 BM273060 456 aJ243212 aJ297935 aa295769 nm_017579 aJ243224 aI492875 aI796676 aJ749838 aa918144 aJ814590 aJ923531
			AU100613 BG9555	5 Ansor79 Ai279072 Aw612904 Ai492104 Ai284510 A1141231 AA513554 Aw662148 Aw769047 AA565985 Aw612888 85 BG95558B AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 Aw769569 T89953 BE934311
40	41 1880 428833 455797	1139083_1 317753_1 1511159_1	BE088101 T05990 Al928355 Al709178 BE091833 BE0918	3 AA436447 A)431274 BF946000
	407244 451049	83923_1	W92422 AA013353	
45	431353 451385	1241126_1 85022_1	AA019761 AA0176	
	442526 446164	450370_1 41648_2	AK026817 AI55970	000 AW277221 AV735848 08 AW273539 AW892886
	438038 438909	2523501_1 4045_1	AI732629 AI73283 AF085839 R69254	1 AA776249 R69137 AW188788
5 0	431169 419721	1235760_1 40816_1	AW971240 AA493 AK026728 AL1381	723 AA493843 36 BF059437 A1657037 AL600872 C15206 C14676 AA001003 AL157562 BG706081 H24162 BF841047 H16952 Ż45355
	*******		AL157565 AV7217 AW197333 R1623	62 AW953127 AA324171 BF476417 R52508 N54211 R46734 BG485659 BF810747 BE786227 AL538364 R19964 T15657 5 R40826 BG152309 AV729035 R45066 AA016969 BE504976 BF593783 N51085 R81284 BE702264 Al216994 Z41068 N72577
55			R37645 AW23701	4 AW197890 AJ359402 AA707906 AL119885 H23480 T16037 AJ950756 T62597 T91664 R40195 D60186 H23014 T89715 H05749 I H15041 C15205 D59987 R13787 R61283 H23479 H07874 R14070 R52555 R21139 H05856 AA948655 AL120460 T62525
				375 AJ361912 H13341 BG150488 AL119338 Z42792 F05695 H07966 F06492 R59866 D31594 H09436 R35726 BI917845 198 AL036526 BG569879 AW195713 R59867 AA016968 H09087 BE841173 AW893631
	446868	15525_1	AK074473 BC0179	997 BIB31060 BF971101 AIBB6394 AX082624 AV708785 W86073 W07772 AVG60737 AIB16793 R52250 BG183529 AA633473 R19947 BF571346 W86257
60	413059	1488711_1	BE083078 BE151	
	TABLE 320	x		
65	Pkey: Ref:	Sequence :		nbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of
	Strand: Nt_position	Indicates D	nosume 22 - Dunnam IA strand from which e Icleotide positions of p	
70	Pkey	Ref	Strand Nt_posi	lden
	400880 402474	9931121 7547175		29336,30363-36580 53628,55765-55920,57530-57757
	406387 404277	9256180 1834458	Plus 116229 Minus 91665-	I-116371,117512-117651 91946
75	402674 404240	8077108 5002624	Minus 39290-	
	405102	8076881	Minus 120922	2-121296
~~	406122 400750	91440B7 8119067		I-199168,199316-199548
80	404394 403421	3135305 9665041		37205,37491-37762,41053-41140,4132 9-126773,139986-140205
	403903 404854	7710571 7143420	Minus 101169 Plus 14260-	5-102597 - 14537

	401854	7770538	Plus	151483-151637,151902-152008,152146-15231
	406422	9256411	Plus	163003-163311
	400498	9743564	Plus	41515-41695
_	402333	8844110	Minus	165693-165856
5	406517	7711431	Plus	7151-7402
	403420	9664969	Plus	159835-159938

10 YABLE 33A: About 800 genes upregulated in lung fibrosis relative to normal lung

15

Pkey: Unique Eos probesat identifier number

Examplar Accession number, Genbank accession number

UnigenalD: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of lung fibrosis Als divided by 90th percentile of normal lung Als, where the minimum value for the numerator and denominator was set to 50

	****	000- poi-000			
	Pkey	ExAcon	UnigenelD	Unigene Title	R1
20	406964	M21305		FGENES predicted novel secreted protein	16.10
2 0	431089	BE041395		ESTs, Weakly similar to unknown protein	12,38
	421110	AJ250717	Hs.1355	catherisin E	11.86
	428330	L22524	Hs.2256	matrix metalloproleinase 7 (metrilysin,	11.62
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.90
25	444381	BE387335	Hs.283713	hypothetical protein BC014245	8.58
	406850	Al624300	Hs.172928	collagen, type 1, alpha 1	8,26
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	8.24
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.72
	4083B0	AF123050	Hs.44532	diublgaltin	7.24
30	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	7.15
	458034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	7.12
	453355	AW295374	Hs.31412	myopodin	6.96
	408562	Al436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88
~ =	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.83
35	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homoto	6.72
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.72
	438089	W05391		nuclear receptor subfamily 1, group I, m	6.62
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56
40	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46
40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	6.32
	439195	H89360		gbcyw28d08.s1 Morton Fetal Cochlea Homo	6.29
	444301	AK000136	Hs.10760	asporin (LRR class 1)	6.28
	414061	NM_000699	Hs.335493	amylase, aipha 2A; pancreatic	6.13
45	423057	AW961597	Hs.130816	ESTs, Moderately similar to 138022 hypot	6.11
43	430702	U56979	Hs.278568	H factor 1 (complement)	6.10
	424878	H57111	Hs.221132	ESTS	6.00
	417878 414217	U90916 A1309298	Hs.82845 Hs.279898	Homo saplens cDNA: FLJ21930 fis, clone H Homo sapiens cDNA: FLJ23165 fis, clone L	6.00 5.94
	408491	Al088063	Hs.7882	ESTs	5.94
50	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	5.92
50	432222	Al204995	113.41002	gb:sn03c03.x1 Stratagene schizo brain S1	5.92
	407857	AI928445	Hs.92254	synaptolegmin-like 2	5.90
	433230	AW136134	Hs.220277	ESTs	5.86
	412719	AW018810	Hs.816	ESTs	5.85
55	407788	BE514982	Hs.38991	\$100 calcium-binding protein A2	5.82
	426759	Al590401	Hs.21213	ESTs	5.72
	418007	M13509	Hs.83169	matrix matalloproteinase 1 (interstitial	6.72
	421814	L12350	Hs.108623	thrombospondin 2	5.71
	4306B7	N66801	Hs.260287	KIAA1841 protein	5.70
60	453870	AW385001	Hs.8042	Homo sapiena cDNA: FLJ23173 fis, clone L	5.62
	436954	AA740151	Hs.130425	E8Ts	5.58
	411573	AB029000	Hs.70823	KIAA1077 prolein	5,55
	432441	AW292425	Hs.163484	introp of hepatocyte nuclear factor-3 at	5.39
15	410606	AW418779	Hs.114889	ESTs	5.38
65	410800	BE280421	Hs.94499	ESTs	5.32
	413195	AA127382	Hs.22404	protesse, serine, 12 (neurotrypsin, moto	5.28
	405687	M31126	11 00000	matrix metalloproteinase 11 (stromelysin	5.28
	417733	AL048678	Hs.82503	H.saplens mRNA for 3'UTR of unknown prot	5.22
70	412622	AW664708	Hs.171959		5.22
70	439841	A!392640 AW005054	Hs.18272	amino acid transporter system A1	5.18
	440575 430299	W28573	Hs.27976B Hs.106747		5.15 5.13
	425177	AF127577	Hs.155017		5.13 5.12
	444314	A1140497	ns. 100017	gb:ow76b09.s1 Soares_fetal_liver_spleen_	5.11
75	444527	NM_005408	Hs.113B3	small inducible cytokine subfamily A (Cy	5.04
, 5	452239	AW379378	1 13.1 1005	protein tyrosine phosphatase, receptor t	4.97
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	4.96
	443B84	N20617	Hs.194397		4.94
	444040	AF204231	Hs.182982		4.94
80	428261	AA194554	Hs.183434		4.93
	440687	AL080222	Hs.7358	hypothelical protein FLJ13110	4.92
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	4.92
	432435	BE218886	Hs,282070		4.92

	422572	814P107000	U- 205326	integrals who by the interpretation	4.90
	422573 430665	AW297985 BE350122	Hs.295726 Hs.157367	integrin, alpha V (vitronectin receptor ESTs, Weakly similar to 178885 serine/th	4.90
	446006	NM_004403	Hs.13530	deziness, autosomal dominant 5	4.90
_	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.82
5	430027	AB023197	Hs.227743	KIAA0980 protein	4.78
	408393	AW015318	Hs.23165	ESTs	4.76
	449509	AA001615	Hs.84561	ESTs	4.72
	416206	AW206248	Hs.111092	hypothetical prolein FLJ22332	4.72
10	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	4.72
10	433226	AW503733	Hs.9414	KIAA1488 protein	4.68
	444745 442994	AF117754 AJ026718	Hs.11861 Hs.16954	thyroid hormone receptor-associated prot ESTs	4.68 4.66
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.66
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.66
15	418005	A1186220	Hs.83164	collagen, type XV, alpha 1	4.65
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spieen	4.64
	424917	A1636208	Hs.96901	hypothetical protein FLJ23049	4.64
	424408	A)754813	Hs.146428	collagen, lype V, alpha 1	4.64
20	418113		, Hs.83484	SRY (sex determining region Y)-box 4	4.62
20	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12951 fis, done NT	4.62
	450086	AW016343	Hs.233301	ESTs	4.61
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	4.60 4.59
	442652 410268	A)005163 AA316181	Hs,201378 Hs,61635	ESTs, Weakly similar to T12545 hypotheti six transmembrane epithelial antigen of	4.58
25	418259	AA215404	115.01055	ESTs	4.54
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (ig),	4.54
	432810	AAB63400		ESTs	4.54
	407112	AA070801	Hs.61615	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.53
	436100	AA704B06	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.52
30	412652	A1801777		ESTs	4.52
	438899	AF085633	Hs.135624	ESTs	4.52
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	4.52
	436252	Al539519	Hs.120969	Homo sapiens cDNA FLJ11562 fia, clone HE	4.52
35	443324	R44013	Hs,164225	ESTs	4.51
33	407690 431393	R47799 AW971493	Hs.266957 Hs.134269	hypothetical protein FLJ14281 ESTs, Highly similar to cytokine recepto	4.51 4.51
	452518	AA280722	Hs.24758	ESTs, Weakly similar to (38022 hypotheti	4.50
	431843	AA516420	1 ADAL TE DO	ESTs, Weakly similar to (38022 hypotheti	4.50
	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.46
40	452561	A1692181	Hs.49169	KIAA1634 protein	4.48
	440273	A1805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	4.45
	442046	AA974603		gbcop34f05.s1 Soares_NFL_T_GBC_S1 Homo s	4.44
	436120	Al248193	Hs.119860	ESTs	4.44
45	423575	C18863	Hs.163443	Intron of periostin (OSF-2os)	4.44
43	429697	AW296451	Hs.24605	ESTS Per OTBook estimates emble CU2 demais	4.44 4.43
	439866 429688	AA280717 BE245169	Hs.6727 Hs.211610	Ras-GTPase activating protein SH3 domain CUG triplet repeat, RNA-binding protein	4.43
	414462	BE622743	Ha.301064	erfaptin 1	4.42
	428698	AA852773	Hs.334838	KIAA1866 protein	4.42
50	420838	AW118210	Hs.42321	ESTs	4,41
	458584	AF217518	Hs.8360	PTD012 protein	4.40
	434340	A)193043	Hs,128685	ESTs, Weakly similar to T17226 hypotheti	4,40
	400076			Eos Control	4.38
55	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	4.38
33	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.36
	420298 433339	Al199510 AF019226	Hs.267912 Hs.8036	ESTs, Weakly similar to ALU7_HUMAN ALU S glioblastoma overexpressed	4,36
	433339	AF019220 AW803564	Hs.288850	Homo saplens cDNA: FLJ22528 fis, clone H	4.35 4.34
	416391	Al878827	Hs.79284	mesoderm specific transcript (mouse) hom	4.34
60	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4.33
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	4,33
	429228	Al553833		ESTs	4.32
	426458	D83032	Hs.169984		4.30
45	408369	R38438	Hs.182575		4.30
65	432476	T94344	Hs.326263		4.29
	434963 436446	AW974957	Hs.288719		4.28
	439556	AW016809 AI623752	Hs.119021 Hs.163603		4,27 4,26
	428179	AM27772	Hs.279696		4.26
70	428411	AW291464	Hs.1033B	ESTs	4.26
	434936	AJ285970	Hs.183817		4.23
	413048	M93221	Hs.75182	mannose receptor, C type 1	4.23
	432608	NM_002104		granzyme K (serine protesse, granzyme 3;	4.22
75	413859	AW992356	Hs.8364	Homo septens pyruvate dehydrogenase kina	4.22
75	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	4.22
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyma E2E 1 (homo	4.21
	421229	AJ056590 AJ264155	Hs.7086	hypothetical protein MGC12435	4.20
	456844 423578	AVV960454	Hs.152981 Hs.222830		4.20 4.20
80	446608	N75217	Hs.257B46		4.20
	424238		Hs.137635		4.19
	450747	AI064821	Hs.318535		4.1B
	420674			bulyrylcholinesterase	4.18

	428227 439593	AA321649 BE073597	Hs.2248 Hs.124863	small inducible cylokine subfamily B (Cy ESTs	4.18 4.17
	442369	AI565071	13 40-000	ESTs	4.16
5	445885	A1734009	Hs.127699	KIAA1603 protein	4.16 4.16
,	459702 452960	Al204995 AK001335	Hs,31137	gb:an03c03x1 Strategene schizo brain S1 protein tyrosine phosphatase, receptor t	4.16 4.16
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	4.15
	407347	AA829847		gb:od40d07.s1 NCI_CGAP_GCB1 Homo saptens	4.14
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.13
)	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.12
	4511B4	T87943	1) 445000	transcription factor 7-like 2 (T-cell sp	4.12
	426174	AA547959	Hs.115838 Hs.11637	ESTs ESTs	4.12 4.12
	431562 417094	A1884334 NM_006895	Hs.81182	histamine N-methyltransferase	4.12
5	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12
•	449437	A1702038	Hs.100057	Homo sepiens cDNA: FLJ22902 fis, clone K	4.12
	425053	AF046024	Hs.154320	ublquitin-ectivating enzyme E1C (homolog	4.10
	444020	R92962	Hs.35052	ESTa	4.10
)	439424	A)478667	Hs.118183	hypothetical protein FLJ22833	4.10
,	416987	D86957	Hs.80712	KIAA0202 protein	4.10
	457121	A1743770 M26939	Hs.180513 Hs.119571	ESTs, Weakly similar to KIAA0822 protein collagen, type III, alpha 1 (Ehlers-Dani	4.09 4.09
	422737 446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.03
	431193	AW749505	Hs.296770	KIAA1719 protein	4.08
5	452144	AA032197	Hs.102558	Homo saplens, clone MGC:5352, mRNA, comp	4.08
	433308	AA582718	Hs.291650	ESTs	4.08
	445756	AA290690	Hs.300776	ESTs	4.08
	431745	AW972448	Hs.163425	ESTs CALL CALL CALL CALL CALL CALL CALL CAL	4.08
)	444610	Al 174783	U. coor	gb;HA2501 Human fetal liver cONA library	4.07
J	440099	AL08005B AA284267	Hs.6909 Hs.221504	DKFZP564G202 protein ESTs	4.06 4.05
	439398 432731	R31178	Hs.287820	fibronectin 1	. 4.06
		. L27479	Hs.77889	Ertedraich steeta region gane X123	4.05
_	433626	AF078859	Hs.86347	hypothetical protein	4.05
5	428055	AA420564	Hs.101760	ESTs	4.04
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04
	413243	AA769266	Hs,193657	ESTs ·	4.02
	431214 453753	AA294921 BE252983	Hs.348024 Hs.35086	v-ral simian leukemia viral oncogene hom ubiquitin specific prolease 1	4.02 4.02
0	414504	AW069181	Hs.115175	stecile-aipha motif and leucine zipper c	4.02
v	434404	AW445034	Hs.256578	ESTs	4.02
	407604	AW191962		collagen, type VIII, alpha 2	4.02
	429412	NM_005235	Hs.2407	POU domain, class 2, associating factor	4.02
_	436772	AW975688		metalfothionein 1E (functional)	4.00
5	443257	A1334040	Hs.11614	HSPC065 protein	4.00
	450187	AA736788	Hs.78521	KIAA1717 protein	3.9B
	433913 415060	AI694106 AJ223810	Hs.72325 Hs.43213	ESTs, Weskly similar to 138022 hypotheti ESTs, Weskly similar to IEFS_HUMAN TRANS	3.98 3.98
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	3.98
0	432374	W68815	Hs.301885	Homo saplens cDNA FLJ11346 fls, clone PL	3.98
	426818	AA554827	Hs.292996	DKFZp434A0131 protein	3.98
	440118	AB040893	Hs.6968	KIAA1460 protein	3.9B
	413836	W92003	Hs.70614	ESTs	3.97
5	442647	AL038436	Hs.31388	ESTS	3.96
)	449188 450656	AW072939 AA010539	Hs.347187 Hs.18912	myotubularin related protein 1 ESTs	3.96 3,96
	410817	A1262789	Hs.93659	protein disulfide isomerase relațeă prot	3,94
	429784	M89796	Hs.30	membrane-spanning 4-domains, subtamily A	3.94
	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	3.94
60	407879	AA045464	Hs.6557	zinc finger protein 161	3.93
	438146	Z36842	Hs.57548	ESTs	3.93
	433658	L03678	Hs,156110	immunoglobulin kappa constant	3.93
	429355	AW973253	Hs.292689	ESTS	3,92
55	437210 432467	AA311443 T03667	Hs.293563 Hs.239388	Homo saplens mRNA; cDNA DKFZp586E2317 (f Human DNA sequence from clone RP1-304814	3.92 3.92
	452416	AA026115	Hs,114777		3.92
	413873	AI310151	Hs.173524		3.91
	400196			Eos Control	3.91
•	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.90
70	453204	R10799	Hs.191990		3.90
	454076	AW204712	Hs.61957	ESTs	3.90
	431183	NM_006855 AW090198	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic KIAA1150 protein	3.90 3.90
	437158 443970	AWU90196 Al280341	Hs.166571		3.90
75	441633	AW958544	Hs.112242		3.90
-	452281	T93500	Hs.28792	Homo sepiens cDNA FLJ11041 fis, clone PL	3.90
	444057	AA316896	Ha.257267	FYVE and coiled-coil domain containing 1	3.89
	411495	AP000693	Hs.70359	KIAA0136 protein	3.88
20	438452	Al220911	Hs.288959		3.88
30	410297	AA148710	11-00-100	lumican	3.88
	427698 436769	AW972594	Hs.335499	ESTs ESTs	3.69 3.66
	436769 417819	AA748675 Al253112	Hs.133540		3.86
	-1(7)	THE STATE OF THE	1 1000		4.00

	445800	AA126419	Hs.32944	inosticl polyphospitate-4-phosphatase, ty	3.86
	425838	NM_014071	Hs.159613	nuclear receptor coactivator RAP250; per	3.86
	422173	BE385828	Hs.250619	phorbolin-like protein MOS019 (CEM15)	3.86
5	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell	3.85
. ·	445693 433700	AW800444	Hs.76507	LPS-induced TNF-alpha factor	3.85
	432706 412636	NM_013230 NM_004415	Hs.286124	CD24 antigen (small cell lung carcinome desmoplakin (DPI, DPII)	3.85 3.84
	436169	AAB88311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	3.84
	418876	AA740516		gb:ny97f11.s1 NCI_CGAP_GC81 Homo sapiens	3.84
10	436110	AA704899	Hs.291651	ESTs, Weakly similar to 138022 hypotheti	3.84
	430317	AB020645	Hs.239189	giutaminase	3.84
	442805	AW294522	Hs.149991	ESTs	3.84
	414320 430512	U13616 AF182294	Hs.75893 Hs.241578	ankyrin 3, node of Ranvier (ankyrin G)	3.82
15	427051	BE178110	Hs.173374	U6 snRNA-associated Sm-like protein LSm8 Homo sapiens cDNA FLJ10500 fis, clone NT	3.82
	430573	AA744550	Hs.136345	ESTs	3.82 3.82
	453394	AW960474	Hs.402B9	ESTs	3.81
	431266	AW149321	Hs.105411	ESTs ·	3,80
20	434987	AW975114		ESTs	3.80
20	452685	Al634651	Hs.30250	V-maf musculoaponeurotic fibrosarcoma (a	3.79
	435176	AA744875	Hs.189413	ESTs	3.78
	437134 430709	AA349944 R34356	Hs.42915	ARP2 (actin-related protein 2, yeast) ho gb:yh85d01.s1 Soares placenta Nb2HP Homo	3,77 3.77
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.76
25	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	3.76
	417228	AL134324	Hs.7312	ESTs	3.76
	418546	AA224827		gb:nc32g04.s1 NCI_CGAP_Pr2 Homo saplens	3.76
	450779	AW204145	Hs.156044	ESTs	3.75
30	412408 443879	D51103 Z28462	Hs.73851 Hs.9927	ATP synthese, H transporting, mitochondr	3.75
30	414812	X72755	Hs.77367	Homo saplens mRNA; cDNA DKFZp564D156 (fr monokine induced by gamma interferon	3.75 3,75
	429494	AA769365	Hs.126058	ESTs	3.75
	447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro	3.75
25	408B22	AW500715	Hs.57079	Homo saplens cDNA FLJ13267 fis, clone OV	3.74
35	419591	AF090900	Hs.91393	Homo sapians cDNA: FLJ21887 fis, clone H	3.74
	448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	3.74
	436260 421485	BE172762 AA243499	Hs.292710 Hs.104800	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.74
	414883	AA926960	125.104000	hypothetical protein FLI10134 CDC28 protein kinase 1	3.73 3.72
40	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.72
	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	3.72
	444099	DB7432	Hs.10315	solute carrier family 7 (cationic amino	3.72
	438607	AW080237	Hs.252884	ESTs	3.72
45	408221 418699	AA912183 BE539639	Hs.47447	ESTs	3.72
73	419900	A)469960	Hs.173030 Hs.170698	ESTs, Weakly similar to ALU8_HUMAN ALU S ESTs	3.70 3.70
	446342	9E298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.70
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23,2	3.70
50	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	3.70
50	413263	R78669	Hs.23756	hypothetical protein similar to swine ac	3.70
	447846	AA324057	Hs.77955	Homo sapiens cDNA: FLJ23527 fis, clone L	3.70
	436198 418300	AKD01125 Al433074	Hs.86882	Homo sapiens cDNA FL 10263 fis, clone HE	3.70
	40B495	W68796	Hs.237731	Homo sapisns cDNA: FLJ21578 fis, clone C ESTs	3.69 3.69
55	424452	N41367	Hs.173002	ESTs, Weakly similar to 138022 hypotheti	3.68
	448479	H96115	Ha.21293	UDP-N-acteylglucosamine pyrophosphorylas	3.68
	431974	AW972689	Hs.200934	ESTs	3.68
	416354	NM_000633	Hs.79241	B-cell CLL/lymphoma 2 (BCL2)	3.68
60	417412	X16896	Hs.82112	Interleukin 1 receptor, type 1	3.68
00	413645 416221	AA130992 BE513171	Hs.79086	gbzo15e02s1 Strategena colon (937204)	3.67
	419111	AA234172	Hs.137418	mitochondrial ribosomal protein L3 ESTs	3.67 3.67
	423979	AF229181	Hs.136644	CS box-containing WD protein	3.66
~-	418875	W19971	Hs.233459	ESTs	3.66
65	451690	AW451469	Hs.209990	E8Ta	3.66
	423032	AJ684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.66
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.66
	428347 426779	A1264161 AA384577	Hs.183773 Hs.93714	golgi autoantigen, golgin subtamily a, 4	3.65
70	435335	A1693150	Hs.137928	ESTs, Weakly similar to T00365 hypotheti ESTs	3.66 3.66
	410577	X91911	Hs.64639	glioma pathogenesis-related protain	3.66
	452933	AW391423	Hs.288555	Homo sepiene cDNA: FLJ22425 fis, clone H	3.65
	429105	D87077	Hs. 196275	KIAA0240 protein	3,64
75	407813	AL120247	Hs.40109	KIAA0872 protein	3.64
13	425863	U43804	Hs.159901	Human triklentified mRNA, partial sequence	3.64
	451678 452420	AA374181 BE564871	Hs.26799 Hs.29463	DKF2P564D0764 protein centrin, EF-hand protein, 3 (CDC31 yeast	3.64 3.64
	45240B	AA306477	Hs.29379	hypothetical protein FLJ10687	3.64 3.64
	441466	AW673081	Hs.54828	ESTs	3.63
80	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.62
	420056	AW043684	Hs.99804	ESTs	3.62
	424886 431774	H88584 RE348813	Hs,96900	hypothetical protein; KIAA1830 protein	3.62
	431774	BE348813	Hs.268561	hypothetical protein FLJ 10726	3.62

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	435990	Alhiteen	11- 424702	COX-	
	433990	A1015862 BE245149	Hs.131793 Hs.82643	ESTs protein tyrosine klnase 9	3.62
	414715	AA587891	Hs.904	amylo-1,6-glucosidase, 4-alpha-glucanotr	3.62 3.62
_	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.62
5	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	3.62
	413823	A1341417	Hs.29406	ESTs	3.61
	435354	AA678267	Hs.117115	ESTs	3.60
	427832 427846	AF038362	Hs.180930	TBP-associated factor 172	3.6D
10	426116	AW499770 AA868729	Hs.180948 Hs.144694	KIAA0729 protein ESTs	3.60
~~	457635	AV660976	Hs.3569	hypothetical protein	3.60 3.60
	443998	A)620661	Hs.296276	ESTs	3.60
	417867	AW952547	Hs.194603	ESTs, Moderately similar to 138022 hypol	3.5B
15	4181B2	AW016405	Hs.16648	ESTs	3.58
15	434941	AW073202	Hs.334825	Homo sepiens cDNA FLJ14752 lis, clone NT	3.5B
	424831	H61453		ESTs	3.58
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.58
	421823 414781	N40850 D50917	Hs.28625 Hs.77293	ESTs KIAA0127 gene product	3.58
20	427393	AB029018	Hs.177635	KIAA1095 protein	3.57 3.57
	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.56
	425465	L18964	Hs.1904	protein kinase C, iota	3.58
	417124	BE122762	Hs.25338	ESTs	3.56
25	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	3.56
25	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-fymp	3.55
	421097 410390	A1280112 AA876905	Hs.125232 Hs.126286	Horno sapiens cDNA FLJ 13266 ffs, clone OV	3.55
	442073	AW973443	Hs.8086	ESTs RNA (guanine-7-) methyltransferase	3.54
	435266	AK001942	Hs.4863	hypothetical protein DKF2p566A1524	3.54 3.54
30	441499	AW298235	Hs. 101689	ESTs	3.54
	453256	A1565587	Hs.32556	KIAA0379 protein	3.54
	414142	AW368397	Hs.334485	hemicaniin (libulin 6)	3.54
	438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	3.54
35	412245	A1952669	Hs.228B3	ESTs, Weakly similar to 138022 hypotheti	3,54
25	424144	AA454033	Hs.41644	AKAP-associated sparm protein	3.53
	446682 431392	AW205632 Al371223	Hs,211198 Hs,288671	ESTs Homo septens cDNA FLJ11997 fis, clone HE	3.52
	433430	AlB63735	15.2000)	ESTs	3.52 3.52
	420394	AB023161	Hs.97403	KJAA0944 protein	3.52
40	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.52
	443547	AW271273		hypothetical protein FLJ12666	3.52
	420576	AJ4347B0	Hs.4248	vav 2 oncogene	3.51
	410590	AA322979	Hs.130266	ESTs	3.50
45	459645 401403	AA074348		ESTs	3.50
73	451166	198171	Hs.185675	Target Exon ESTs	3,50
	418836	AI655499	Hs.161712	ESTs	3.50 3.50
	421462	AF016495	Hs. 104624	aquaporin 9	3.50
	414555	N98569	Hs.76422	phospholipase A2, group IIA (piatelets,	3.50
50	432401	NM_013330	Hs.274479	NME7	3.49
	408392	U28831	Hs.44566	KIAA1641 protein	3.49
	425836	AW955696 AK000196	Hs.90960	ESTs	3.48
	452327 418721	NM_002731	Hs.29052 Hs.87773	hypothetical protein FLI20189	3.48
55	433627	AF078865	Hs.284298	protein kinase, cAMP-dependent, catalyti Homo sepiens cDNA: FLJ22993 fis, clone K	3.48 3.48
	422960	AW890487	TRILO ILUO	cadherin 13, H-cadherin (heart)	3.48
	430570	Al417881	Hs.292464	ESTs	3.48
	406387			Target Exon	3.47
60	4165B5	X54162	Hs.79386	leformedin 1, smooth muscle (LMOD1) (Thy	3.48
OV	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo saplens	3.46
	412240 450937	H72176 R49131	Hs.26267	hypothetical protein FLJ13169	3.46
	443634	H73972	Hs.134460	ATP-dependent interferon response protel ESTs	3.46 3.46
	422963	M79141	Hs.13234	ESTs	3.46
65	424954	NM_000546	Hs,1846	tumor protein p53 (LI-Fraumeni syndrome)	3.46
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	3.46
	425100	AF051850	Hs.154567	supervilla	3.45
	450680	AF131784	Hs.25318	Homo sapiena clone 25194 mRNA sequence	3.45
70	444250	R40816	Hs.12396	ESTs, Weakly similar to 2004399A chromos	3.44
70	428386 447764	R17298 NM_003776	Hs.295923	seven in absentia (Drosophila) homolog 1	3.44
	411251	R19774	Hs.19500 Hs.22B35	nuclear localization signal deleted in v HHGP protein	3.44 3.44
	432648	AA557952		gb:nl17c05.s1 NCL_CGAP_HSC1 Homo seplens	3.44
es E	428708	NM_014897	Hs.190386	KIAA0924 protein	3,44
75	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	3.43
	451743	AW074266	Hs.23071	E8Ts	3.42
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	3.42
	448705 414489	H05072 A1620677	Hs.124984 Hs.73105	ESTs, Moderately similar to ALU7_HUMAN A	3.42
80	429732	U20158	Hs.2488	ESTs lymphocyte cytosolic protein 2 (SH2 doma	3.42
	435841	R28522	Hs. 186937	ESTs	3.41 3.41
	424130	AL050136	Hs.140945	Homo sepiens mRNA; cDNA DKFZp586L141 (fr	3.40
	451198	AW984541		hypothetical protein FLJ21127	3.40
				100	
				476	

	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	3.40
	436023 449656	TB1819 AA002008	Hs.302251	ESTs	3.40
	437739	AW579216	Hs.188633 Hs.264610	ESTs ESTs, Moderately similar to lbd1 (H.sapi	3.40
5	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	3.40 3.40
	448474	Al792014	Hs.13809	hypothetical protein FLJ10648	3.40
	456505	AA504695		ESTs	3.40
	439867	AA847510	Hs.161292	ESTs	3.40
10	442113	BE6221B7	11 400	ESTs, Weakly similar to 138022 hypotheti	3.40
10	425922 435299	AL157466	Hs.162751	Homo saplens mRNA; cDNA DKFZp761E2423 (f	3.40
	421263	A1745458 AB020638	Hs.343026 Hs.103000	ESTs, Weakly similar to T20593 hypotheti	3.40
	410300	AW903988	Hs.62119	KIAA0831 protein hypothetical protein FLJ14B00	3.40
4	440028	AW473675	110102110	ESTs, Weakly similar to T17227 hypotheti	3.39 3.39
15	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	3.38
	432572	A1660840	Hs.191202	ESTs, Weeldy similar to ALUE_HUMAN IIII	3.38
	442426	Al373062	Hs.332938	hypothetical protein MGC5370	3.38
	428412 448772	AA428240 AW390822	Hs.126083	EST\$	3.38
20	417057	A3001417	Hs.301528 Hs.81086	L-kynurenine/alpha-aminoadipate aminotra solute carrier family 22 (extraneurona)	3.38
	413714	A1560944	Hs.71428	ESTs	3.38
	415663	AW296841	Hs.313332	ESTs	3.38 3.38
	407904	W44735	Hs.9286	Homo sepiens cDNA: FLJ21278 fls, clone C	3.37
25	421114	AW975051	Hs.293156	ESTs, Weakly similar to 178885 serine/th	3.37
23	440214	AA247118	Hs.7049	hypothetical protein FLI11305	3.37
	440980 411975	ALD42005 Al916068	Hs.1117 Hs.144583	tripeptidyl peptidase (i ESTs	3.36
	450330	AW500775	Hs.24817	hypothelical protein FLJ20136	3.36
• •	414783	AW069569		unactive progesterone receptor, 23 kD	3.36 3.36
30	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.36
	411213	AA676939	Hs.69285	nsuropilin 1	3,36
	420613 417534	A1873871	Hs.7041	ESTs, Weakly similar to A47582 B-cell gr	. 3.35
35	431598	NM_004998 A1492369	Hs.82251	myosin IE ESTs	3.35
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3,35 3.35
	441623	AA315805		desmoglein 2	3.34
	420729	AW964897	Hs.290825	ESTs	3.34
40	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	3.34
70	448369 452820	AW268962 N46161	Hs.111335 Hs.35274	ESTS ESTS	3.34
	453271	AA903424	Hs.6786	ESTS	3.34
	428839	Al767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.34 3.34
46	418832	X04011	Hs.88974	cylochrome b-245, beta polypeptide (chro	3.34
45	443291	AA325633	Hs.136102	KIAAD853 protein	3.33
	418720 452107	Al381687 AB020681	Hs.39526	ESTs	3.33
	439943	AW083789	Hs.27973 Hs.124620	KIAA0874 protein ESTs	3.33
	433282	8E539101	1 24 (24020	hypothetical protein	3.33 3.33
50	410344	AW978436	Hs.62515	KIAA0494 gene product	3.33
	417259	AW903838	Hs.81800	chandroitin sulfiste proteoglycan 2 (vers	3.32
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.32
	434210 431923	AA665612 Al741770	Hs.292690	ESTS	3,32
55	453199	Al336266	Hs.32353	ESTs, Weakly similar to 138022 hypotheti mltogen-activated protein kinase kinase	3.32
	419534	AA443691	Hs.90858	Homo sapiens clone 25023 mRNA sequence	3.32 3.32
	448939	BE267795	Hs.22595	hypothetical protein FLJ 10637	3.32
	433312	AJ241331	Hs.131765	ESTs, Moderately similar to 198937 DNA/R	3.32
60	422092 412262	AB007883	Hs.111373	KIAA0423 protein	3.32
00	412202	W26406 NM 013989	Hs.154424	seven in absentla (Drosophila) homolog 1 delodinase, iodothyronine, type II	3,32
	446094	AK001760	Hs.13801	KIAA1685 protein	3.32
	446493	AK001389	Hs.15144	hypothetical protein DKFZp5640043	3.32 3.32
<i>C</i> =	420339	AW968259	Hs.186647	ESTs	3.31
65	447735	AA775268	Hs.6127	Homo saplens cDNA: FLJ23020 fis, clone L	3.31
	432331	W37862	Hs.274368	MSTP032 protein	3.31
	433697 419231	AA600357 Al046294	Hs.239489	TIA1 cytoloxic granule-associated RNA-bi	3.31
	430950	AA489525	Hs.136245	ESTs, Weakly similar to T17227 hypotheti ESTs	3.31
70	409758	AW474960	Hs.182258	ESTs, Weakly similar to 178885 serine/th	3.30 3.30
	417958	AA767382	Hs.193417	ESTs	3.30
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.30
	419543 454024	AA244170	17- 50000-	gb:nc05h02.s1 NCI_CGAP_Pr1 Homo saplens	3.30
75	454024 452039	AA993527 AI922988	Hs.293907 Hs.172510	hypothetical protein FLJ23403	3.30
	443798	R07848	Hs.188522	ESTS ESTS	3.30
	449378	AW664026	Hs.59892	ESTs	3.29 3.29
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	3.28
80	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	3.28
OU	444291 424084	A1598022 A1940675	Hs.193989	TAR DNA binding protein	3.28
	437330	AJ940675 AL353944	Hs.20914 Hs.50115	hypothetical protein FLJ23056 Homo spojens mRNA: aDNA DMEZaze4 (4442.4	3.28
	443774	AL117428	Hs.9740	Homo sepiens mRNA; cDNA DKFZp761J1112 (I DKFZP434A236 protein	3.28 3.28
				ACIC	

	425657	T89839	Hs.119471	ESTs	3.28
	406672 419905	M26041	Hs. 198253	major histocompatibility complex, class	3.28
	425332	AW248229 AA633306	Hs.93659 Hs.127279	protein disultida isomerase related prot	3.27
5	418529	AW005695	Hs.250897	ESTs TOK Sured core	3.27
_	417944	AU077196	Hs.82985	TRK-fused gene collagen, type V, alpha 2	3.27
	433618	AA502539	Hs.345494	ESTs	3.27 3.27
	408530	AA748009	Hs.173328	ESTs	3.26
10	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	3.26
10	415102	M31899	Hs.77929	excision repair cross-complementing rode	3.26
	432526	AA471098	Hs,278544	acetyl-Coenzyme A acetyltransferese 2 (a	3.26
	429493	AL134708	Hs.145998	ESTs	3.28
	445860 450256	AA332145 AA286887	Hs.13392	telhering factor SEC34	3.26
15	426083	AW962712	Hs.24724 Hs.126712	MFH-amplified sequences with feucine-ric	3.26
	420059	AF161486	Hs.94769	ESTs, Weakly similar to AF191020 1 E2:G5 RAB23, member RAS oncogene family	3.26
	448412	Al219083	Hs.42532	ESTs, Moderately similar to ALUS_HUMAN A	3.26
	436758	AW977167	Hs.155272	ESTs	3,26 3.26
20	438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.26
20	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	3.25
	426860	U04953	Hs.172801	isoleucine-IRNA synthetese	3.25
	437830	AB020658	Hs.5867	KIAA0851 protein; suppressor of actin 1	3.25
	453368 409939	W20296	Hs.288178	Homo sepiens cDNA FLJ11968 fts, clone HE	3.25
25	413715	AA463437 AW851121	Hs.11556 Hs.75497	Homo sapiens cDNA FLJ12566 fis, clone NT	3.25
	407939	W05608	Hs.312679	Homo saplens cDNA: FLJ22139 fis, clone H ESTs, Weakly similar to A49019 dynein he	3.24
	418283	S79895	Hs,83942	cathepsin K (pychodysostosis)	3.24
	414405	Al362533	11000012	KIAA0306 protein	3.24 3.24
	445893	Al610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.24
30	434423	NM_006769	Hs,3844	LIM domain only 4	3.24
	408951	AW407227	Hs.227591	hypothetical protein FLI 11088	3.24
	408949	AF189011	Hs.49163	putalive ribonuclease III	3.24
	410337	M83822	Hs.62354	cell division cycle 4-like	3.24
35	409010 400419	A1648675 AF084545		Homo sapiens, Similar to RIKEN cDNA 1700	3.24
	454078	AA601518	Hs.22209	Target secreted modular calcium-binding protein	3.24
	422461	NM_003417	Hs.117077	zinc finger protein 254	3.24
	441604	A1683049	Hs.201282	ESTs	3.24 3.24
40	411960	R77776	Hs.18103	ESTs	3.23
40	414895	AW894856	Hs.116278	Homo saplens cDNA FLJ13571 fis, clone PL	3.23
	430522	N75750	Hs.242271	KIAA0471 gene product	3.23
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23
	405268 429165	AW009886	12-140000	ENSP00000223174*:KIAA0783 PROTEIN.	3.23
45	427196	AW967522	Hs.118258 Hs.191593	prostate cancer associated protein 1 ESTs	3.22
•••	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	3.22
	417727	AL133823	Hs.82501	similar to mouse Xm1 / Dhm2 protein	3.22
	410853	H045BB	Hs.30469	ESTs	3,22 3,22
50	411962	AA099050		gbtzk85d12.r1 Soares_pregnant_uterus_NbH	3.22
50	451099	R52795	Hs.25954	Interieukin 13 receptor, elpha 2	3.22
	440452	Al925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22
	427480 444623	BE148769 A1183829	Hs.334477	hypothetical protein FLJ11328	3.22
	424006	AF054815	Hs.202111	ESTs	3.21
55	435874	AA86868B	Hs.137548 Hs.93102	CD84 antigen (laukocyte antigen) ESTs	3,21
	443801	AW206942	Hs.253594	introx of: trichorhinophalangeal syndro	3.20
	434982	AW975084	1,0,00001	gb:EST387190 MAGE resequences, MAGN Homo	3,20 3.20
	430929	AA489166	Hs.156933	ESTs	3.20
60	426316	NM_002430	Hs.268515	maningioma (disrupted in balanced transl	3,20
vv	430378	729572	Ha.2556	tumor necrosis factor receptor superfamil	3.20
	422109 451110	S73265	He.1473	gastrin-releasing peptide	3.20
	451119 414893	AAB05417 AA215295	Hs.64753 Hs.77578	ESTS	3.20
	432676	A1187366	114.7 7310	ubiquitin specific protease 9, X chromos gb:qf29c01.x1 Soares_lestis_NHT Homo sap	3.20
65	428820	AA436187	Hs.172631	integrin, sipha M (complement component	3.19 3.19
	422040	AA172106	Hs.110950	Rag C protein	3.18
	437838	Al307229		ESTs .	3.18
	408761	AA057264	Hs.23B936	ESTs, Westdy similar to (defline not eve	3,18
70	420789	A1670057	Hs.199882	ESTs	3.18
70	419135 446019	R61448	Hs.106728	ESTs, Wealdy similar to KIAA1353 protein	3.18
	43084B	Al362520 AW021726	Un SAEANÓ	histone descriylase 3	3.18
	425375	AA631977	Hs.345490 Hs.155995	gb:df27e02.yf Morton Fetal Cochiea Homo KIAA0643 protein	3.18
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.18
75	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18 3.18
	453111	AB014598	Hs.31720	haphaestin	3.18
	454042	H22570		hypothetical protein F1J20093	3.18
	407756	AA116021	Hs.38260	ubiquitin specific protesse 18	3.18
80	447183	A1554733	Hs.173182	ESTa	3.18
30	437446 431831	AA788946 AW023204	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.18
	420664	AN023204 A1681270	Hs.302743 Hs.99824	ESTs BCE-1 protein	3.18
	451582	A1963026	Hs.28995B	ESTs, Weakly similar to putative p150 [H	3.18
				· · · · · · · · · · · · · · · · · · ·	3.17

	******	110000			
	432954 444990	A1076345 A1912410	11- 27475	ESTS	3.17
	427373	AB007972	Hs.27475 Hs.130760	Homo saplens cDNA FLI12749 fls, clone NT	3.17
_	408832	AW085690	Hs.63428	myosin phosphetase, target subunit 2 ESTs, Weakly similar to Z195_HUMAN ZINC	3.17
5	441889	A1090455	Hs.268371	hypothetical protein FLJ20274	3.17 3.17
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.16
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.16
	420623	BE245485	Hs.99437	Homo saplens mRNA; cDNA DKFZp586G1924 (f	3.16
10	451475	T19093	Hs.26450	KIAAD725 protein	3.16
10	452066 429556	AA772149 AW139399	Hs.16979	ESTs, Weekly similar to A43932 mucin 2 p	3.16
	448514	AB020628	Hs.98988 Hs.301866	ESTs KIAA0819 protein	3.16
	443732	Al188B03	Hs.153944	ESTs	3.16
	436805	AA731533	Hs.270751	ESTs	3.16 3.16
15	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	3.16
	417511	ALD49176	Hs.82223	chordin-like	3.16
	423595	R82826	Hs.220702	EST ₃	3.16
	445837	Al261700	Hs.145544	ESTs	3.16
20	418068 430253	AW971155 AK001514	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	3.16
20	414183	AW957446	Hs.236844 Hs.301711	hypothetical protein FLJ 10652	3.16
	433194	AB040883	Hs.83243	ESTs KIAA1450 prolein	3.16
	453915	AA588721	Hs.286218	nitrosomal protein L44	3.16 3.15
0.5	407725	BE388094	Hs.21B57	ESTs	3.15
25	437412	BE069288	Hs.34744	Homo saplens mRNA; cDNA DKFZp547C136 (fr	3.14
	440937	AF202724	Hs.7531	KIAA0810 protein	3.14
	449057	AB037784	Hs.22941	RAA1363 protein	3.14
	446126 407204	AW085909 R41933	Hs.140237	pleckstrin homology domain interacting p	3.14
30	419145	N99638	ПБ. 14023/	ESTs, Weakly similar to ALU1_HUMAN ALU S gb:za39g11.r1 Soares fetal liver spleen	3.14
	418757	Al864193	Hs.169728	hypothetical protein FLI13150	3.14 3.14
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	3.14
	437296	AA350994	Hs.20281	KIAA1700	3.14
35	441381	H22195	Hs.31874	ESTs	3.14
22	457250	AAB11987	Hs.125779	ESTs	3.14
	422900 442787	AA641201 W83048	Hs.222051 Hs.250723	ESTS	3.14
	430589	AJ002744	Hs.246315	hypothetical protein MGC2747	3,14
••	419355	AA42B520	Hs.90061	UDP-N-acetyl-alpha-D-galactosamine:polyp progesterone binding protein	3.14 3.14
40	409509	AL036923	Hs.322710	ESTs Process	3.14
	417308	H60720	Hs.81892	KIAA0101 gene product	3.14
	409799	D1192B	Hs.76845	phosphosedne phosphatase-like	3.14
	429160	AW663083	Hs.144469	ESTs	3.14
45	452679 451107	Z42387 AAZ35108	Hs.83883	transmembrane, prostate androgen induced	3.14
	444034	AL161957	Hs.17639 Hs.10177	Homo sapiens ubiquitin protein iligase (L)	3.14
	451518	AW340925	Hs.174918	pleckstrin homology domain interacting p ESTs	3.14
	435702	Al033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3,14 3.13
50	439208	AK000299	Hs.180952	dynactin 4 (p62)	3.13
50	451838	AW005866	Hs.193969	ESTS	3,13
	426369	AF134157	Hs.169487	Kreisler (mouse) mai-related leucine zip	3,13
	446945 453920	Al 193115 Al 133148	Hs.16611 Hs.36602	tumor protein D52-like 1	3.13
	411529	AA430348	Hs.317596	I factor (complement) Hamo sapiena cDNA FLJ12927 fis, clone NT	3.13
55	417105	X60992	Hs.81226	CD6 antigen	3.13 3.12
	433854	AA610649	Hs,333239	ESTs	3.12
	408089	H59799	Hs.42844	thioredoxin-like	3.12
	453686	AL110326	Hs.304579	ESTs, Moderately similar to Z195_HUMAN Z	3.12
60	428187 452195	AF039023 AA994712	Hs.167496	RAN binding protein 6	3.12
00	416580	T61572	Hs.116878 Hs.79385	ESTs Human clone 23574 mRNA sequence	3.12
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12
	424801	W67883	Hs.137476	paternally expressed 10	3.12 3.12
CE	4345B4	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3,12
65	433401	AF039698	Hs.284217	serologically defined colon cancer antig	3,12
	409245	AA361037		tRNA isopentenyipyrophosphate transferas	3.12
	414290 400294	ai568801 N95796	Hs.71721	EST8	3.12
	429819	AL133011	Hs.278695 Hs.225108	Homo sapiens prostein mRNA, complete cds	3.12
70	448873	NM_003677	Hs.22393	Homo septens mRNA; cDNA DKFZp434P201 (fr density-regulated protein	3.11
	428471	X57348	Hs.184510	stration	3.11 3.11
	436288	Al361722	Hs.192410	ESTs	3.10
	433376	Al249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.10
75	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	3.10
13	453468 412340	W00712	Hs.32990	DKFZP566F084 protein	3.10
	439716	AA101809 AA814903	Hs.182685 Hs.155113	ESTS ESTs	3.10
	419440	AB020689	Hs.90419	KIAA0882 protein	3.10
00	433017	Y15067	Hs.279914	zinc finger protein 232	3.10 3.10
80	428513	BE220806	Hs.184697	plexin C1	3.10
	437866	AA156781		metallolhioneln 1E (functional)	3.10
	451027 448030	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	3.10
	*********	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10

	**-*				
	435445	AA737345	Hs.294041	ESTs	3.10
	420997	AK001214	Hs.100914	hypolhetical protein FLI10352	3.09
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	
	405122	,	100170200		3.09
5		\$ 400C44E		Target Exon	3.09
	435272	AA906415	Hs.110041	ESTs	3.09
	410726	AI623859	Hs.15936	ESTs	3.09
	413063	AL035737	Hs.75184	chilinase 3-like 1 (cartilage glycoprote	3.08
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	
	417538	AW050865	Hs.275711	hypothesical ambala AACCOACC	3.08
10	434938			hypothetical protein MGC2452	3.08
10		AW500718	Hs.8115	Homo saplens, cione MGC:16169, mRNA, com	3.08
	434733	Al334367	Hs.159337	ESTs	3.08
	434421	A1915927	Hs.34771	ESTs	3.08
	407930	AAD45847	Hs.188361	Homo sapiens cONA FLJ12807 fis, clone NT	
	424939	AK000059	Hs.153881	Home serious NV DEN 50 N This	3.08
15	458332		113.10001	Homo sapiens NY-REN-52 antigen mRNA, par	3.0B
1.5		AI000341		ESTs	3.08
	445034	AW293376	Hs.143659	ESTs	3.08
	446570	AV659177	Hs.127160	ESTs	3.08
	429920	AW473208	Hs.115572	ESTs. Weakly similar to I38022 hypotheti	
	459513	AI032946		chine (C=00 of Connect field the control	3.08
20			11. 40000	gb:ox06g09.s1 Soares_felal_liver_spleen_	3.06
20	419038	AW134924	Hs.190325	ESTs	3.06
	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	3.06
	417386	AL037228	Hs.82043	D123 gene product	3.06
	453108	At311457	Hs.99472	ESTs	
	44932B	AI962493	***************************************	ESTs	3.06
25	428656	AB037798	U. 400700		3.06
			Hs.188790	KIAA1377 protein	3.06
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06
	447957	NM_014821	Hs.20126	KIAA0317 gene product	3.06
	417226	AW505054	Hs.4283	ESTs	
	452248	AA093668	Hs.28578		3.05
30				muscleblind (Drosophila)-like	3.05
50	426279	A1648520	Hs.169084	tebby like protein 3	3.05
	433814	AA609738	Hs.16525	ESTs	3.05
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.05
	431341	AA307211	Hs.251531	protessome (prosome, macropain) subunit,	
	441789	D52059	Hs.7972	KIAA0871 protein	3.04
35	456437				3.04
55		AI924228	Hs.115185	ESTs, Moderately similar to PC4259 femi	3.04
	438771	NM_016289	Hs.6406	MO25 prolein	3.04
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.04
	416240	NM_001981	Hs.79095	epidermal growth factor receptor pathway	
	409038	T97490	Hs.50002	email indusible exterior externity to the	3.04
40	424776			small inducible cytokine subfamily A (Cy	3.04
-10		Al867931	Hs.164595	ESTs	3.03
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.03
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famili	3.03
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	3.03
	431625	AW750627	Hs.6634	Horno sapiens cDNA: FLI22547 fls, clone H	
45	451144	AW956103		TOTAL SOPIETS CLIVE, FLIZZOGY 115, CKING H	3.03
			Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	3.02
	432274	AK000382	Hs.274251	hypothetical protein FLI20375; KIAA1797	3.02
	408683	R58665	Hs.46847	TRAF and TNF receptor-associated protein	3.02
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (3.02
	440603	AL121733	Hs.7299	Morel human gone manine is the second	
50	415443	T07353	H₂.7948	Novel human gene mapping to chomosome 1	3.02
				ESTs	3.02
	439981	A1348408	Hs.124675	ESTs. Weakly similar to T14742 hypotheti	3.02
	406685	M18728		gb:Human nonspecific crossreacting antig	3.02
	446013	Al360167	Hs.152774	EST8	3.02
	433902	AW292820	Hs.144905	ESTs	
55	41261D	X90908			3.02
-			Hs.74126	fatty acid binding protein 6, fleat (gas	3.02
	432505	AW274526	Hs.277721	KIAA0049	3.01
	440040	BE219431	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.01
	433255	A1274270	Hs.96840	KIAA1527 projein	
	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.01
60	417258	N58885	. no i ad 17	approximate tropic i	3.01
		Af248285	11- 440010	gb:yy60e09.s1 Soares_multiple_sclerosis_	3.00
	435800		Hs.118348	ESTs	3.00
	44483B	AV6516B0	Hs.208558	ESTs	3.00
	456760	AW961251	Hs. 127828	guanine nucleotide binding protein (G pr	3.00
	408360	A1806090	Hs.44344	hypothetical protein FLJ20534	
65	427982	NM_016156	Hs.181326	KIAA1073 protein	3.00
	436396			Mary 1073 protein	3.00
		AI683487	Hs.152213	wingless-type MWTV integration site fami	3.00
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00
	412095	A1624707	Hs.5921	Homo saplens cDNA; FLJ21592 fis, clone C	3.00
~~	425955	T96509	Hs.248549	ESTs, Moderately similar to S65857 elpha	
70	450247	AF123303	Hs.24713	himsipolary antica in among white	2.9B
	417865			hypothetical protein	2.9B
		AW086059	Hs.6529	ESTs, Weakly similar to 178885 serine/th	2.98
	415457	AW08171D	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.98
	438543	AA810141	Hs.192182	ESTs	298
~-	415503	U36601	Hs.78473	N-deacelylase/N-sulfotransferase (hepara	
75	42913B	AB020657	Hs.197298	MO1 hindles and le	2.98
. –			175. 131230	NS1-binding protein	298
	447881	BE620886		GCN1 (general control of emino-acid synt	296
	425481	AW978162		ESTs	2.96
	453315	BE544203	Hs.24831	ESTs	2.96
00	440638	Al376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	
80	433208	AW002834	Hs.24095	EGL*	2.95
			· 13.24U33	ESTs	2.95
	442495	Al184717		EST ₃	2.94
	418858	AW961605	Hs.21145	hypothetical protein RG083M05,2	2.94
	408170	AW204516	Hs.31835	ESTS	2.94
					207

	430382	AA477908	Hs.282267	ESTs, Moderately similar to 138022 hypot	2.94
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALUB_HUMAN A	2.94
	407361 407910	AA744622 AA650274	Hs.292645	ESTs, Weakly similar to ALUS_HUMAN ALU S	2.94
5	438005	BE551650	Hs.41296 Hs.15B126	fibronectin leucine rich transmembrane p Homo sapiens cDNA FL/13350 fls, clone OV	2.93 2.93
	44945B	AI805078	Hs.208261	ESTs	293
	449317	AW293413	Hs.132906	19A24 protein	2.92
	411118 449494	N27944 AW237014	Hs.221476 Hs.315369	ESTs, Weakly similar to AF108480 1 ubinu Homo sepiens cDNA: FLJ23075 fis, clone L	2.92
10	416311	D80529	1 10.0 10005	gb:HUM081H05B Human fetal brain (TFujiwa	2.91 2.91
	43306B	NM_006456	Hs.28B215	stelyltransferase	2.90
	429272	W25140	Hs.110667	ESTs	290
	432519 445467	AI221311 AI239832	Hs.130704 Hs.15617	ESTs, Weakly similar to BCHUIA S-100 pro ESTs, Weakly similar to ALLI4_HUMAN ALU S	2.90 2.88
15	426782	R14614	Hs.33846	ESTs	2.88
	426216	N77630	Hs. 13895	Homo saplens cDNA FLJ11654 lis, clone HE	2.88
	413882 421554	AA132973 AW137676	Hs.184492	ESTs ESTs	2.88
	446488	AB037782	Hs.97775 Hs.15119	KIAA1361 protein	2.88 2.84
20	421391	AW304350	Hs.191958	inmunoglobulin superfamily receptor tran	2.84
	424527	AW138558	Hs.334873	ESTs, Weekly similar to 154374 gene NF2	2.82
	419284 415788	AW820869	Hs.21565B	ESTs, Moderately similar to ZN91_HUMAN Z	2.82
	448481	AW628686 W15284	Hs.78851 Hs.74832	KJAA0217 protein ESTs	2.82 2.82
25	410491	AA465131	Hs.64001	Horno saplens clone 25218 mRNA sequence	2.80
	443441	AW291196	Hs.92195	ESTs	2.80
	422725 431926	AA315703 AW972724	Hs.199993	ESTs, Weakly similar to ALUS_HUMAN IIII gb:EST384816 MAGE resequences, MAGL Homo	2.80
	420406	AA741024	Hs.88378	ESTs	2.60 2.79
30	437678	AA829860	Hs.122834	ESTs	2.78
	440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.78
	439883 446428	AL359652 AW062270	Hs.171096 Hs.12496	Homo sepiens EST from clone DKFZp434AD41 ESTs, Weekly similar to ALU4_RUMAN ALU S	2.78 2.77
	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.76
35	435154	AA668764		ESTs	2.76
	432451 442703	AW972771	Hs.292471	ESTs, Weekly similar to ALU1_HUMAN ALU S ESTs	2.75
	419341	AL044949 N71463	Hs.116299 Hs.118688	ESTS, Weakly similar to ALU1_HUMAN ALLUS	2.74 2.74
40	435881	AF254956	Hs.16608	candidate (umor suppressor protein	2.72
40	42D137	AA308478	Hs.95327	CD3D antigen, delta polypeplide (TTT3 co	2.70
	438441 428158	AW664960 NM_001982	Hs.205319 Hs.199067	ESTs v-erb-b2 avian erythroblastic laukemia v	2.70
	432862	NM_013257	Hs.279696	serum/glucocorticold regulated kinasa-li	2.67 2.66
45	416239	AL038450	Hs.48948	ESTs	2.62
45	434792	AA649253	Hs.132458	ESTS	2.60
•	424852 425638	Al222779 NM_012337	Hs.144848 Hs.158450	ESTs nasopharyngeal epithelium specific prote	2.58 2.57
	419551	AW582256	Hs.91011	anterfor gradient 2 (Xenepus (aevis) horn	2.56
50	450571	AF158240	Hs.60397	ESTs	2.56
50	442435 424148	A1988208	Hs.244760	ESTs, Highly similar to 934087 hypotheti	2,56
	445784	BE242274 Al253165	Hs.1741 Hs.146065	integrin, befa 7 ESTs	2.66 2.53
	408072	BE005566	Hs.16773	Homo sapiens clone TCCCIA00427 mRNA sequ	2,52
55	434779	AF153815	Hs.50151	potassium inwardly-recitiying channel, s	2,52
<i>J J</i>	450295 440381	A1766732 AA917808	Hs.210628 Hs.190495	ESTs ESTs	2.48
	433923	A2823453	Hs.148625	ESTS	2.46 2.44
	420302	U22376	Hs.1334	v-myb avian myeloblastosis viral encogen	2.44
60	429670 437908	L01087 A1082424	Hs.211593	protein kinase C, theta	2.44
00	438676	AA813745	Hs.123446	ESTs ESTs	2.43 2.37
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28
	444969	A1203334	Hs.160628	ESTs	2.28
65	446423 435517	AW139855 AA928626	Hs.150120 Hs.130177	ESTs ESTs	2.27 2.27
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26
	439180	AI393742	Hs.199067	v-erb-b2 avisn erythroblastic leukemia v	2.00
	429073 433834	AA446167 AA620742	Hs.47385 Hs.130786	ESTs ESTs	1.98
70	417365	D506B3	Hs.82028	transforming growth factor, beta recepto	1.72 1.52
-	414521	D28124	Hs.76307	neuroblestoma, suppression of turnorigent	1.30
	402550			Target Exon	1.09
	TABLE 33	IB:			
75					
	Pkey:	Unique Eos	probeset iden	tifler number	
	CAT numi Accession	ber: Gene cluste	r number cession numb	Orn	
	· evroggith	CANDON C	Andreas (1)	913	
80	Pikey	CAT Number			
	431089 456034	125941_2 685586_1	BG9401	89 AW063489 AA715980 BF001091 BF880066 AA66610	02 AA621946 AA491826
	407192	2200202_1	AA6029	53 AA136656 AW450979 AA984358 AA809054 AW2380 64 AA609200	20 W4485013 RF108842

	438089	22448_4	BM475665 0E644917 AW770789 AW952971 N64863 BM263259 Al224545 Al184866 N69114 AW518902 Al440169 AA809472 AV654440 AA281642 AU185230 AW337382 Al872923 Al537113 N73882 T83378 H63731 BF671764 AW897824 Al811204 AA344646 BE009112 BG899664 H91240 R60548 N41701
5	439195 432222 406687	21979_1 539529_1 0_0	AF086037 H89360 H89546 BG207209 BE166299 At204995 BG199355 AW969908 AA528755 AW440776 BI044354 M31126
10	444314 452239	10279B4_1 10116_4	AW749625 AW749626 AW749644 Al140497 BG034B53 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 Al751258 Al090486 BE939504 AW631492 Al768270 Al862133 AA417652 BE378218 AA699207 AW794702 AA024968 AA446024 Al148235 Al191710 Bl493797 Al272646 Bl493796 AA634323 Al754332
10	433586 418259	32908_1 133853_1	AA258414 C05155 AI218226 AI039656 AI350380 AI084688 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743 BC011194 AW517087 AA601054 T85512 BM310925 AA426110 BM310629 BF434288 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI468252 AI624726 AA843768 AA782158 AI336058 AI097532 AW451563
15			AA459408 AA459633 AA418444 W23607 BG940150 Al93345 AW054729 Al221929 Al868744 AA215405 AA766713 AA621546 BF928317 BE454132 Al990909 AW271459 Al262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689588 R69057 BF766886 BE769254 W95240
20	432810	101919_1	BG292389 C05094 Al666930 AW104534 AA310513 AA830127 AW134897 AA046963 AW966490 Al810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 Al276287 Al684428 Al524234 Al335035 AW014704 Al911443 AA972102 Al367512 Al126670 AW016017 Al286003 Al147163 AA626033 Al539156 AA565542 Al094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400
20	412652	18858_2	H17550 Al991439 R46187 BE929954 AA333976 D63102 BF744491 Al801777 BE677762 AW008210 AW009441 BE350994 BE207949 Al091475 Al802774 Al827533 Al075363 Al659979 AA687856 Al078125 Al090285 AA670056 AA602411 AA683472 Al436058 AA612825 Al038932 BE057726 A167355 BF449023 Al289476 AW074381 BF972912 Al991780 AA689119 AL537472 239730 Al669853 Al192337 BE812978 BE812939 AA115248 H99006 Al915784 F08973 116748 D20458 AA609899 BF081234 AA14528 BE813978 BE813978 DE813092 BE813098 BE813099 AA115238 F08973 116748 D20458 AA609899 BF081234
25	431843	445334_1	AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 AW970134 AA516420 AA543007 BG057526 Bl001430 Al498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D80184 D60856
	442048 429228	750422_1 215430_1	AW340495 AI984319 AA974603 BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE468B12 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
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	407347	810943_1	T23514 Al655785
	451184	1531_4	Z99386 AV716301 BE222333 AI949687 BF732426 AV494086 AV721430 AW577332 N68315 BE672030 A(084440 A)260908 N69901 AA757364 BF515264 A1186231 BE466038 AW631313 AA993514 N54411 BG057615 AW013895 N77963 AA708723 A)273295 N59093 AA522665 A)871574
35			AA505521 AA812256 AA533841 AW467057 W68650 AI168772 AA988308 AA910057 AI868258 AA918322 AI335847 AA621494 AA904390 AI760007 AL1146694 AV758440 BM142562 N66507 AI674563 AW628584 AI253902 BF223368 AI090490 AI452918 N71423 AA062767 T94332 AA016003 BG681608 AA082426 AA028451 N71873 BF437845 T54154 AV741757
	444610 407604	2145292_1 43771_1	A174783 R12271 R83569 AK074129 A1.138071 A1803793 A1453544 AXX84616 BF062435 BE672932 A1828296 BF062464 A1803443 A1264326 A1280956 A1743547 AW285227
40	401004	1017 L	AW139967 AI972561 AI863570 AW062752 AW062756 AW062756 AW176904 AW062765 AW062765 AW062749 AW176886 A1751694 BG251391 AAU43621 W30872 BI524827 N94581 AU84614 AA776978 AI377572 A1751695 AI016756 AW4839994 AW194255 AW627763 AA6685249 AI079870 AW022524 AI968640 AI24380 AA702490 AAG4385 AA631513 AW176883 AW751767 AW1476887 AW062748 AW062745 AW176862 AW176815 AW176814 AW176846 AW176841 AW176871 AW176874 AW176819 AI927437 AW191962 R36548 AA853713 AW198059 AA618567 AW176819 AW176814 AW176846 AW176841 AW176871 AW176874 AW176819 AI927437 AW191962 R36548 AA853713 AW198059 AA618567 AW176818
45			AW082764 AW062751 AW062746 AW176888 AW751772 AW176859 AW751765 AW751762 AW176833 AW176873 AW751745 AAB94513 AA780815 AW176857 AW176834 AW176839 AW751771 AW176878 AW176843 AW176842 AW751755 AW176847 AW176842 AW176845 AW176849 AW176844 AW176877 AW751757 AW176850 AW176851 AW751758 AW751746 AW176858 AW176853 AW751766 AW176845 AW176872 AW176840 AW176876 AW176852 AW751754 AW176836 AW176856 AW751773 AW751760 AW751751 AL138070 AA639738 AL802588 AAB53712 AA317570 R38469 AW291669
50	436772 437158	1239464_f 59575_1	AA156151 Z25109 C05177 AW975888 AA731063 N67084
30	437 (35	25310_1	ALOSDOBS AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630760 AI597717 AIB07128 AA623012 AI366250 AW451857 AA974203 AI762577 BF512562 AW007307 BE675286 AW450602 AA96207 AW516069 AI582546 BF221924 BF222543 AI801808 AW488599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H39588 AW090188 AW043993 R39847
55	410297	2990_1	BC013939 BI494690 BI491211 AI928393 AA843540 BC938644 AL185628 BI495842 AW173255 BM052709 A1743999 A6690144 A1922209 A1740907 AW340368 AA928769 AW118737 BF513970 AA707807 BF435285 AL339463 AL\$73842 AL43809 BE222382 AA602308 AA428281 AL60355 AW662760 AW888037 AL34208 AA722416 W78151 N64362 BE221848 AW025901 AA452120 A1150479 A1016166 AA778515 AA61781 BM745307 BIB11169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BMA61961 BG681160 BI602483 BE885892 AW954311 BM052988 BI962893 AL989929 Z42328 BF022804 T35668 BG602802 AU185770 A1023271 AA147719 AL43079 AL56000 A1276488 AA992453 AA342821 AA648303
60			Alsassa Alostoob Aaszesat aaseoba awottast nizizas aarbatsb aacesat nizizeb awatose aaceteto aasteet aaceste a R70463 alsasse Abeztisb basaktz awoztosa basakt aagestoo aaacesi basakt awozese aaceast eeztitbo aasteet aabez D59858 nisiste aabez abeztitbo bisata arzaata ncesst eeges aasteet aaceste abezet abezet abezet abezet alsasta Nisista aasteet abezet abezet abezet aasteet aasteet aasteet aasteet abezet abezet abezet abezet alsasta alsasta aasteet aasteet aasteet abezet a
65	436769 412636	1239572_1 1438_1	AW975904 AA748675 AA731008 M77830 NM_004415 A1731005 BG681115 BG740377 BI712964 BG000856 AA128470 BI438324 H27408 BEB31630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739776 B)765807 BM353403 BM353248 AW177784 AW205789 AW961576 AW848592 BE182164 BF149266 BE940187 B1080445 B1080444 BF350983 BE720095 BE720069 BE715164 BE082844 BE082578 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM402504 BE931734 BF149264 AA340777 BF381183 BG621737
70			AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA352212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG890873 BI040954 BF919911 AU140155 AB51786 AI434518 AW804674 BF762969 BE837009 BE925826 BF149285 AW995615 BE814264 BI039784 AU140407 BE14243 BE703963 0F985842 BE001923 BF933510 AW365328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082525 BF476666 BF086994 BF692276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804163 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421
75			BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 CO4715 BF095124 BE865341 AW799304 AL603116 BE1469760 BE705967 BE705966 BE705966 AW848723 AW376699 AW376897 AW376897 BG005097 BF751115 BE698084 AW848731 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE666474 BE186187 BE166821 BE716089 BE713297 BE713298 BE175915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE00551 BG959922 BF094833 BF094748 BF094583
80			AW377699 AW807238 BE002519 AW377700 BF34947 A190590 At54403 A192926 AU168477 B1467252 AU159819 A750816 BF002516 AM38101 AA451923 A1340326 A1590975 B1791553 A1700983 A1142882 AA039975 AA946936 AA644381 BM314884 AA702424 A4417612 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA126864 AIB30049 AW780435 AU078449 A)819984 A)858282 B1468588 A)860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207 A)205283 BF082491 AW021347 A1558096 BE939862 AA088666 D12062 AA066527 AA782109 W19287 W02156 AW150038 AA022701 T87181

			H44405 Al910434 BF082513 Al494069 Al270027 Al635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745630 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 Al571075 BE067786 AV721320 AV022862 N29754 CX3378 N84767 AA131077 H30146 BE714290 Al686869 Al568892 Al915596 AW105614 Al887258 Al538577 BE926474
5			BE067737 BG319486 AA247685 AW7198883 AW103521 BF389173 AW860878 BE939707 BE186750 BE714084 BE713903 BE713868 BE713763 BG950164 BE713810 AW3651518 BG955489 BE005272 BF915937 AW365148 AI905927 BF9192780 AW863812 BG954443 BI770623 TGG979406 BG740832 BG671087 BG6698430 AA455100 T67267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG877012 BG741970 AA025480 BE70599 BG677157 BE005090 BG681378 BE712291 BG961498 BG678984 BI040041 AA357270 AW384371 AW847442 BI058559 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW995245 BE711801 AW284090
10	418876	121279_1	BE064323 BE719390 BE940148 BG991212 BF375714 BF349622 BG996267 T48793 BI013292 BE001925 AW366156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 AA740616 AA654854 AA229923
15	434987 430709 418546	121985_1 1234627_1 242836_1	AW975114 AI096634 AI767001 AA658384 AW517542 AW969880 AA484613 AA501874 R34356 T59708 AA224827 T59843 BE166903
	414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI038982 AA700926 AU154749 AI459432 AI423513 AL094597 AA740817 AI991988 AI090262 AI312104 BI255707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA3939239 AI146955 BF514270 N92892 AI346943 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA23549 BF108854 AA964344 N49882 AI457100 AW659407 AW300758 BE220715 BE220898 BE569091 BM009647 BF903351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
20	436198 413645 424831 433430	28727_1 1234345_1 1272834_1 2181751_1	AK001125 AU120581 AU145612 AW301393 AA130992 AW869837 AA503935 H61453 AA838765 Al693104 AA721107 AA961588 AIB83735 AA588325
0.5	443547	137089_2	AV645808 AA701657 AW271273 AY795734 AI472316 AI017631 AI081178 BF109096 AA548964 N83806 AA131648 AA156589 BE708349
25	459645	722255_1	AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63B41 R78995 N87474 AW292984 AA724304 AA074346 AA074368
	422980	11862_2	BF090249 AW954947 AW690487 A\305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 A\350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF476488 D60383 D81751 BE699260
30	432340 412240	1619980 <i>_1</i> 8235 _ 1	AA534222 AA632632 781234 BF963346 BI460763 BI599382 AI188089 AY055003 AW959185 AA187681 AI692282 AU153608 BI493898 BI493899 AI797349 BE550679 AI701137
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45	456505 442113	15472_2 43919_1	AW005891 AID55933 AA971813 AA334937 N58441 AA536020 AW874174 AL565960 AW607532 H44647 BCD17965 AW989075 AA279882 AA504611 A1219979 AA504595 A1245579 AA278181 BG485019 BI049312 AK074156 A1401548 BE002083 BE002086 BE002084 BG113650 AW5810909 AA632959 BG610861 BG436183 BF436017 AI568608 A1085503 A1204208 AW244158 BE622614 N52349 BE0422940 A1085658 AA978119 AA833838 A1620854 AA456105 AA971569 A1246289 A1336635 AA994082 A1260060 A1095710 AA605125 AA291672 BEA63947 N52870 AA287563 A1149093 AA581802 W31684 AA610159 BF247061 BG258954 BE176866
50	440028	598730_1	BE177041 AA332106 BE967020 AW473675 Al190744 W69997 AW104913 Al221098 W69996 AA885487 AA861491
	414783 431698	262554_1 6468_7	BE972567 AW069569 AJ392889 H85161 AJ074962 AA423935 BE671254 AA912627 H39845 H69083 AA280259 N67746 AA155722 BM423504 BE075913 AJ492369 AJ831729 AA807134 A0057292 BF059761 AA918209 BE858647 AW036707 AJ676269 AJ462916 BF593014
		_	Al480099 Al522283 Al628681 Al470402 BF058360 AW236830 AA514206 BF055812 Al796201 BF055617 BF054827 Al288301 AA705763
55 60	441623	3362_1	BC022413 BE355396 BF754175 AA506621 BE706665 BE706678 AA723159 BE155169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE163241 BC017410 AJ37912 AU99244 AW090300 BE219837 A4623661 BE501576 BE501734 AV742222 A/023964 AJ456424 AA975373 A/288904 A)984583 AA890325 N32562 AJ358102 AW241694 A/03674071 A/016389 AA576391 AA977874 AW189392 W37448 AA612894 AJ277648 H89561 AJ897674 H89362 AA316805 AW579188 BC014584 BC014584 BW780125 AJ672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA628775 W37573 BE041644 AW366504 BM129622 BM129624 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AJ373653 R75904 BF979185 BF691393 BG495595
00	433282	759_1	BI094458 BET06702 BG49659 BF246973 BG494800 BI094458 BET06702 BG49659 BF246973 BG494800 BC015150 BM471660 BM478941 BI759769 BI094332 BE005819 BE005834 BM023432 BE179013 BE675522 Al680275 AA515794 AA256503 F01634 AF002990 BG288697 Al091616 AW002917 Al691085 AW182664 BE501232 AI922168 BF838783 Al631078 BE464544 AI376986 AW503774 AA424131 AW511849 AA872169 BF084885 Al432024 Al491908 BF197906 AA580599 Al274418 AW269225 AW058288 Al611346 AA236200
65			COO417 BE689899 Al468149 BMA60137 Al685282 Al902714 BG990066 BF894391 T83393 T84298 BF609721 BE925494 AV755948 BF928512 BF894494 BF908642 AA256740 BF694347 BE928708 H06072 AA199607 BI85300 Al983233 AL521122 BE168896 BE302848 X76770 BC000927 NM_032632 BG707103 BG913867 BG613824 BG613257 BM313077 BI561132 BL461428 BE389811 BE391509 BE164848 AA746371 AV750611 BE176813 AA332440 BG200997 BG485576 AL043706 AV715984 BF903156 AV8020459 AU132824 BF941136 BE643211 AA521432 AW887568 BF809523 AW614570 AU129338 AW880782 AA371070 BG515427 BI657976 BI598706 BI599341 BE889166 BG502432 NM_020144 AF218840
7 0	424540	T4004 4	BI461106 BI562235 BI462594 BI458763 BF195561 BFR32738 BE890148 AI678629 AL135238 AJ1129571 AW\$00045 AA382478 AW\$02738 BI561031 BE280163 BF037226 BM480024 AW804395 BE707050 R72668 BF038861 BF895070 BG036594 BE551809 BF326901 BG286626 AW962888 BE544939 AW363399
	434210	54921_1	AK057015 AI025834 BE857936 AA149091 AI742972 AW439172 AI253168 AA255813 BF513175 AI005006 T03406 AW338149 AA836442 AA420530 R88566 AI61 I672 AA4393916 AA442855 BF063008 AA812568 AI889706 AA215513 AA768539 AA767520 AA686371 AA404380 A&665412 BE9658A2 AA706388 AI6560376 AA87489 AI44750 LYZDSTA MAGAREN LYZDSTA MAGAREN AA768539 AA767520 AA686371 AA404380 DEGGS AA768539 AA767520 AA6706378 AI6576378 AA87489 AI44750 LYZDSTA MAGAREN LYZDSTA MAGAREN AA768539 AA767520 AA686371 AA404380 DEGGS AA767520 AA767520 AA767520 AA67489 AA767549 AI64750 LYZDSTA MAGAREN LYZDSTA MAGAREN AA768539 AA767520 AA686371 AA404380 DEGGS AA767520 AA767520 AA767520 AA87489 AA87527 AMAGAREN LYZDSTA MAGAREN AA768539 AA767520 AA686371 AA404380 DEGGS AA767520 AA767520 AA686371 AA404380 AA87520 AA687520 AA767520 AA687520 AA767520 AA687540 AA767520 AA687540 AA767520 AA687540 AA67520 AA687540 AA67520 AA687540 AA67520 AA687540 AA67520 AA687540 AA67520 AA687540 AA67520 AA67540 AA67520 AA687540 AA67540 AA67520 AA687540 AA67540
75	412262	4362_1	AA665612 BF056442 AA706386 Al650676 AA627448 Alf41769 H78227 AW901862 H78221 BE701982 BF689273 AA397464 N33072 R60218 AW968247 H14833 AA768305 AA043348 R56470 BF739832 R51827 A474963 BG494574 AA149090 BF238154 Al802210 BE000129 BF734513 R41964 H21055 R85253 R17705 R40844 BF799216 BG386356 BF093037 AA73133 AA377348 W24822 AK056051 AB971258 Al681134 AU146134 Al803300 AA917325 AA923663 BF895058 Al304442 A167464 Al284188 AA054272 AA829262 AJ551910
			T90930 Al886230 U70056 AU119916 BF446537 BE503207 BE502849 Al698102 AA258553 AV718529 AV719917 BF724133 BH38668 Al804000 BE349103 Al912294 BE645117 AA227954 AA446520 AAB79147 AA281770 AW136872 AA807907 Al435989 Al339628 Al383274 AA418512
80			BE771804 BF894509 AA455093 A1379061 Al150855 BF769906 R17298 AU138740 BF808607 BE674633 AV700132 AA227789 AA253099 AW975199 AA95418 T74315 F12666 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810 RA2784 R44804 R41278
	430950	594908_1	AI525877 AA489525 AW088177

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	419543 455657 414405	251903_1 1490185_1 112689_1	BE065209 AL047596 /	A244170 AA244355 BE065364 BE065110 BE065111 AA393792 A1670731 A1037957 AW874364 A1038137 N62286 A1241379 BE501096 AW090596 A1927369 A1669226 A1369437 A1371075 A1686711 A1183289 AA477717 A1076122 AA635190 AA700984 AA781508 D81020 BF575223 A1356183 D79312 A1375558 H81111
5	409010	10331_1	BG283489 AL575207 AA059411 Al580336 A	BE090666 BE090664 BE090662 126545 AL551714 BM014781 BG542863 BG771232 AA429722 A1377511 AI770155 AA716665 BG003427 AA810B11 AA442760 AA128610 AI756263 AH94075 AI572127 AA420992 BF436063 AI648675 AA878813 BI486614 BG700886 AA128609 AV702879 AA731146 AI373224 AA919169 AI758175 AA976350 BG701414 BF057794 AW135598 AA062683 BI549631 AI185077 AA933879 AW024454 AA045194 BG9226396 BE856883 BF435859 AA186423 AW237471 RB9289 D61992 BE856637 BF368270 AA194235 N51319 AA383499
10	411962	2307710_1	N63065 BG	548812 BF027898 BG779448 AA098526 T47733
	434982 432676	121871_1 3503_22		T90204 AA658177 VA618478 AA558869
15	437838 446019	2512601_1 658727_1	A1362520 F	N307229 AA769348 D25917 A1670784 A1742347 AW269789 A1270700 AW610641 AW793036 AW793036 AW610540 AW362220 AW362166 AW362214
	454042	30254_1	AJ420458	; AW362228 AL119827 AI018523 AA708688 BF849633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI664847 AW874199 AI206120
20			W27787 H A\431587 (R43035 T65767 AW103715 W28478 BF953052 H45926 BF807569 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137288 AI366488 N64350 AA779107 AW029596 R49056
	432954	2159612_1	A\0763457	R55722 AW771106 F04969 Z38381 F01659 H17396 B1493714 A1880103 AW771447 A1202561 AA768851 A1494436 BF856114 H22570 A1887648 AA572691
25	446126	610_2	AA336407 AI458885 A AIG00008 A	BF946218 BF851494 AL536879 AA457150 AL590194 AL582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322 AA337222 AA319240 BI026817 BI027058 AL536860 AL63827 AA651730 AT701013 BM066789 AW339506 AA293021 BF991108 AA937223 AW974652 AI761251 AL655763 AA628063 BE047125 AW085916 AL129587 N52070 AW172361 AA052951 AW085909 AA982570 AJ371342 AJ364207 AA664514 AJ962506 AJ824603 AW376300 AA058439 AW361192 AV656680 N50282 BF820514 BF891008 F891112 BE708029 AW043567 AA056762
30	419145 409245	248375_1 3199_2	BM456602 AF030234 AW467027 AW960844 BF093291	2 AV706711 9F379357 H90994 AA234436 AA558020 BF351723 AA328271 R94815 N99638 BG223375 AW973750 N59599 BC017465 BC008526 AW505550 9M460141 N47324 AA361037 AA321632 N45806 AV752798 AV657116 AA296832 AU137857 7 AT74080 Al654350 H58206 AA478518 AW439997 AW393565 AW393523 Al659753 Al608732 R66056 H01374 Bl257369 Bl259930 75 RM4666252 AW506813 BE768647 AV658853 BM065248 BF372070 BF372056 BF372061 AA347852 AA905863 BG505070 AV654024 AW021929 H22650 AA469715 BC496341 BE697763 Bl254209 BG499543 H42946 Bl059780 Bl086741 H87896 H87599 BF691752 BG940948 W37195 BF372041 BE683796 BF372042 BF367329 BF909744 AW968003 AV714014 Bl492868 Bl495144 AA921845
35			Al693426 AW66524 AA884954 AA948472	AIGSZ147 AI435449 NAT325 A1434429 AA573137 A1163423 A182962 AI332556 BF513937 A1189561 AI221962 A1378034 AW118987 7 AW340077 N41605 AA478619 AA463875 A1858260 AA483379 AI292305 BE045947 AA971089 A112820 BG940947 AI080245 1 A1125702 A1382934 AA931835 A1358631 AW4339905 A1027833 A139648 A1014533 AA347851 AA738261 NG7374 NG9081 A1768867 2 A1819214 AA293133 A1186725 AA888214 A1222635 B1495143 N29605 N48812 AA76904 A1492769 D56771 AA096911 BE222062 W3722265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 B1255749 B1492848
40	437856	34257_1	H16217 H U52054 A BM19413 AA837481	21980 H22651 H38179 H87364 H44052 H25165 H44128 L5B1000 AA156860 AW293839 B1335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 4 AN956609 W84374 BF916380 AA385173 W84386 AA383743 BF903598 AA043776 W84421 AA778445 AW444904 BF446960 1 AV755539 AW468444 AW468002 AA811830 AA581806 AJ86686 AJ572124 AA687333 D20160 AA812489 AU185004 1 AJ536733 BM144850 AJ471883 AA040926 BF507639 AA043777 AWB74142 BE832523 BE163972 B1022546 B102104
45	458332 459513 449328	1139685_1 417837_1 3030726_1	A1000341 AV70406	3 Al36033 BW184030 A44 1663 A464032 BF307 653 A46407 F A4614142 BE602223 BE10037 2 Bio2234 G1021204 Al766341 AW873274 2 BE162284 Al032946 BF380636 Al652383 Al851694 Al838744 Al982493
	405685 417258	O_0 400835_1	M1872B	1 BI914326 BI030196 N58885 N63406 AV683374 N59892 BG110601 AA333708 AA359583 AW963123 N95562 N95696 N95587
50	447881	44623_1	AK07429 AA72218 AW81419 AW31658	1 AW293424 BE676135 AI632125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575697 AI672039 F28618 BF924261 4 BF934174 BE004328 AV749301 BE680282 BI019788 BI019389 BF926776 AW813409 AV726604 AA077560 BE2772975 BF849119 15 BE679126 AI697926 BF694155 BE205787 BF069313 N35828 AJ946557 AJ433839 AI378679 BG056182 AI589094 N23123 AA588805 31 AI0802772 AJ421980 AJ493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 6 W01350 H05495 AJ243785 Z39622 AA887432 AJ350659 R46102
55	425481 440638 442495	334120_2 371165_1 928718_1	AL52049 BG00950 AI184717	6 alw978162 ai610475 ai688960 aw470054 aa609426 ai167391 aa815231 aa358241 10 ai376561 aa897445 t87714 7 aw518883 af121173
	416311 431926	1280744_1 1237041_1	AW97277	6 AA357794 D91719 D80529 C14833 24 AA877998 AA522631 AU185388 53 AA688764 AA804491 AW665688 AA765069
60	435154 437908	126605_1 13268_11		55 AADT1806 BES00996 AW204531 AID82424 AID33879 BF093176 AA771764 D38676
	TABLE 33	C:		
65	Pkey: Ref:	Sequence a	source. The 7 omosome 22	nding to an Eos probeset I digit numbers in this column are Genback Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of Dunham, et al. (1999) Nature 402-489-495.
	Strand; Nt_position			m which exons were predicted. tions of predicted exons.
70	Pkey 401403 406387	Ref 7710966 9256180	Strand Plus Plus	Nt_position 146180-146294 116229-116371,117512-117651
75	405268 406122	4156151 9144087	Minus Minus	24404-24521 30940-31386
75	402550	7652009	Minus	80413-80573

80 TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific interatibal pneumonitis

Pkey: ExAcon;

Unique Eos probeset Identifier number Examplar Accession number, Genbank accession number

UnigenelD: Unigene number Unigene Title: Unigene gene title

R1

90th percentile of IPF Ats divided by 90th percentile of HP Als, where the minimum value for the numerator and denominator was set to 50 R2: 90th percentile of IPF Als divided by 90th percentile of NSIP Als, where the minimum value for the numerator and denominator was set to 50 5 Pkey UnigenelD Unicene Title 405443 Target Exon 9.66 7.50 418007 M13509 Hs.83169 matrix metalloproteinase 1 (Interstitlat 7.23 3.66 10 446619 AU076643 Hs.313 secreted phosphoprotein 1 (osteopontin, collegen, type XVII, alpha 1 6.63 3.03 422511 AU076442 Hs.117938 4.84 2.81 M21305 406964 FGENES predicted novel secreted protein 4.73 5.69 425259 AL049280 Hs.155397 Homo seplens mRNA; cDNA DKFZp564K143 (fr 4.14 4.34 407244 M10014 fibrinogen, gamma polypeptide 4.14 5.88 15 421823 N40850 Hs.28625 ESTs 4.12 1.80 419R75 AA853410 Hs.93557 proenkephalin 3.90 201 409542 AA503020 Hs.36563 Hs.86693 hypothetical protein FLJ22418 388 2.90 418310 AA814100 3.66 2.84 442006 AW975183 ESTs, Weakly similar to \$72482 hypotheti 3.60 3.13 20 438315 FL56795 Hs.82419 3.49 425071 NM_013969 Hs.154424 dalodinasa, iodofnyronine, type 11 3.47 1.38 serine (or cysteine) proteinase inhibito hypothetical protein PRO2834 bullous pemphigoid antigen 1 (230/240kD) Predicted gene: Eos cloned; secreted w/V 409632 W74001 Hs.55279 3.46 3.46 AF119903 434233 Hs.138453 3.28 2.51 408000 L11690 Hs.198689 3.26 25 447033 AI357412 Hs.157601 3.19 212 AL044056 420185 Hs.251385 ESTs 3.1B 3.01 420195 N44348 Homo sapiens ceNA FLJ11177 fis, clone PL 3.16 3.16 428682 8E0099VA Hs.2056 UDP glycosyltransferase 1 family, polype 3.08 3.18 408221 AA912183 Hs.47447 3.07 1,98 30 417079 U66590 interleukin 1 receptor antagonist Hs.81134 3.02 2.36 419216 AU076718 Hs.164021 small inducible cytokine subfamily B (Cy 298 1.72 prominin (mouse)-like 1 Homo sapiens mRNA; cDNA DKFZp434F1135 (f KJAA0455 gene product 422163 AF027208 Hs.112360 2.87 1.48 4224D4 AL133571 Hs.336189 2.80 2.66 445745 AB007924 Hs.13245 2.78 1.65 35 407938 AA905097 Hs.85050 nhosoholamban 2.78 2.46 423575 C18863 Hs.163443 intron of periostin (OSF-2os) 1.55 2.78 446859 A1335361 Hs.226376 2.74 1.56 425383 D83407 Hs.156007 Down syndrome critical region gene 1-lik 2.74 1.85 2.72 437620 AW976930 FSTR 2.72 40 414591 A1888490 Hs.55902 ESTs, Weakly similar to ALUS HUMAN ALU S 2.05 leiomodin 1, smooth muscle (LMOD1) (Thy 416585 X54182 Hs.79386 2.66 1.47 425707 AF115402 Hs.11713 E74-like factor 5 (ets domain transcript 2.66 2.62 2.66 430712 AW044647 ESTa 2.62 453111 AB014598 Hs.31720 hephaestin 261 1.72 45 455099 R52795 Hs.25954 interleukin 13 receptor, alpha 2 2.59 1.27 414290 AJ568801 Hs.71721 2.59 1.23 2.58 417601 AA417383 Hs.62582 integrin, beta-like 1 (with EGF-like rep 2.58 412639 AW9812B4 Hs.203838 ESTa 2.29 2.58 423720 AL044191 Hs.23388 hypothetical protein DKFZp434F0318 2.57 1.74 50 AW452355 429757 Hs.256037 257 1.60 429504 X99133 Hs 204238 lipocalin 2 (oncogene 24p3) (NGAL) 2.57 1.00 412228 AW503785 Hs.73792 complement component (3d/Epstein Barr vi 2.56 1.12 compenent component (sourcessum tout vi nephroblastoma overexpressed gene ghtm30f03.x1 NCL_CGAP_Thy4 Homo sapiens C16001440*:gl[12330704[gb]AAG52890,1]AF3 C16001416*:gl[12743112[ref]XP_010131.2] similar to S88401 (cattle) glucose Induc 430223 NM_002514 Hs.235935 2.56 411880 AW872477 2.54 2.54 3.38 55 401645 2.53 401673 2,47 2.83 Z45051 H58721 449048 Hs.22920 2.46 1.18 416316 Ns.271628 2.42 2.40 3,44 453B74 AW591783 collegen, type XIV, alpha 1 (undulin) RNA binding motif protein 8B mucin 5, subtype B, tracheobronchial Hs.36131 7 69 60 451149 AL047586 2.40 1.95 421190 U95031 Hs.102482 2.40 410036 Hs.57975 Hs.205353 R57171 calsequestrin 2 (cardiac muscle) 2.40 2.40 1.27 429525 N92540 ectonucleoside triphosphate diphosphohyd C4001445:gi|12697999|dbj|BAB21818.1| (AB 2.39 405120 2.38 2.98 65 AW189460 432224 418663 Hs.208358 ESTs 2.38 2.00 AK001100 Hs.41690 desmocollin 3 2.38 2.37 2.38 412622 AW664708 Hs.171959 **ESTs** 1.53 1.52 1.22 424012 AW368377 Hs.137569 turnor protein 63 kDa with strong homolog 2.37 442767 Al017208 Hs.131149 **ESTs** 70 401785 NM_002275":Homo sepiens keralin 15 (KRT1 2.35 2.35 1.79 411800 N39342 Hs.103042 microtubule-associated protein 1B 1.18 2.34 pro-platelet basic protein (includes pla ESTs 427535 R29543 Hs.2164 234 444009 Al380792 Hs.135104 234 207 435143 R12375 Hs.19460D ES7s 2.33 1.68 75 402333 Target Exon 3.15 1.10 429609 AF002246 Hs.210863 cell adhesion molecule with homology to 233 454078 AA601518 secreted modular calclum-binding protein Hs.22209 2.32 1.90 R50956 452242 Hs.159993 gycosyltranslerase 2.32 1.45 41B693 AI750878 He R7409 thrombospondin 1 2.32 232 80 428411 AW291464 Hs.10338 ESTR 2.32 1.54 1.98 459702 Al204995 gò:an03c03.x1 Stratagene schizo brain S1 428839 A1767758 Hs.82302 Homo sapiens cDNA FLJ14814 lis, clone NT 2.31 2.49 427138 N77624 Hs. 173717 phosphatidic acid chosphatase type 28 2.31 1.32

	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.30	2.30
	456536	AW135986	Hs.257859	ESTs	2.28	2.28
	428166	AA423849	Hs.79530	M5-14 protein	2,27	1.88
~	456936	M81349	Hs.1955	serum amylold A4, constitutive	2.25	2.16
5	417728	AW138437	Hs.24790	KIAA1573 protein	2.25	1.37
	453070	AK001465	Hs.31575	SEC63, andoplasmic reticulum translocon	2.24	2,42
	409159	AW673312	Hs.50848	hypothetical protein FLJ20331	2.24	2.24
	404942			splicing factor, arginine/serine-rich 9	2.24	264
4.0	410286	Al739159	Hs.61898	DKFZP586N2124 protein	2.24	2.46
10	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.24	1.94
	421574	AJ000152	Hs.105924	defensin, bela 2	2.23	1.35
	418005	A\$186220	Hs.83164	collagen, type XV, alpha 1	2.22	1.37
	421948	1.42583	Hs.334309	keratin 6A	2.20	2.20
	407788	BE514982	Hs.38991	\$100 calcium-binding protein A2	2.19	1.61
15	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.18	2,40
	431089	BE041395		ESTs, Weakly similar to unknown protein	2.16	2.46
	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	2.16	2.00
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.16	1.26
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.16	1.99
20	403362			NM_001615*:Homo saplens actin, gamma 2,	2.16	1.61
	432374	W68815	Hs.301885	Homo saplens cDNA FLJ11346 fis, clone PL	2.15	211
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spieen	2.15	2.24
	402643			C1002296:gi 6677817 ref NP_033126.1 rep	2.14	2.74
	418235	AW994005	Hs.337534	ESTs	2.14	2.14
25	413059	BE151498		gb:RC0-HT0295-291199-031-E11 HT0295 Homo	2.14	2.14
	432437	W07088	Hs.293685	ESTs	2.14	2.14
	428398	A1249368	Hs.98558	ESIs	2.14	2.14
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.12	1.43
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	2.12	1.93
30	436391	AJ227892	Hs.146274	ESTs	2.12	2.12
	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.11	2.17
	407443	AF227138		gb:Homo saplens candidate taste receptor	2.11	2.36
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Cit	2.10	1.29
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.10	2.10
35	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	2.10	2.00
	440273	AI805392	Hs.325335	Homo saplens cDNA: FLJ23523 fis, clone 1.	2.10	1.37
	450271	A1693900	Hs.200920	ESTs	2.09	2.34
	432222	Al204995		gb:an03c03.x1 Stratagene schizo brain S1	2.09	1,40
	458208	A)380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	2.08	2.00
40	405600			C12001673:gi]9631264[ref]NP_048045.1] or	2.07	1.97
	434554	A1825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	2.07	2.52
	439261	At126020	Hs.145674	basic transcription factor 3	2.05	1.45
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	2.04	2.04
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RBF1 Homo sepiens	2.04	2.04
45	423151	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	2.02	1.33
	412505	AA974491	Hs.21734	ESTs .	2.02	2.02
	443180	R15875	Hs.259576	slaudin 12	2.02	2.02
	431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.02	2.02
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	2.02	2.17
50	452571	W31518	Hs.34665	ESTs	2.02	2.09
- •	405061			Target Exon	2,01	2.52
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	201	2.41
	402327	000 101	***********	Target Exon	2.00	2.44
	418786	A1796317	Hs.203594	Homo saplens uncharacterized gastric pro	2,00	2.00
55	447343	AA256641	Hs.236894	ESTs, Highly similar to \$02392 alpha-2-m	2,00	2.00
	438634	AW340400	Hs.126728	ESTs	1.99	2,43
	416127	N49B43	Hs.79022	GTP-binding protein overexpressed in ske	1.97	1.41
	423961	D13666	Hs.136348	periostin(OSF-2os)	1,96	1.48
	430397	Al924533	Hs.105507	bicarbonate transporter related protein	1.96	1.31
60	411010	AWB13339	1,01.00001	gb:MR3-ST0192-101299-013-c05 ST0192 Homo	1.96	273
	439628	W81007	Hs.58628	ESTS	1.96	1.28
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.96	1.58
	431726	NM_015361	Hs.268053	KIAA0028 protein	1.95	1.72
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.95	1.87
65	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	1.95	1.06
	417552	AVV888754	Hs.134126	crystalilin, gamma S	1.95	214
	424480	AA341442	Hs.205299	ESTs	1.94	1.94
	404342		INILLIGIO	C7002192*:gi[7299207 gb]AAF54404.1] (AE0	1.92	1.32
	443320	AI051607	Hs.16335	ESTs	1.91	2.1B
70	449780	AA443241	110.10000	ribosomei protein L44	1.90	1.76
	423337	NM_004655	Hs.127337	axin 2 (conductin, axii)	1.89	2.16
	434416	AA805903	Hs.59498	cell division cycle 2-like 5 (cholinests	1.89	2,04
	457505	AL044659	Hs.43791	ESTs	1.89	2.34
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pt	1.88	1.26
75	413585	AL137023 AL133452	Hs.75431	Sentestretime kinesa wili Do- atu pi	1,88	
, ,	428231	U17989	Hs.183105	numogen, gankta porypepude nuclear autoantinen	1.88	1.88
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	1.88	1,88 1.88
	404429	,-w:uzzz		Target Exon	1.88	2.18
	447644	AW861622	Hs,108646	Homo sapiens cDNA FLJ14934 fis, clone PL	1.88	3.04
80	406641	AJ235667	110,100040	gicthomo sapiens mRNA for immunoglobulin	1.86	
~	417059	AL037672	Hs.81071	gothomo saprens natova for immunogicousia extracellular matrix protein 1	1.86 1.88	2.57 1.48
	454565	BE141231	HUILING	gb:MR0-HT0075-081199-003-e09 HT0075 Horno	1.86	1.40
	415115	AA214228	Hs.127751	hypothetical protein	1.85	1.23
			1 80. 14,1731	The suppose by Apple	1.00	1.20

	432306 414085	Y18207 AA114016	Hs.303090 Hs.75746	prolein phosphatase 1, regulatory (inhib aldehyde dehydrogenase 1 family, member	1.85 1.84	1.45 1.44
	403344	AVX114010	f15./5/40	NM_000341:Homo sapiens solute carrier fa	1,84	1.84
	447245	AK001713	Hs. 17860	hypothetical protein FLJ10851	1.84	2.33
5	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.84	2.02
	401593			Yarget Exon	1.83	2.34
	434392	AW983709	Hs.250824	Homo saprens cDNA: FLJ23435 fis, clone H	1.83	2.12
	406461 455657	BE065209		hypothelical protein, clone 24751 gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.83 1.83	2.01 1.26
10	400609	112003203		C10001147:gi 12698926[gb]AAK01739.1]AF33	1.82	2.08
	422095	Al868872	Hs.282804	hypothetical protein FLJ22704	1.81	1.14
	422867	L32197	Hs.1584	cartilage offgomeric matrix protein (pse	1.81	1.22
	417412	X16895	Hs.82112	interleukin 1 receptor, typa i	1.81	2.10
15	426521 429610	AF161445	Hs.170219	hypothetical protein	1.81	2.08
13	423915	AB024937 AF03901B	Hs.211092 Hs.135281	LUNX protein; PLENC (palate lung and das alpha-actinin-2-associated LIM protein	1.81 1.80	1.64 1,34
	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.80	1.80
	459189	AI909090		gb:IL-B7198-010499-007 BT198 Homo saples	1.80	1.80
20	412429	AV650262	Hs.75765	GRD2 cncogene	1.80	2.55
20	402674			Target Exon	1.80	3.41
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.79	1.57
	454824 401677	AW833646		gb:CV4-TT0008-161199-033-d09 TT0008 Homo BAN-associated protein 3	1,78 1,78	1.94 2.28
	426291	U58913	Hs.169191	small Inducible cytokine subtamily A (Cy	1.78	1.53
25	430028	BE564110	Hs.227750	Target CAT	1,78	1.59
	445988	BE007663	Hs.13503	inactivation escape 2	1,78	2.10
	452272	AW292249	Hs.252739	hypothetical protein DKFZp434P0316	1.78	2.08
	418205 400425	L21715 AY004252	Hs.83760	troponin I, skeletal, fast BB domain exatelling 12	1.78	2.70
30	400419	AF084545	Hs.287365	PR domain containing 12 Target	1.77 5.77	2.02 2.67
-	447169	AI989803	Hs.157289	ESTs	1.77	2.21
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	1,77	2.12
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1.76	2.54
35	432808	NM_015985	Hs.278973	angiopoietin-3	1.76	1.76
33	437400 422487	AB011542 AJ010901	Hs.5599 Hs.198267	EGF-like-domain, multiple 5 muckt 4, tracheobronchial	1.75 1.75	2.00 1.47
	444986	Al204197	113.150205	ESTs	1.75	2.48
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	1.74	1.69
40	413524	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.74	1.74
40	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	1.74	2.26
	405579 405797			C22000151:gij6806921[refjNP_004165.1] so CX001015:gij11322384[amb]CAC16687.1] (AJ	1,74 1,73	2.12 2.66
	405159			ENSP0000243337*:CDNA FLI13984 fis, clor.	1,73	2.01
	450569	AW192334	Hs.3821B	ESTs	1.73	2.08
45	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.73	1.24
	445261	T79759	Hs.250651	ESTs, Weakly similar to 138022 hypotheti	1.73	2.52
	454231 429500	AW450669	Hs.45058 Hs.289114	hypothetical protein DKFZp434l143	1.73	1.64
	422259	X78565 AA307584	ns.209114	hexabrachion (tenascin C, cytolactin) gb:EST178498 Coton carcinoma (HCC) cell	1.72 1,72	1.37 1.72
50	456034	AW450979		gb:UI-H-BI3-ela-a-12-0-UI.s1 NCL_CGAP_Su	1.72	1.34
	451862	H09260	Hs.32333	ESTS	1.71	2.16
	403520			Target Exon	1.71	1.39
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	1.71	2.26
55	428603 418387	AA382291 R18085	Hs.22279	gb:EST95683 Teetis I Homo saptens cDNA 5 gb:yg16b12.rl Soares Infant brein 1NIB H	1.70 1.70	1.70 1.70
	433417	AA587773	Ha.8859	Homo sapiens, Similar to RIKEN CONA 5830	1.70	1.87
	402538			C1001634:gi[12521136]ref[NP_075245.1] Ba	1.69	1.57
	414844	AA296874	Hs.77494	deoxyguanosine kinasa	1.69	2,06
60	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.69	1.63
UU	446563 456235	AB021179 AA203637	Hs.15299	HMBA-inducible gb:zx58b12.r1 6oares_fetal_liver_spleen_	1.69 1.68	2.02 2.12
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	1.68	2.03
	433930	AA620338		ESTs	1.68	2.28
10	404151			Target Exon	1.68	1.B0
65	429392	AL109712	Hs.295506	Homo sepiens mRNA full length insert cDN	1.67	2.18
	430070 400496	AF197927	Hs.231967	ALL1 fused gene from 5q31 ENSP00000224716*:GTP-binding protein SAR	1.66	216
	413464	AL121500		ESTs	1.66 1.66	2.13 2.03
	411188	BE161168		gb:PM0-HT9425-170100-002-a10 HT0425 Homo	1.66	2.12
70	446281	H69416	Hs.14606	hypothetical protein FLJ20271	1.65	2.28
	443282	T47764	Hs.132917	ESTs	1,65	2.04
	423217	NM_000094		collagen, type VII, alpha 1 (epidermolys	1.65	1.67
	453355 432375	AW295374 BE536069	Hs.31412 Hs.2962	myopodin S100 calcium-binding protein P	1.65 1.65	1.66 1.54
75	437929	T09353	Hs.106642	ESTs, Weakly similar to 109052 hypotheti	1.65	2.04
	410295	AA741357		Algodeu (eusciju)	1.64	2.30
	437767	AA830103	Hs.293331	ESTs	1.64	1.26
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	1.64	3,38
80	450795 421847	AW173371 NM 018717	Hs.60435	ESTs	1.64	1.64
50	403010	NM_014717	Hs.10B884	KIAA0390 gene product C21000152:gij6226483 spjQ52118 YMO3_ERWS	1.84 1.54	2.75 2.03
	406387			Target Exon	1.64	1.78
	440423	AW293995	Hs.192277	ESTs	1.63	2.05

					4.44	a 07
	444381	BE387335	Hs.283713	hypothetical protein BC014245	1.63 1.63	2.07 1.65
	442802	AL133035	Hs.8728	hypothetical protein OKFZp434G171 ESTs, Moderately similar to B34087 hypot	1.62	2.40
	442424 402885	Al342715	Hs.129569	Target Exon	1.62	1.18
5	402000 408786	AA773187	Hs.294027	ESTs	1.62	1.59
9	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.62	1.63
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart,	1.62	2.10
	406838	AAB27569	Hs.153	ribosomal protein L7	1.61	1.41
	441600	AA939347	Hs.127223	Homo saplens cysteine knot protein (ZSIG	1.61	2.32
10	420693	NM_001972	Hs.99863	elastase 2, neutrophil	1.60	2.37
	412649	NM_002206	Hs.74369	Integrin, alpha 7	1.60	1.23
	432331	W37862	Hs.274368	MSTP032 protein	1.60	1.23
	454034	NM_000691	Hs.575	aidehyde dehydrogenese 3 family, member	1.60 1.60	1.69 1.56
15	400279	********	U- 40505	NM_004581*:Homo sapiens Rab geranyigeran	1.60	2.42
13	437865	A1472305	Hs.19565	ESTs prostete cancer associated protein 1	1.60	1.29
	429165	AW009886 BE018682	Hs.118258 Hs.166196	ATPase, Class I, type 8B, member 1	1.60	211
	442993 410684	AA088500	Hs.170298	ESTs	1.59	1.46
	433149	BE257672	Hs.42949	hypothetical protein HES6	1.59	2.22
20	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	1.59	1.41
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.59	1.26
	427654	AA410183	Hs.137475	ESTs	1.59	2.83
	411662	D80541	Hs.285519	Homo saplens cDNA FLJ11904 fis, clone HE	1.59	2.18
0.5	440383	AA884208	Hs.30484	ESTs	1.58	219
25	408690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.5B	1.58
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase 8	1.58	1.47 1.51
	407857	A)928445	Hs.92254	synaptotagmin-like 2	1.68 1,57	1,29
	411573	AB029000	Hs.70823	KIAA1077 protein	1.57	1.17
30	433336	AF017986	Hs.31386 Hs.184510	secrejed frizzled-related protein 2 stratifin	1,57	1.55
20	428471 429249	X57348 X81479	Hs.2375	egi-like module containing, mucin-like,	1.57	1.19
	407986	AA295052	Hs.38516	Homo saplens, clone MGC:15887, mRNA, com	1.57	2.12
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.57	1.05
	430469	AW603667	Hs.286742	Homo saptens cDNA: FLJ22712 fis, clone H	1.56	1.56
35	445511	AA845512		Homo saplens cDNA FLJ14459 fis, clone HE	1.55	2.08
	404501			nucleoside phosphorylase	1.55	2.54
	429107	AJ470451	Hs.99075	ESTs	1.55	2.05
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.55	1.45
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.54 1.54	2,61 1.54
40	458091	AF150286	11- 400004	gb:AF150286 Human mRNA from cd34 stem ca	1.54	2.06
	439280	Al125436	Hs.123654	ESTs Homo sapiens, cione IMAGE:3868989, mRNA,	1.53	1.55
	428096 414221	AW291771 AW450979	Hs,42239	gb:UI-H-BI3-gla-a-12-0-UI.s1 NCL_CGAP_Su	1.53	1.39
	451712	AA019290	Hs.110469	ESTs	1,53	1.99
45	402487	AND 13230	113.110403	Target Exon	1.53	2.02
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.53	1.29
	452887	Al702223	Hs.107253	hypothetical protein DKFZp761F241	1.53	1.21
	410253	T51823		ESTs	1.52	2.03
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	1.52	1.37
50	432985	792363	Hs.178703	ESTs	1.51	1.48
	422166	W72424	Hs.112405	\$100 calcium-binding protein A9 (calgran	1,51	1.15
	429259	AA420450	Hs.292911	Piekophiin	1.51 1.51	1.31 1,19
	429289	A1400746	Hs.62187	phosphatidylinositol glycan, class K	1,51	2.08
55	441457	AW996651 AF026944	Hs.43838 Hs.293797	EST8 ESTs	1.51	2.74
55	433365 425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homoto	1.51	1.21
	424386	BE146577	Hs.285132	ESTs	1.50	1.53
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	1.50	1,29
	442391	AW450544	Hs.220751	ESTs	1,50	1.65
60	414341	D80004	Hs.75909	KIAA0182 protein	1.50	2.10
	438222	At208737	Hs.122810	Homo saplens cDNA FLI11489 fis, clone HE	1.50	2.16
	442264	A127B777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	1.50
	443878	AW292499	Hs.139709	hypothetical protein FLJ12572	1.50	1.37
65	430152		Нв.234642	equaporin 3	1.50 1,49	1.43 0.91
65	447762		Hs.10593B	lactotransferrin opioid receptor, kappa 1	1.49	1.36
	404455		Hs.98132	ESTs	1.49	1,30
	424106 433095		Hs.302480		1.49	2.02
	409361			sine ocuis itomeobox (Drosophila) homolo	1.48	1.50
70	456256		Hs.82771	vaccinla related kinase 2	1.48	1.42
	439310		Hs.102793		1.48	1.48
	407102			glycerol-3-phosphate dehydrogenase 1 (so	1.48	1.15
	437981	AA774445	Hs.145365		1.48	2.36
مبر پینو	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.47	1.21
75	414799		Hs.77326	Insulin-like growth factor binding prote	1.47	1.25
	453864		Hs.21068	hypothetical protein	1,47	2,18
	401057			ENSP00000252105":CDNA FLJ1 2240 fis, clon	1.47	1.81
	456054			gb:601151545F1 NIH_MGC_19 Homo saplens c	1.47 1.47	1.99 2.03
80	402324		Hs.82503	C19001982:gij3043638jdbj]BAA25483.1\ [AB H.sapiens mRNA for 3'UTR of unknown prol	1.47	1.29
OU	417733 457734			hypothetical protein FLJ11526	1.47	2.26
	402013		i iadur 30	Target Exon	1.46	2.42
	429295		Hs.99216	ESTs, Moderately similar to ALUS_HUMAN A	1.46	2.09
	,		,,	400		

					4.40	2.46
	430920		Hs.248132	goosecoid-like	1,46 1,46	2.46 2.02
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium cadhedn 3, type 1, P-cadherin (placenta	1.46	1.43
	431958	X63629	Hs.2877		1.46	1.46
5	427719	AJ393122 AJ863735	Hs.134726	ESTs ESTs	1.46	1.15
J	433430 423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	1.46	2.36
	444083	Al123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.45	2.29
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	1.45	1.50
4.2	420859	AW468397	Hs.100000	\$100 calcium-binding protein A8 (calgran	1.45	1.17
10	456664	AW963354	Hs.334409	matallothionein 1G	1.45	2.20
	438158	A1796556	Hs.187884	ESTs	1.45	1.18
	409883	AW452419	Hs.296098	ESTs	1.45	2.00
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.45 1.45	1.27 1.36
1.5	413048	M93221	Hs.75182	mannose receptor, C type 1	1.45	2.08
15	457462	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	1.44	1.28
	452679	Z42387	Hs,83883	transmembrane, prostate androgen induced	1.44	2.19
	401116	AA528295		Target Exon. gb:nh26e06.s1 NClCGAP_Pr3 Homo saplens	1.44	2.30
	419618 452281	T93500	Hs.28792	Homo saplens cDNA FLJ11041 fis, clone PL	1.44	2.03
20	426125	X87241	Hs.166994	FAT turnor suppressor (Drosophila) homolo	1.43	1.48
20	428330	1.22524	Hs.2256	matrix metalloprotelnase 7 (matrilysin,	1.43	1.51
	418742	AW451197	Hs.113418	ESTs	1.43	1.24
	418335	R63267	Hs,28399	ESTs	1.43	1.14
	408404	AW192518		gb:xl45h08.x1 NCI_CGAP_Pan1 Homo saptens	1.43	2.08
25	448175	BE296174	Hs.225160	hypothetical protein FLI13102	1.43	2.29
	431846	BE019924	Hs.271580	uroplakin 1B	1.43	2.12
	459557	N58315		gbtyv68g06.s1 Soares fetal liver spleen	1.43 1.43	2,00 1.33
	449925	A1342493	Hs.24192	Homo saplens cDNA FLJ20767 fls, clone CO	1.43	1.10
20	442321	AF207654	Hs.8230	a disinlegrin-like and metalloprotease (1.43	1.55
30	454843	AW834536	Hs.258549	gb:MR2-170014-241199-012-506 T70014 Homo Homo saplens clone 23928 mRNA sequence	1.43	1.38
	410281	AF076812	Hs.166186	NM_002463*:Homo sapiens myxovirus (influ	1.42	2.16
	402998 443709	AI082692	Hs.134662	ESTs	1.42	2.22
	435259	AA152106	Hs.4859	cyclin L anla-6a	1.42	2.01
35	454407	AW578420	Hs.118843	gb:RC1-CT0249-120100-022-b04 CT0249 Homo	1.42	1.76
22	453359	AA448787	Hs.24872	ESTs	1.42	1.33
	434126	Al13B589	Hs.118205	ESTs	1.41	2.06
	417944	AU077196	Hs.82985	collagen, type V, sipha 2	1.41	1.46
	442316	Z75331	Hs.8217	stromal antigen 2	1.41	2.20
40	438330	AW450572	Hs.257316	ESTs	1.41	2.20
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	1.41	2.02
	455885	BE153524		gb:PMO-HT0339-241199-002-C03 HT0339 Homo	1.41 1.41	1.33 1.24
	405550	4 4 0 4 7 9 7 7 7		C7001981*:gt565157[gb]AAB31881.1] T-cel	1.41	1.99
15	451385	AA017656	14 4 5 2 9 5 7	gb;ze39h01.r1 Soares retina N2b4HR Ногно	1,40	2.64
45	424925	NM_002432		myeloid cell nuclear differentiation ant ESTs	1.40	1.26
	431022	AA490B15	Hs.208351	glial cells missing (Drosophila) homolog	1.40	2.72
	439781 429379	AA845538 NM_014840	Hs.200598	KIAA0537 gene product	1,40	1.05
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprole	1.40	1.26
50	430702	U56979	Hs.278568	H factor 1 (complement)	1.39	1.1B
-	451331	AK002039		Homo saplens cDNA FLJ11177 fis, clone PL	1.39	1,26
	459198	A1086347	Hs.15113B	ESTs	1.39	1.22
	442344	AJ022925	Hs.79368	epithelist membrane protein 1	1.39	1.35
	402917			ENSP00000202587*:Bicarbonale transporter	1.39	1.44
55	418211	SE244746	Hs,247474	hypothelical protein FLJ21032	1.39	2.08
	437158	AW090198		KIAA1150 prolein	1.3B	2.07
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	1.38 1.38	1.24 2.15
	433911	Al923092	Hs.8899	ESTs	1.38 1.3B	1.38
60	402504	A142003040	Hs.78054	C1003823*:gi 4826521 emb CAB42853.1 (AL. gb:QV4-TT0008-251099-016-e11 TT0008 Homo	1.37	2.22
vv	409465	AW393810 T92251	Hs.198882	ESTs	1.37	2.38
	449426 405491	132201	118.150002	Target Exon	1.37	2.74
	406685	M18728		gb:Human nonspecific crossreading antig	1.37	1.34
	442418		Hs.197680	ESTs	1.37	1.56
65	407701			ESTs	1.35	2.02
-	400818			Target Exon	1.36	2.10
	406475			C15000508*:gi[2558825]gb]AAC53387_1[(AF	1.36	2.78
	426935	NM_000088		collagen, type I, alpha 1	1.36	1.41
	414171		Hs.865	RAP1A, member of RAS oncogene family	1.36	2.20
70	444195		Hs.10587	KIAA0353 protein	1.35 1.35	0. 94 1.22
	447918		Hs.115175	ESTs, Highly similar to JC5818 gamma-act	1,35	1.40
	421314		Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA, protesse, serine, 11 (IGF binding)	1.35	1.24
	412992		Hs.75111	NM_004055":Home sapiens calpain 5 (CAPN5	1.35	1.30
75	401025 452862		Hs.8687	ADAMTS2 (a disinjegdo-like and metalio	1.34	2.12
,5	425308		Hs.155585		1,34	1.02
	402306		110,100,000	Target Exon	1.34	1,21
	428416		Hs.184222		1.34	1.40
	407242	2 M18728		gb:Human nonspecific crossreacting antig	1.34	1.22
80	410741		Hs.324473		1.34	2.05
	43933	5 AA742697	Hs.62492	NM_052863:Homo saplens secretoglobin, fa	1.34	1.12
	43125		9 Hs_251385	murine retrovirus integration site 1 hom	1,33	1.21
	405213	3		Target Exon	1.33	203

	447000	DEC (0004		Mark Mark Committee Commit		
	447990	BE048B23	Rs.20144	small inducible cytokine sublamily A (Cy	1.33	1.05
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha	1.33	2.09
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.33	1.32
_	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.33	1.18
5	430385	AA113437		N-myc downstream-regulated gene 3	1.32	1.48
	447731	AA373527	Hs.19385	CGI-58 protein	1.32	2.22
	400740			hypothetical protein FLJ14280	1.32	2.01
	410481	R34107	Hs.321450	pregnancy specific bela-1-glycoprotein 2		
	440274	R24595			1.32	1.32
10			Hs.7122	scrapie responsive protein 1	1.32	1.32
10	406867	AA157857	Hs.182265	keralin 19	1.32	1.42
	456855	AF035528	Hs.153863	MAD (molhers against decapentaplegic, Dr	1.32	2.30
	443144	BE248335		hypothetical protein MGC14797	1.32	2.03
	432810	AA863400		EST\$,	1.32	4.01
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.31	1.24
15	424075	Al807320	Hs.227630	RE1-silencing transcription factor	1.31	2.17
	440099	AL080058	Hs.6909	DKFZP554G202 protein	1.31	1.53
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein		
	438874	H02780	115.10-61	abudded 4 Peans stanged NATA News	1.31	1.31
	402825	102100		gb:yj41a11_1 Soares placenta Nb2HP Homo	1.31	2.03
20		1100070	11. 440514	Target Exon	1.31	1.24
20	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dan)	1.31	1.45
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.31	1.19
	417640	D30857	Hs.82353	protein C receptor, andothelial (EPCR)	1.31	1.12
	436027	A1864053	Hs.39972	ESTs, Weakly similar to 138588 reverse t	1.30	2.06
	407409	AF060168		gb:Homo sapiens AS10 protein mRNA, parti	1.30	2.16
25	400221			NM_002082*:Homo saptens G protein-couple	1.30	2.02
	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A		
	450008	H52970	Hs.36688		1.30	2.44
	441591	AF055992	Hs.183	WAP four-disulfide core domain 1	1.30	1.19
		AFUSSBBZ	U2'10'	Duffy blood group	1.29	1.03
30	405973			Target Exon	1.29	1.32
20	424604	AW8653BB	Hs.151076	KIAA1243 protein	1.29	0.92
	410899	AW809716		gb:MR4-ST0124-241199-026-h09 ST0124 Homo	1.29	2.06
	405818			CX001073;glj4176497 emb]CAA20116.1] (AL0	1.29	2.05
	402621			Target Exon	1.29	3.06
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	1.28	2.35
35	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.28	
	453331	A)240665		ESTs		1.44
	439791	H77774	Hs.35755	ESTs	1.28	2.36
	431385	BE178536			1.28	2.00
			Hs.11090	membrane-spanning 4-domains, subfamily A	1.28	3.00
40	407266	AJ235664		gb:Homo sapiens mRNA for Immunoglobulin	1.2B	1.28
40	446526	H89616		Homo saplens cDNA FLJ 13357 fis, clone PL	1.28	1.28
	455577	BE006341		gb:RC2-BN0127-240300-011-505 BN0127 Homo	1.28	1.28
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.28	2.10
	407711	AI065846	Hs.25522	KIAA1808 protein	1.28	1.23
	E40714	NM_004369	Hs.80988	collagen, type VI, alpha 3	1,28	1.19
45	420136	AW801090	Hz.195851	actin, alpha 2, smooth muscle, aorta	1.27	1.24
	418203	X54942	Hs.83758	CDC28 protein Knase 2		
	448515	H6B441	Hs.13528		1.27	2.08
	444418	AL034417		hypothetical protein FLJ14054	1.27	2,05
			Hs.11169	Gene 33/Mig-6	1.27	1.98
50	427809	M26380	Hs.180878	lipoprotein Ilpase	1.2 7	1.09
20	414690	BE410103	Hs.12313	hypothetical protein FLI14566	1.27	1.36
	439919	AA970710	Hs.128064	ESTs	1.27	2.28
	401311			Target Exon	1.27	2.05
	444235	AW207346	Hs.143202	ESTa	1.27	2.00
	430858	AFC07190		Homo saplens SIB 297 Intestinal mucin (M	1.26	1.23
55	448186	AA262105	Hs.4094	Homo septens cDNA FLJ14208 fis, clone NT	1.26	2.40
	400161			Eos Control		
	444239	R57988	Hs.10706		1.28	1.33
	438369	177886		epithelial protein lost in neoplasm beta	1.26	1.20
	441944		Hs,83428	nuclear factor of kappa Eght polypeptid	1.25	1.26
60		AW855861	Hs.6025	Homo sapiens clone 23767 and 23762 mRNA	1.28	1.12
90	431142	AA852596	Hs.250641	tropamyosin 4	1.26	1.23
	434229	R56378	Hs.1B1223	hypothetical protein PRO2801	1.26	2.04
	406733	AA976565	Hs.297753	vimeกนึก	1,26	1.29
	422292	Al815733	Hs.114360	transforming growth factor beta-stimulat	1.25	1.16
	424137	AA335769	Hs.16262	ESTs	1.25	1.27
65	434868	R50032	Hs.159263	collagen, type VI, alpha 2	1.24	1.50
	42440B	A1754B13	Hs,146428	collagan, type V, alpha 1		
	433750	H15448	Hs.31330	Homo saplana clone HQ0319	1.24	1.29
	447299				1.24	1.27
		AFD43B97	Hs.18075	chromosome 9 open reading frame 3	1.24	1.13
70	438357	Al042101	Hs.294107	ESTs	1,24	204
70	409959	BE349470		mucin 6, gastric	1.23	2.22
	439897	NM_015310	Hs.6763	KIAA0942 protein	1.23	244
	421982	AF206019	Hs.110347	REV1 (yeast homolog)- (ike	1.23	2.14
	407207	T03651	Hs.336780	tubulin, beta polypapiide	1.23	1,32
	416956	AA810664	Hs.101660	hypothetical protein MGC5391	1.23	2.39
75	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevin)	1.23	1.06
	442941	AU076728	Hs.8867	cysteine-rich, anglogenic inducer, 61		
	452304	AA025386	Hs.61311		1.23	1.51
	414359	M62194		ESTs, Wealdy similar to \$10590 cysteine	1.23	1.01
			Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1,22	1.41
80	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.22	1.17
GU	421341	AJ243212	h	deleted in malignant brain ternors 1	1.22	1.09
	406850	A1624300	Hs.172928	collagen, type t, aipha 1	1.22	1.52
	452167	N75238	Hs.13075	Homo saplens cDNA: FLJ23013 fis, clone L	1.22	2.55
	423189	M59371	Hs.171595	EphA2	1.22	1,15
						-,

	401899			Target Exon	1.22	1.22
	403579			Target Exon	1.22	2.34
	415954	AA171850	Hs.42251	ESTs	1.22	2.24
5	429171	AJ743173	Hs.169095	ESTs, Weekly similar to ARL2_HUMAN ADP-R	1,21	1.14
3	444071	A1627808	Hs.110524	ESTs	1.21	2.23
	424344	AF036973	Hs.145477	HCGIV-6 protein	1.21	2.15
	434051	AF116622	N- 44 10 10	gb:Homo sapiens clone FLB4217 mRNA seque	1.21	1.25
	422311 404600	AF073515	Hs.114948	cytokine receptor-like factor 1	1,21	1.39
10	429751	LISENIA	Lie 44 toon	Target Exon	1.21	1.29
10	430392	M55210 NM_000627	Hs.214982	laminin, gamma 1 (formerly LAMB2)	1.21	1.03
	422687	AW068823	Hs.241257 Hs.119205	latent transforming growth factor bele b	1,21	1,21
	424855	AW204725	Hs.25560	insulin-like growth factor binding prote ESTs	1.21	1.23
	418890	AA232134	Hs.19002B	ESTs	1.20	1.98
15	413232	BE073258	Hs.133988	hypothetical protein FKSG28	1,20 1,20	1.33
	414154	AW205314	Hs.323060	ESTs	1.20	2.18
	416784	AA334592	Hs.79914	lumican	1.20	1.34
	410933	C15974	*	gb:C15974 Clordech human aorta polyA mRN	1.19	1.27 2.05
	415388	AF018081	Hs.78409	collagen, type XVIII, alpha 1	1,19	1,11
20	406731	AI559131		gb:tq31g07.x1 NOL_CGAP_Ut1 Homo saplens	1.19	1.19
	447563	BE536115	Hs.160983	EST	1.19	1.14
	405531			Target Exon	1.19	2.02
	400363	NM_001403		sukaryotic translation elongation factor	1.19	1.21
0.5	426611	BE178050	Hs.171271	caterin (cadherin-associated protein), b	1.19	1.18
25	427876	AA394062	Hs,300772	tropomyosin 2 (beta)	1.18	1.16
	413929	BE501689	Hs.75617	collegen, type tV, aipha 2	1.18	1.20
	413856	D13639	Hs.75586	cyclin D2	1,18	1.20
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	1.18	1.12
30	422287	F16365	Hs.114346	cytochroma c axidase subunit VIIa polype	1.18	1.05
50	412758 446868	Y07818	Hs.74566	dihydropyrimidinase-like 3(ULIP)	1.18	1.06
	417613	AV680737	U- panc	ESTs	1,18	1.18
	405542	AV654351	Hs.82306	destrin (actin depolymerizing factor)	1.18	1.17
	41990B	AW971327	Hs.293315	Tanget Exon ESTs	1.18	1.98
35	434095	AA011117	Hs.3745	milk fat globute-EGF factor 8 protein	1.17	2.02
•-	407230	AA157857	Hs.182265	keralin 19	1.17	1.19
	448413	Al745379	Hs.42911	ESTs	1.17	1.35
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.17 1.17	2.87
4.0	424572	M19650	Hs.179600	2',3'-cyclic nucleotide 3' phosphodieste	1.17	1,39 2.08
40	440109	AK001138	Hs.333149	hypothetical protein FLJ10276	1,17	1.06
	405131			C1002509:gli9938010 ref[NP_064684.1 odo	1,17	2.22
	422354	U20982	Hs.1516	insulin-like growth factor-binding prote	1.17	1.19
	442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 fis, clone PL	1.17	1.11
15	400060			Eos Control	1,18	2.53
45	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	1.1B	2.00
	412802	U41518	Hs.74602	aqueporin 1 (channel-forming integral pr	1.16	1.30
	429207	AA447941	Hs.123423	ESTs	1.16	1.27
	415149 400231	X12451	Hs.78056 _,	cethepsin L	1,16	1.12
50	416553	AA768553	Do 40244E	Eos Control	1.16	1.17
50	422813	AV658571	Hs.193145 Hs.121068	metallobionein 1E (functional)	1.16	1.16
	43931B	AWB37046	Hs.6527	trensmembrane 4 superfamily member 6	1.16	1.10
	422424	Al186431	Hs.296638	G protein-coupled receptor 55 prostate differentiation factor	1.16	1.15
	432745	AI821928	1 44200000	gbxnt78f05.x5 NCL_CGAP_Pr3 Homo sapiens	1.16 1.15	1.21
55	412477	AA150864		microsomal glutathlone S-bransferase 1	1.15	2.00 1.23
	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	1.15	2.31
	424512	X53002	Hs.149848	Integrin, beta 5	1,15	1,15
	449924	W30681	Hs.146233	Homo saplens cDNA: FLJ22130 fis, clone H	1.15	1.24
CO	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.15	1.07
60	456076	BE243877		ATPase, Na? transporting, betz 3 polypep	1,15	2.00
	403026			Target Exon	1.15	2.32
	422545	X02761	Hs.287820	fibronectin t	1.15	1.17
	412719	AW016610	Hs.B16	ESTs	1.15	1.05
65	421848 422087	X15880	Hs.106885	collegen, type VI, alpha 1	1.15	1.14
0.5	413936	X58968 AF113876	Hs.111301	matrix metalloproteinase 2 (gelatinase A	1.15	1.16
	449B45	AW971183	Hs.297681 Hs.6019	serine (or cystaine) proteinase inhibito	1.14	1.13
	430202	T85775	£19.0019	DnaJ (Hsp40) homolog, sublanily C, membe	1.14	2.07
	418806	AA485970	Hs.191718	gb:yd60g02.r1 Soares fetal liver spleen ESTs	1.14	1.14
70	424017	AA333789	10.102110	gb:EST37925 Embryo, 9 week Homo saptens	1.14	2.14
-	422003	AA361760	Hs.296326	усто 137320 свяжус, а меек пото зарівдв ESTs	1.14 1.14	2.16 1.17
	437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.14	
	438367	N79688	Hs.204354	res homolog gane family, member B	1,14	2.17 1.23
75	453152	AK001933	Hs.31945	hypothetical protein FLH 1071	1.13	2.36
75	406849	AA454B09	Hs.172928	collegen, type I, alpha 1	1,13	1.33
	422110	Al376738	Hs.111779	secreted protein, acidic, cystelne-rich	1.13	1.06
	425335	BE394327	Hs.296267	follistatin-like 1	1.13	1.08
	434795	BE620794	Hs.4147	translocating chain-associating membrane	1.13	1.08
80	417426	NM_002291	Hs.82124	laminin, bela 1	1.13	1.11
ŲΨ	452924 416379	AW580939 N28857	Hs.97199	complement component C1q receptor	1,13	1.01
	421464	N38857 AA291553	Hs.34145	ESTS	1.12	1.12
	442420	A1024834	Hz.190086 Hs.131729	ESTs ESTs	1.12	201
			120.101123	2010	1.12	1.15

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	405369			NM_005569":Homo sapiens LIM domain kinas	1.12	1.99
	421730	AW449808	Hs.334534	glucosamine (N-acelyl)-6-sulfatase (Sanf	1.12	2.08
•	405932			C15000305;gfj3806122 gb AAC69198.1 [AF0	1.11	2.01
5	453542	AW836724		Homo sepiens mRNA expressed only in plac	1.11	2.00
J	437585	AW976857		EST8	1.11	2.01
	412524	AA417B13	Hs.44208	hypothetical protein FLJ23153	1,11	1.05
	449931	AW875786	Hs.25734	ESTs, Weakly similar to BING1 [H.saplens	1.11	1.03
	407085	270759	11-47002	gb:H.saplens milochondrial 16S rRNA gene	1.10	1.12
10	447191	NM_014521	Hs.17667	SH3-domain binding protein 4	1.10	1.04
10	406713 432675	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.10	1.07
	432731	Al791855	Hs.105884	ESTs	1.10	2.30
	430763	R31178 AA4B5468	Hs.287820	fibroneciln t	1.09	2.12
	438855	AW946276	Hs.6441	DNA fragmentation factor, 45 kD, alpha p	1.09	2.10
15	405156	MISTURIO	115,0441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	1,09	1.04
~~	409031	AA376836		NM_003213*:Homo sapiens TEA domain famil ESTs	1.09	219
	422608	AW160644	Hs.118695		1.09	2.22
	440704	M69241	Hs.162	potassium voltage-gated channet, subfami Insulin-tike growth factor binding prote	1.09	2.26
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	1.09	1.28
20	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (eifin)	1.0B	2.64
-	452219	AA024860	Hs.61224	ESTs	1.07 1.07	1.02
	430108	AA465294		ESTs	1.07	2.09 2.11
	402174			Target Exon	1.07	2.11
~ ~	416952	A1767736	Hs.290070	gelsolin (amyloidosis, Finnish type)	1.07	1.00
25	410199	AW377424	Hs.205126	Horno saplens cDNA: FLJ22667 ffs, clone H	1.07	1.13
	442670	BE410050	Hs,11859	hypothetical protein FLJ13188	1.07	2.21
	442310	AF033199	Hs.8198	zinc finger protein 204	1.06	2.04
	405536			NM_005805:Homo saplens 26S protessome-as	1.06	2.20
20	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.06	1.05
30	423017	AW178761	Hs.22794B	serine (or cysteine) proteinese inhibito	1.06	1.06
	425371	D49441	Hs.155981	mesothelin	1.06	1.27
	429925	NM_000786	Hs,226213	cylochrome P450, 51 (lanostero) 14-aipha	1.06	2.37
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkall, smo	1.06	1.05
35	409407	AW987370	Hs.342855	Homo saplans cDNA FLJ13289 fis, clone OV	1.05	2.00
33	406109	A10004000		Target Exon	1.05	2.04
	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.05	2.67
	403162	NEL AGGTO	11- 02702	C2000231*:gi[9802031[gb]AAF99597.1[AF239	1.06	2.07
	431020	NM_006770	Hs.67726	macrophage receptor with collegenous str	1.05	1.07
40	407225 41 6 955	J04617	II. goene	aukaryotic translation elongation factor	1.05	1.02
-	451989	AW889150 AF169797	Hs.80595	NM_004552*;Homo sapiens NADH dehydrogena	1,05	1.10
	410276	Al554545	Hs.27413	adaptor protein containing pH domain, PT	1.04	2.12
	446921	AB012113	Hs.16530	angiopoletin-2	1.04	1.04
	406712	M31212	Hs.77385	small inducible cytokine subfamily A (Cy	1.04	1.04
45	406773	AAB12424	Hs.76067	myosin, light polypeptide 6, elkali, smo heat shock 27kO protein 1	1.03	1.05
	452082	N51905	Hs.125133	hypothetical protein FLJ22501	1.03	1.10
	419150	T29618	Hs.89640	TEK brosine kinase, endothellal (venous	1.03 1.03	2.01
	417204	NB1037	Hs.1074	surfactant, pulmonary-associated protein	1.02	2.24 1.00
	408339	R97502	Hs.30443	sentrin/SUMO-specific protesse	1.02	2.19
50	400247			Eas Control	1.02	2.04
	4300 <u>á</u> 0	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	1.01	1.01
	442275	AW449467	Hs.54795	ESTs	1.01	1.04
	4D6786	AW161678	Hs_111334	ferrilin, light polypeptide	1.01	1.06
E E	439403	BE265745		ESTs, Weekly similar to ALUC_HUMAN !!!!	1.01	2.11
<i>55</i>	428043	T92248	Hs.2240	uteroglobin	1.00	1.06
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1,00	1,02
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU 8	1.00	2.16
	450724	R55428		gbtyj79b05.r1 Soares breast 2NbHBat Homo	1.00	0.99
60	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	1.00	1,0B
UU	432077 427687	AL134685 AW003867	U- ACTO	gb:DKFZp547M126_r1 547 (synonym; hfbr1)	1.00	2.05
	435256	AF193766	Hs,1570	histamine receptor H1	1.00	1.00
	420026	AI831190	Hs.13872	cytokine-tike protein C17	1.00	1.00
	455128	AW861555	Hs.166676 Hs.314372	ESTs EST	1.00	1.00
65	410685	AA497117	Hs.58893	ESTs, Moderately similar to ALU1_HUMAN A	1.00	1.00
	401404		1 10.00030	Target Exon	1.00	1.00
	449625	NM_014253		odz (odd Oz/tan-m, Drosophile) homolog 1	1.00	1.00
	443458	R05385	Hs.143509	hypothetical protein FLJ2(924	1.00	1.00
	452744	A1267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	1.00	1.00
70	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, aip	1.00 1.00	1.00 1.00
	447947	N33033	Hs.270215	ESTs	1.00	1.00
	419236	AA330447	Hs.135159	Home sapiens cDNA FLI11481 fts, clone HE	1.00	1.00
	455047	AW852530		gb:PM1-CT0243-071099-001-g05 CT0243 Homo	1.00	3.00
T.F	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	1.00	1.00
75	444963	A1916973	Hs.213603	ESTs	1.00	1.00
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.00	1.00
	442849	R10099	Hs.269805	ESTs ·	1.00	1,80
	420407	AA814732	Hs.145010	Epopolysaccarida-specific response 5-li	1.00	1.00
80	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	1.00	1.00
υŲ	418454	AA315308	Hs.195870	hypothetical protein FLJ 14991	1.00	1,00
	459045 455500	N69101	Hs.40730	ESTS	1.00	1.00
	455500 411745	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	1.00	1.00
	771140	AW867826		gb:MR0-SN0039-300300-001-502 SN0039 Homo	1.00	1.00
				45.5		

						4.00				
	429932	A1095005	Hs.21586	ESTS	1.00 1.00	1.00 1.00	•			
	432365	AK001106	Hs.274419	hypothelical protein FLJ10244	1.00	1.00				
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t CTP synthase	1.00	1.00				
5	431374 443162	BE258532 T49951	Hs.251871 Hs.9029	DKFZP434G032 protein	1.00	1.50				
,	432128	AA127221	Hs.296502	ESTs	0.99	2.33				
	45183B	AW005866	Hs.193969	ESTs	0.9B	3.26				
	438414	AA806794	Hs.131511	ESTs	0.97	3.61				
4.4	435872	AA701357	Hs.192759	ESTs	0.97	0.96				
10	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.97	1.08				
	424001	W67883	Hs.137476	paternally expressed 10	0.96 0.96	2.25 2.07				
	418869	AW516565		gb:xq01d05.x1 Soares_NHCeC_cervical_tumo	0.94	2.18				
	458659	AW749895	Hs.332520 Hs.85226	Homo sapiens mRNA; cDNA DKFZp434A1014 (f lipase A, lysosomal acid, cholesterol es	0.94	1.31				
15	418458 432728	AA332941 NM_006979	Hs.27B721	HLA class II region expressed gene KE4	0.94	2.12				
13	432093	H283B3	110.210121	gb:yl52c03,r1 Soares breast 3NbHBst Homo	0.94	2.19				
	452239	AW379378		protein tyrosine phosphatase, receptor t	0.94	0.79				
	403167			Target Exon	0.94	2.06				
	402209			Targel Exon	0.92	2.04				
20	453500	AJ478427	Hs.43125	esophageal cancer related gene 4 protein	0.92	0.74				
	424090	X99699	Hs.139262	XIAP associated factor-1	0.91 0.91	2.11 2,15				
	432B16	N38913	Hs.221575	ESTs	0.91	2.14				
	451779 406851	AW968616 AA609784	Hs.296234	ESTs, Weakly similar to T31613 hypotheti major histocompatibility complex, class	0.89	1.04				
25	427698	AW972594	Hs.335499	ESTs	0.89	0.90				
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-E	0.88	2.42				
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.87	1.14				
	426024	Z43405	Hs.75668	Homo saplens, Similar to RIKEN cDNA 1700	0.87	2.04				
	400986			NM_024085*:Homo saplens hypothetical pro	0.87	2.10				
30	430353	AW952337		citrate synthese	0.86 0.86	2.28 2.50				
	404975	2000	1). 400050	uncharacterized hypothalamus protein HT0	0.86	1.94				
	406673	M34996 AW970623	Hs.198253	major histocompatibility complex, class pb:EST382705 MAGE resequences, MAGK Homo	0.80	2.08				
	431323 404926	AWSTUDZS		Target Exon	0.79	2.01				
35	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	0.77	0.86				
	437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	2.10				
	421566	MM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	0.76	266				
	406646	M33600	Hs.306026	major histocompatibility complex, class	0.76	1.09				
40	442195	NM_001430		endothelial PAS domain protein 1	0.76	2.00 0.78				
40	415457	AW081710	Hs.7369	ESTs, Weekly similar to ALU1_HUMAN ALU S	0.76 0.73	2.06	•			
	413916 453716	N49813	Hs.75615 Hs.152675	apolipoprolein C-II ESTs	0.73	2.10				
	437802	AA037675 A1475995	Hs.122910	ESTS	0.70	2.08				
	422282	AF019225	Hs.114309	apolipoprolein L	0.68	2.95				
45	410361	BE391804	Hs.62661	guenylate bloding protein 1, interferon-	0.54	2.11				
	424917	A1636208	Hs.96901	hypothetical protein FLJ23049	0.53	0.53				
		_								
	TABLE 3	4B:								
50	Dham	l'hirus Es	s probeset ident	Mor gumbor						
50	Pkey:	nber: Gene chis		DIGITION TO THE PROPERTY OF TH						
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	1 IDDECOIC									
	Play	CAT Numi	ber Accessio	m						
55										
	442006	1239046_	1 AW9751	183 AA973583 A1365103 A1699495 A1301787	22 ALIA 92000 ATARGGI	04.4 SOLVONALE 44.0	CC100 DETROOTS NAARAR AIRBOOTS			
	420195	28714_1	AK0020	39 Al 117524 AV714494 AW954901 AL045243 BF9551 77 N66571 AA999864 AU157344 AI817146 R54821 BE	85 AU151 BOU AVVOOL 222107 AAAEERRO A	JB 13 AYYOOU486 AA& I344769 DE480910 K	2487 M24033 M323020 M306145			
			AA4000	77 N66571 AA599164 AO 137344 AIG17146 R34621 BE 21 AI584169 AI250173 AY440227 AA669696 AW244040	41358404 AI570333	AM1R315 N94787 R7	2348 N94780 BF944396 BF75469B			
60			AWINGS	MY MORRS 1 REPORTOAT RESPRESS A 431R076 AW60147	4 AWBR3910 H10056	N63481 BEB3B574 B	3F909132 B)084973 BG257295 BG818471			
v			DESARA	AO ALADOGDA AWYY1213 REDARYAA WAAGAD ARRYAAD	AW903942 AA97591	9 AA312915 BF9480:	57 R55120 H10110 BI045196 AW069645			
	437620	9575_20	AW9769	330 AW292808 AW451798 BF514112 A1806378 A16685	103 A1769457 AW599	455 A1625525 A15385	S1 Al660609 AA761825 AA973287			
		_	AA8614	83 W73065 A1735361 W60499 W76663 BG959557	_					
~~	430712			347 A1670953 A1656180 AA484715 A1659205 BF92347	2					
65	411880		.1 BE0881	01 T05990 AW872477	nen A1740070 A18MCI	1000 AIGC	979 AMEZESOS DEGERÁSS AMINAASINS			
	451149	4941_2	AF2315	12 AW300273 BG779015 AW510935 AI989816 AA197 59 AA886718 AI753144 AA626885 AI018092 AI263010	101 111 0 100P 11A 20U 101 100 0 100P 11A 20U	1001 MG02020 M000 R AA256288 AW5710	37 2 A1070302 DE000001 AVV044100			
			660777	የፋፍ ል) የበማይያው ልልየፊያያያያለ ሲሆንያበዊያያ ል) የ157573 ልልበ15867	7 N73713 ALII47588 <i>I</i>	AVV840954 AA256196	3 AW840357 AWB40504 T35684 Z36755			
			AVANCE.	ልንተ ልልንለፕለንለ ልነበናዩርናስ T31 የRD RIG1በለንጽ ዝጸዓለጸዓ RG	1675223 AA443427 B	E879501 AA478530 I	R72977 AA29856B BF792417 AA356982			
70			95922/	199 BE764808 RE565836 RE903986 RE331881 N42207	' BG623760 BG61109	30 BF735387 BE6977	'57 BE697755 BE718853 N/8560 AI984095			
7 🗸			AA137	140 AA053711 N59865 A1078134 AA643796 T57803 A/	018642 N66799 A10	04600 BG896323 BF8	195104 N73684 N73606 N73B11 AW900267			
			AA0180	541						
	459702			209 BE166299 AI204995 BG199355 AW969908 AA528	756 AW440776 BIO4	4354				
75	417563			701 R86895	400 14004040 8446	14000				
75	431089			189 AW063489 AA715980 BF001091 BF880065 AA660	7 IUZ PVIDZ 1240 PIRAS	1020				
	455797 413059			833 BE091874 BE091871 078 BE151503 BE151498						
	417430			732 AW827432 AA199662 AA610519 R54983						
	432222									
80	458208	45807_4	AIGGNE	AG A13R0016 SIM273298 BM273060			con process a process			
	45774	120741_	1 BK0179	168 BE044740 BI017768 AW827360 BF380597 BI0179	O BF / 46974 BF 3805	82 BF380592 BF908	17691 6465909 BIN17766 BIN17065			
				634 BE166581 BE161439 BF908606 BI017961 BE0447 160 B1017798	10 AVY027623 BF90	1700 BIU I BOT AWSZ	10211010 00111010 00000991			
			RI0.1\2	NG ING 17 (30						

	411010	1066474_1	AW813381 AW816094 AW813357 AW814469 AW813293 AW816099 AW813295 AW813425 AW813331 AW813325 AW813351 AW813427
			AW813339
	449780	31099_2	BG721806 BG623574 AA367501 BG436403 BG619828 BG570704 BF086115 BF086118 R78932 BG620860 BG571920 BF997723 AA368244
5			BG620631 BG621967 BG435818 BG620442 BG621618 H12650 BG573175 H6160 R67494 H01715 D78811 BG435953 BF107266 D79043 R67255
,			H01310 BG570941 BG570693 R21776 AA327133 R32578 R30775 BG570963 T86946 H61601 W86279 BF991104 R21732 BF990905 BG622861 BE929694 A)090290 BE929277 BE929284 AA367783 AA082581 D78839 H78318 N91085 BE929344 D63217 BE929334 H53536 R80360 H54070
			8532994 AW962470 R00900 R6919988 R6823946 H9918 BE929345 AA004287 BP957177 R6820685 BF086421 T87029 C17044 H60972
			BG573514 AA131924 D78838 BG003560 C16615 W86323 R09737 R02529 AA367502
	406641	0_0	BG376314 Art 31842 U 1000 B GUUDOSIO U 100 B WOUSE 1703767 TWEEE AVAIGNOUSE
10	454565	1061836_1	AZ25000 AZ25000 AZ25000 AZ25000 AZ25000 BE14167 BE141807 BE141806 BE141805 AW807591 AW807590 AW807596 AW807583 BE141803
10	404000	1001030_1	PER 100 DE 141201 DE 141131 DE 141141 DE 141101 DE 141001 DE 141001 DE 14100 ANDRIGHT ANDRIGH
	455657	1490185_1	REGISCAP BEDGS364 8EGGS110 BEG65111
	459189	MH1945_5	AV683451 AV057494 BG718853 BM152866 BG390826 BE709644 AI864727 BI045181 BI459637 AI909102 AI909090 BG722507 BI023834
	454824	1073655_1	AW833783 AW833646 AW833525 AW833351 AW833526 AW833825
15	444986	704733_1	AW258472 Al204197 AW592537
	413524	1518859_1	BE145894 BE145837 BM263472
	422259	140437_1	BF821471 AW795791 BF844843 BF821371 AA307584 AW795790 BF833724 BE154067 BE084709
	456034	686586_1	AA136663 AA136666 AW450979 AA984358 AA809054 AW23B038 AA492073 BE168945
	426603	1299162_1	AA994657 AA382291
20	456235	1979764_1	AA203637 AAB32266 H67452
	433930	19851_15	AW873618 AA62033B
	413464	415532_1	AL527514 AI732432 AA133309 AI225224 AV700997 BF589361 AW291763 AL121500 AA129708
	411188	1072487_1	AW621260 BE162466 BE161168
25	410295	2817_1	BG402852 BG545086 AA150252 AL038760 AA452480 AI033258 W68776 W83372 N31248 AI052219 AI367635 W89374 N88610 R58194 BI524854
25			B197111 BF940043 A1129268 A1359798 A1056480 AA121421 A1042150 AW445003 A1418180 A119420 A1356058 BF832243 A1349330 A135948
			W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE30214B AW022281 AW960273 AA121288 AJ336371 AJ989381 AJ131425 AJ147483 AJ311637 AW338638 AJ141849 AA709414 AJ187177 AA780884 AJ333805 AA045312 AJ623918 AJ349421
			W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 A1869152 N93462 N71889 A1657432 R71628
			VRDSTSS WIGSTANDSTATE AND MODEL WIGSTAND MODEL WIGGE TO A WIGSTAN AND AND AND AND AND AND AND AND AND A
30			AUG83980 A1148372 H99951 AW183001 A127/0317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67493 R80715 AW149812 N78914
50			A)362034 W61122 AW023118 W69375 T88917 T47994 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79947
			N21313 BFB74610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BFB32310 A1249109
	460279	2140_1	Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091905 BI917641 Al023762 AA587230 BF436086 Al264282 Al687392 Al810535
			AW589886 AI244419 AA749261 AA535436 AW205689 AI765770 AI765431 C02466 AW305347 AI818456 AA322111 AW381845 AW381829
35			AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051
			AAB31504 AA134052 AI871759 AW089048 BI913532 AA367709 BGB28155 BF093014
	445511	9560_8	BM471219 BED93160 BG171761 BI254009 A1905474 AA453162 AA829759 A108G559 AA776022 A1377446 BF589018 AA452822 AW614566
			AA443980 AA476733 AW970674 A3393291 AA988283 A)905528 AW384956 D78656
40	458091	452694_1	AF150286 AV739062 AA835857
40	414221	685586_1	AA136653 AA136656 AW450979 AAB84358 AA809054 AW238038 AA492073 BE168945 AA774785 AA584875 AA577705 AA883178 AA083204 AW362057 T92332 T51823 T02858 AA083975 T92381
	410253 407102	132134_1 7177_2	AY945170 BF930905 F33652 BG357818 AJ368018 A421495 AJ300352 A5378526 AJ264177 AJ276281 AJ245302 AJ281050 AJ190036 AW451438
	401 102	1117,44	AW243903 AA910870 F22289 F19647 F22775 AW4773816 BF445785 AA774528 F33447 C01077 AW772227 F17769 H42812 R09701 AA349096
			R45772 H42892 H42597 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970
45			H42536 H24495 R48875 H42951 H22079 R86018
	456054	1263570_1	BF314481 BE313241 BI196333 BE383148
	409368	110612_1	AA071059 AA885201 AA085020
	433430	2181751_1	AA961586 AI863735 AA588325
50	423790 444083	886344_1	BE152393 AA330984 BE073904 BF176271
50	41961B	10908_12 252691_1	BU336699 AN123195 BG168298 AA247945 AA528295 AW971284
	408404	658475_1	BF30898 BE299629 BF299766 AW192518 BE299614 BE300025 BF307463
	459557	859794_1	BG622239 N53315 A1524952
	455885	1524553_1	BE153524 BE153576 BE153583
55	451385	85022_1	AA019751 AA017656 AA017374
	439781	2592493_1	A8845538 AA890229
	451331	28714_1	AKOO2039 AL117624 AV714494 AW954901 AL045243 BF955185 AU137860 AW880616 AW880496 AA256290 BE767078 N44348 A886676
			AA455877 NG6571 AA999864 AU157344 A1817148 R54821 BE223107 AA455880 Al365752 BF689210 N63487 A1924033 A1923020 A1308145
~ ^			A1919421 A1584169 A1250173 A1440227 AA669696 AW244040 A1358104 A1570333 A1418315 N94787 R72348 N94780 BF944396 BF754698
60			AW005707 N98931 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N634B1 BE838574 BF909132 BI084973 BG257295 BGB18471
	*****		BE348449 AJ420523 AW271213 BE048764 W44882 AJ867849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645
	437158	59575_1	ALOSOGO AA160485 AW173544 AW296506 AW439860 AI521563 AT702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 A1807128 AA523012 AI366250 AW461857 AA974203 AI762577 BF512652 AW007307 BE676286 AW460802
			BF58,5502 AAB50766 AB59777 ABD7128 AA523012 AJ550250 AW401657 AA574203 A1702677 BF51,2652 AW007507 BE51,0208 AW400002 AA523057 AW516059 AJ582546 BF221924 BF222543 AJ601808 AW468559 AW000736 AJ666625 AW235356 BM021837 AA511956 AJ680606
65			W35516 T03370 AW511634 H41653 Al465349 H19586 AW090198 AW043993 R39867
OJ	406685	0_0	M18728
	430385	MH497_B	NM 032013 AB044943 AF308609 BI769254 AI819262 AA845839 AI289073 BE670187 AA207127 T33098 AA533492 BE328324 AI083620 AI204945
			AA903471 A372802 AI049838 AJ049737 BF000101 AI686167 BF436896 AI659189 T32971 AA311302 AW733149 AM35981 T03438 AA879206
			AI972177 T33083 AA613910 AI971019 AKX27140 AA853739 AI620528 AI637519 AI972307 BF054861 AKX27865 BF082751 AI698127 T33663
70			AA204743 BE086660 F12132 T25372 BF765338 AA323106 AA322907 BI037062 BE315235 AV722868 BE254381 T66212 BE566142 T09034
			AA405202 BF843940 A1743855 AA113356 BG990583 BE085729 BE535539
	443144	16112_3	ABOS8726 ALGS1414 BE245990 BE245765 BF439734 AAG48422 AAO40639 AL340156 AA255928 AA278385 BE766296 AA280771 AL555662
			AJ474638 AJ863068 BI260946 AK027039 BG615852 AJ698039 AA252016 AA255886 EE905205 AW501157 BF514117 BJ857400 AW297001
75			AI624923 AA125900 AW272165 AA190967 AA280729 AA035532 AW125692 AA125899 BG528645 BE614599 BE464693 AI560128 AA551511
13	450045	404040 4	AJ351149 AL556561 BG292389 C06094 AJ668930 AW104534 AA310513 AAB30127 AW134897 AA046963 AW966490 AJ810530 BF092924 AA334151 AA334725
	432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AAB30127 AW134697 AA046963 AW966490 AIB10530 BF092924 AA334161 AA334725 D31302 R20723 AA263003 BIB24635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017
			D31302 N20123 AA263003 BB24635 A1276207 A1684420 A1524234 A1536036 AWVT4704 A1681443 AA672102 A1687672 A1726670 AWVT6017 A1286003 A147163 AA626033 A1569156 AA565542 A1094253 AW512612 BE88628 AA744762 BE646306 AW471324 AA6999975 AA863400
			N200003 H14 (5) NOQUO ADDITIO MODERA NICESCA WELZO IZ DEGESSED PAT 41(5) DEGESSED WHAT IS A ANSESY O ANGULADO H17500 A1991439 R46187 BE929954 AA33976 D53102 BF74491
80	438874	52147_1	AF075017 R66779 R22463 H02780
	400221	9257_3	NM_002082 L16862 BG826886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823162 H16710
	437751	643238_1	AW978796 AA767373 AW173343 AA836163 N27563 AA905328 R97032

	410899	1063474_1	BF374577 AW809840 AW809996 AW809798 AW809695 AW809646 AW809738 BF374582 AW809716 AW809826 AW809802 AW809747 AW810152
5	453331	16559_1	BG571303 AA410388 AA035018 BG572117 BG820022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 F68598 R25671 R31935 R25110 R363678 BE157487 AW663674 AA190993 H31642 BF510304 AA626915 AA746852 A161014 AA099554 BG572534 A18093329 A1809765 AA411449 A1378760 AA976929 A1378620 AA909684 R75632 A1360919 A1350463 AW069127 AA411621 AA742532 H12461 BE208298 H30612 H12899 N58761 R75957 BF996484 A1240665
	446526	11131 17	BF989591 BI056086 BG001590 BF107035
10	455577		AK023419 BE464935 BE221668 A148685 BI859909 Al374780 AA766892 Al347967 Al582917 AA477117 AA229236 AA652637 AA636109 AU334580 P21288 BR802607 BE769124 AV658991 H89616 AV659853 BEACCEST BECACAST BEACCESTS
10	430858 400161	1475566_1 73704_1	BE006307 BE006341 BE006311 AF007190 AW820705 BE169489 AF007192 BF753303 BG978971 BG978568
15	455101	2656_2	U44839 NM_004651 BC000350 BI458316 AU117940 BG759024 BG749694 BE799505 BGB31537 AI816335 AA325352 AL547005 AW157038 AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE20603 AI369814 AI884369 AW157545 BE221486 H99016 AU159025 AI074496 AI494516 BE245950 AA704385 AA280962 AH79595 AI369776 BE671398 T05538 AA682249 BI677303 BE845336 AI369434 H92068 D52699 D53609 D54715 T06015 BE222174 AI954706 D53218 D63787 R69889 W86896 AI497670 R70771 BF309414 BE620147 BC910597 AW964968 BE836120 AL579715 H56612 D55956 BI044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764 D52367 W22034 BC618979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088
20	409959 421341	2781_3	BG119517 W23267 W21941 AA328817 AW513804 BE179199 BE179195 BE179198 BE179204 BE182686
20	421341	1407_1 73505_1	NM_007329 AFT69456 AJZ43212 AJ297935 AA295769 NM_017679 AJ243224 AJ492875 AJ796676 AJ749838 AA918144 AJ814590 AJ923531 BF513992 AJ720725 AJ150879 AJZ79072 AW612904 AJ492104 AJ284510 AJ141231 AA613554 AW662148 AW769047 AA566985 AW612888 AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311 AF116622 AJ114507 AA640834 BF111602 AA377999
25	410933 406731	1064624_1 0_0	C15024 C15974 AW811066 AW811052 AW811020 AISS9131
23	44686B	15525_1	AK07473 BC017997 BIB31060 BF971101 AIB96394 AI082824 AV708785 W66073 W07772 AV660737 AIB16793 R52250 BG183529 AA633473 A191256 R44783 R19947 BF571348 W86257
	400231	MH494_5	BC013310 AF261095 BC004109 AY007133 BC009081 BC001601 NM_002046 M33197 BC020308 J02642 M38164 BE794233 AY721080 BE255459 BG926429 BG389312 BG477333 Al031799 B1763443 B1260432 AA989106 AY728576 BI091380 AA402499 Al200513 A1284734 A1223995 A1289749
30 35			BG283291 BM013814 AW438544 BM450203 F35435 F33262 BE890952 AA401181 BG939668 F35525 BK088182 F34674 F33506 BM471328 F34677 AW276712 AA187508 F34856 AA114245 AA522581 N23935 AU75923 AI018005 BE4879774 BM456837 A753078 BG222159 AA595947 BF970917 B1094125 AA719841 BE893087 BG775178 BE798393 BE797071 BF339134 BE4809272 BE266456 BE796770 BE745957 BG755835 BE286758 BE2563758 BE2563758 BE2563758 BE2563758 BE2563758 BM450181 BG748174 BE299322 BM425887 BM467637 BM452687 BM47516 BM452420 BE273297 BM466364 BM450640 BM476743 BM459048 BM455306 BM47504 BM450516 BM455644 BM450640 BM476743 BM459048 BM455586 BM47504 BM450640 BM476764 BM450640 BM476764 BM450640 BM476764 BM450640 BM45076 BM450640
33	432745	112643_1	BF569359 BM452924 BM455329 BM471815 Bi862301 BG331738 H04903 AA374894 BE902964 AA658826 AIB21926 AI791191 AA635129 AA564492
40	412477	8669_2	AIZ20117 AI857837 AIZ18371 BM091400 AI304964 AI198508 AI400738 AW571549 AW950042 AI089943 AA437ZE0 AU150878 BF197070 AI267984 BF594181 BF195688 AI433152 AI338921 AI620364 AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121 AI281153 N51899 AI087072 AA954788 AW069054 AI346309 BIC520629 AI340135 BF083036 AI167365 AW819657 AA935468 AI467868 AW148701
,,			AJ383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AJ553922 AJ560688 AW950043 AJ961682 AV706506 R01853 AA128514 N62757 AJ56693 AJ926052 AA18720 N99964 AJ56933 AJ915737 AJ000691 A1185358 N48996 N88575 H82624 H60037 AJ247247 T95664 BF593863 AJ749637 AW088541 AA991284 AA887452 AJ073726 AA633132 AA629674 AA629649 AA629656 AA578595 AJ168758 AA804572 AJ085785 AA994396 AA991209 AA948663 AA929054 AA927852 T87001 AA928210 AA629296 AW802267 AW384129 BF7444400 AA194110 AJ382839 AA194837 A4406284 AJ250750 R37035 AJ525586 W01244
45	456076	8455_1	BG210376 BG217800 BE925778 W39114 BG682395 N70844 BE709097 AW275615 BC001469 AL564898 A1086126 AW003852 BF792438 AA161295 AW970131 A1127310 AW029307 AW192534 AA843144 AW606235 BE221641 A4V008111 AA224203 AA864507 AW794761 AA134005 AA126850 N99165 AW768981 AW816302 A1269871 BE503027 AW401627 AA486431 AA486417 AA191542 AA028128 AA159991 A1498090 A1241024 BM145449 AA774661 A1628021 C18251 BE195811 AA291517 N38898 N59222 A1245611 AA169207 A1286572 AA169585 A1131139
50			AA157900 Al433993 Al208276 AA930061 WG7305 AW337587 A1357055 W04739 Al214517 AA617789 AW241277 Al880213 Al582789 Al143996 BE814848 N49964 Al936222 Al817819 F09976 AA039349 AW805002 T35117 N94388 Al68250 AW394673 AW384556 AW384573 AW384573 AW384566 BG194342 BG204579 BG27538 AL578075 AA328769 AW384466 BG194342 BG204579 BG27538 AL578075 AA389553 AW794940 878568 AW511211 R26588 R36111 BG170598 BE937009 BG678833 AA862899 H96612 H02273 AA768487 BF211173 N32570 AA088287 R68451 AA287663 H16847 R60865 AA421891 W68402 R28378 R64119 R70109 R77661 R67963 BG701844 H68670 AA169664 AA114111 BG715243 R69317 BE715252 BE713804 BG336586 NM_001679
55	430202	1233214_1	EC011835 U51476 BM463117 AU119746 BI462090 BI227086 BG706303 BF059073 BG706532 BI544716 AI568735 BE858747 AU122881 AU125210 AI168547 AU134705 BE281323 AI147220 BE263020 AW973937 BG281863 BE858367 BE278941 AI262814 AI001194 AI391616 AI200862 N32564 AI161064 AI089818 BF514359 AI370916 AI341797 BE263166 AI218416 AI131098 AI285310 AI928440 AI086642 AI375442 AW028327 AI217792 AI161020 AI342854 AI221544 AI304700 AI343005 BM148839 AA831636 AW074258 BF940509 AI149876 AI914574 AA298442 AI241343 AA66886 AW272172 AI160537 BG209220 AA028152 AA025989 AW968345 AA468998 T85775
60	424017 437272	888651_1 176_2	AW35617 AA34317 AA333769 AW356107 AA334317 AA333769 AB075828 BG107763 AW021313 BI492345 AW385707 AW680860 AW296117 BE072066 AW680775 BF679498 AW580828 BE003666 BEC03672 AW3560651 AW580908 BI037146 AW580994 AW38094 H17858 NS0343 NS4223 F05578 F07398 F05578 AA773248 AA354359 AA330257 C20685 BE548300 AW968728 AW968554 AA777644 AA706896 AA682517 AA832267 BG165087 NS1097 NS1567 R95837 BI256803 W89042 R95836 R97864 AW975957 AA747943 AA811289
65	453542 437585 430763 409031	885_22 596968_1 1400_7 9531_1	BF588186 BF899745 AW896724 BE249668 AW976857 AI6U9001 AA769369 AW102732 AA761235 AL578301 Al397389 AI671302 AA978185 BF591738 AJ765912 BF036043 AW190446 BG194731 AW682036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167
70			Albs7345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW763711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF79073 AW381624 AV727105 BF439618 AA443174 AI018009 N42950 AW573242 AI417258 AA463483 AI676131 A1051710 AA636827 AAA43828 AW592822 AA25129 AA730278 AW49062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R15650 R39478 R39479 R394368 BG540916 BM314745 AA251087 D54231 D55274 BF085605 D31589 AW5966405 AW994425 D31879 BE093545 AW901107 AA383628 BI021552 R55620 N39976 AA573281 R82565 AA234955 BE093539 AW367006 BF358697 BE093545 AW901107 AA383628 BI021552 R55620 N39976 AA573281 R82565 AA234955 BE093539 AW367006 BF358697
75			BF365318 AA663856 BE702099 BF035969 Al267384 Al267232 BE348320 AA621574 AAB61212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483588 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA183411 AW444709 AW952455 AI887612 BF431948 BI496876 Al284159 BM128481 AI624657 AI689301 AI969467 AA881685 AA251596 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI689301 AI969447 I8495332 BE858113 AI863860 H00660 T69849 AW780389 C14567 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
80	430108 410276 400247	1233254_1 641443_1 2764_1	A4928B10 AW989393 AA468294 AA811301 AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552 BC022339 BC009610 BC010537 X79805 NM_006713 U12979 BM467814 BM450743 AU132951 AU137129 BG493426 AV758819 BG708412 BG705885 BG702217 AV716638 BG777009 BI545689 BI552153 BM476712 BG770858 BG527656 BG528277 BG391388 AV716861 BI602928

5			A)308856 B)5 AV647719 B0 AA252476 A1 AL599291 A1 BE935104 A1	1867398 BM451469 B1867173 B1602139 BG532171 B1669216 B1544727 BG721852 AV716503 AV701327 BM090738 B1492000 SA4504 AL 599813 AV716829 AV716505 AV714505 AV717902 BF668072 AV716385 B1461927 BM090954 AV717826 BG503676 G501392 BG428433 BEB95629 BM313117 AW021050 BG435032 BM152910 AA313503 AA872377 BG574714 AV712054 AV732696 AV712759 AL 599643 BE790872 BG664930 W73337 AW675377 AV760376 AV725139 AV716379 AA887185 BEB330003 AW023796 902948 BG944042 F00781 AA352483 BG217897 N33888 AW581924 BG654730 D31410 AA353088 D31288 AA253029 H95170 U139980 BG772593 BG776470 BG532512 BG105449 B1545421 AV716456 AW386083 BG699714 AL535832 AL514940 BG190861 W999254 H95138 AA353863 BE764809 N50378 BE0701258 BG701258 BB60846 B1832485 BG168159 BG028647 BE548301 H909737 BG702363 BG614141 BG611137 BG700121 BF031492 N85802 AV715940 N51590 BG993478 BE172016 AW893622
10		1937_10 10161_1	AK056692 A BF060834 B AA564758 A	F086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145 1019088 AW862002 AK056737 AA429638 AW663311 AW440655 AW7231970 AA428584 AA995028 AW854593 AA984131 AA552874 A528743 BG927275 BE045117 AW975234 AA664937 BF749390 BG928948 AA984546 BE009153 AV732487 BE078167 AW872716 AA578441 AB207014 A132283 R65428 BF999154 BF880485
15	449625 2 455047	452948_1 249224_1 1092329_1	AL134685 AV BI918168 AV BG986917 T AW852530 /	W972760 AA525319 AA526644 AA525342 AA526632 AA526296 AV739423 AW972765 N779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG966750 N45526 161382 R49391 R45432 A120107 R35004 F07491 R25094 R35360 AV8652526 AV862527 AL597969 AV8634706 AV841904 A148411124 AV8411157 AW811054 AW811087
		1064652_1 1063489 1	AURIDA DODA 1	DESTARSS AWARDADA AWARDATS RESTATAR RESTASAS AWARDING AWARDING AWARDING AWARDAZO AWARDAZO AWARDAZO AWARDA DE S
20		_	BF374641 B BF374682 A BF374716 A	IF374764 BF374744 AW810552 BF374678 BF374658 BF374659 AW810168 AW810170 BF374611 BF374676 BF374617 AW810353 IW810154 BF374688 BF374555 BF374757 BF374637 BF374743 BF374719 AW809664 BF374643 BF374680 BF374714 BF374708 IW810432 BF374691 BF388066 AW810006 AW810345 AW809860
	411745 418869	1228737_1 43036_8 12789_14	AV704306 E AA229762 /	BE064192 BE054169 BE152580 AW963587 BF368760 AW867826 AW859896 AA230035
25	452239	1237011_1 10116_4	BG034853 / AA417652 I AA258414 I	AA526908 H28359 H28383 ANY173315 AN303375 BG190225 BG839153 BF057308 AA600736 A1751258 Al090486 BE939504 AW631492 A1768270 A1862133 BE378218 AA598207 AW794702 AA024968 AA446024 A1148235 A191710 B1483797 A1272646 B1493796 AA634323 A1754332 C05155 A1218226 A1039658 A1350380 A1084698 A1754989 A1673545 A1432010 A1751035 AA375571 AA446297 BG216743
30	406851 430353	0_0 10288_1	BE2630201	RB7304 AL660552 AU133296 AU133086 BE268567 BE268523 BI544879 BE398161 BG473088 BI544445 BE259021 BE296338 BE255040 BG706790 AL598627 AW952337 BG758113 AW512753 BE267666 BE253415 BI225718 BE268350 BE268245 BI224965 AW772805 BE397782 BI196341 BG702880 AI878949 AL600437 AA416759 BE259917 AI031582 BF512142 AI088248 BE560328 A\802823 AL597585 AW768563 AI816352 BF732831 BI225687 AA833686 AA722593 AA807750 AW068064 AA405187 AI923226 NG1593 AL527710
35			BG282576 AW848862 AW752602 AW848981	AL525927 AL525971 BIBG9547 A\064725 R91856 H46814 H20112 W01682 AW848670 AW648855 AW376602 AW746895 AW746893 AW34662 AW756821 AW346812 AW746821 AW756821 AW376821 AW376821 AW376823 AW376622 BE706047 AW752691 AW752674 AW752652 AA379167 AW752610 AW752684 AW752613 AW752690 AW848709 AW848978 AW8489155 AW848980 AW848979 AW848976 AW7848973 AW848916 AW7848713 AW848708 AW848642 AW7848641 AW848639 AW848673 AW764802 AW784890 AW7848888 AW7848973 AW848933 AW7848752 AW7848708 AW782698 AW762697 AW782682 AW782681
40			AW752680 AW752608 AW848718 BI7525817) AWT52679 AWT52664 AWT62651 AWT52638 AWT52637 AWT52638 AWT62638 AWT62626 AWT62624 AWT62619 AWT62696 I ALEB2019 BE875587 ALE22175 AW868686 BG666208 AA259073 BE696973 AA459543 AA358314 W40564 BF926427 AW849000 I AW846515 AW848507 AW848444 AW848440 AW848222 AW848222 AW762657 AW376786 AW376781 AW376615 AW376614 AA534520 AI748906 AA047799 A1014753 AL514480 AL581982 BG743146 W24771 H20102 H11227 AW752607 AW006596 AW130378 AW752651 AW88238 BE349577 AW752612 AW752632 AW848910 NM, 004077 AF047042 AL550606 B1765896 B1196831 B1855656
45			BF326302 BI463171 AA157518	BG749937 BE535486 BE019810 AA313713 AA992542 AA332541 AA682985 AA356125 BE140478 BG750945 BI457548 BGD25661 AA325019 BG980576 AA337466 AA321974 BG949285 BG427585 R23979 BG611485 BE550678 W16977 N50379 BG824101 BG471750 WD4591 AU099360 BG471590 BM011999 BE282945 BE559801 BF756438 BE881957 BE314546 BG811831 BG150811 BG112017 IT92368 AW752820
50	431323 442195	1235269_1 15007_1	UB1984 N BF998789	3 AA502839 AA502819 M_001430 BE907085 BI333232 AI021986 AU138476 C186D1 U51628 AU100617 BI054387 AU076970 BE786454 BG010080 AW377189 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757867 AL649361 AL544018 BE002870 BE929314 BE090199 AL046650 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403
	TABLE 34C	:		
55	Pkey: Ref:	Sequence so	urce. The 7 di	ing to an Eos probeset git numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of
60	Strand: Nt_position:	Indicates DN	A strand from	unham, et al. (1999) <u>Nature</u> 402:489-495. which exons were predicted. ns of predicted exons.
60	Pkey 405443 401645	Ref 7408143 7657839	Strand Plus Minus	Nt_position 90716-90887,101420-101577 34986-35133
65	401673 405120 401785	7689903 8099940 7249190	Minus Plus Minus	122587-122705,122765-123047 140176-140340 165778-165996,166189-166314,166408-16656
	402333 404942 403362	8844110 7382153 8571772	Minus Plus Plus	165693-165856 92095-92252 64099-64260
70	402641 405600 405061	9958129 5923640 7656744	Minus Plus Minus	122598-125136 26662-27225 132492-132932 108675-108770,109801-109910
75	402327 404342 404429 403344	7656695 9638093 7407979 8569726	Minus Plus Plus Plus	115854-116033 31352-3149B 70823-70990
80	401593 406461 400609 402674 401677 405579 405797	7230957 9756020 9887671 8077108 9965537 6456174 1934909	Plus Minus Minus Minus Minus Minus Minus Minus Minus	10368-10572,11293-12356 158842-159135 92037-92247 39290-39502 62856-63086,63603-63884 100996-101542 5399-5881,5921-6104

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	405159	9966252	Plus	79659-79804		
	403520 402538	7684483 9801137	Minus Minus	97621-98084 96314-96539		
	404151	7534014	Minus	69038-69399		
5	400496	9743564	Plus	41515-41695		
	403010	3132346	Plus	78385-79052		
	406387	9256180	Plus	116229-116371,117612-117651		
	402B85 404501	9926751 7229859	Plus Minus	71919-72049 37270-37526		
10	402487	9797538	Plus	75677-75843		
	404455	7677926	Minus	26927-27611		
	401067	5764724	Minus	153366-153509		
	402324	7630361	Plus	26052-26803		
15	402013 401116	7407997 9966559	Plus Plus	174540-174634,175449-17556B 123579-124447		
10	402998	2996643	Minus	17175-17373		
	405550	1552494	Plus	91720-92115		
	402917	7405502	Minus	1034-1177,3143-3266		
20	402504	9797871	Plus	12366-12614		
LU	405491 400818	5801645 8559994	Plus Plus	81857-82045 172644-172765,173085-173200		
	406475	9797684	Pips	125417-125563,128052-128180		
	401025	8117518	Minus	179287-179483,181044-181166,181844-18203		
25	402308	7340295	Minus	92080-93638		
25	405213	6892345	Minus	50267-51151 79920-80510,80578-80746		
	400740 402825	7329267 6165330	Minus Minus	78572-78607		
	405973	B247789	Plus	103859-104254		
	405818	4071056	Plus	29055-29196		
30	402621	9930950	Plus	130806-131036		
	401311	9212516	Minus	180124-180754		
	401B99 403579	7230209 8101179	Minus Minus	155620-155815 36167-36365		
	404600	8705107	Plus	118354-118444,118649-118792		
35	405531	9665194	Plus	35602-35803		
	405542	9857564	Plus	71331-72183		
	405131 403026	8516051 7670575	Minus Plus	136764-137594 56521-56840		
	405369	2078469	Minus	34183-34357,35686-35751		
40	405932	7767812	Minus	123525-123713		
	405156	9966228	Plus	146733-146860,147899-147961,153127-15325		
	402174	B575912	Plus	253499-253674		
	405536 405109	9795661 9127147	Plus Minus	164091-164162,164397-164516,166720-16679 58328-58485		
45	403162	98380B5	Phis	82652-83613		
	401404	7710968	Plus	136474-136646		
	403167	9838127	Plus	162599-162935		
	402209	8576119	Minus	53315-63472		
50	400986 404975	8085497 3419864	Minus Minus	63140-63319 86096-86605		
50	404926	7341919	Mines	150411-151484	•	
55						
55	TABLE 35	A: About 323	делеє цртеди	ated in hypersensitivity pneumonitis relative to idiopathic p	ulmonary fibrosis or non	-specific interstitial pneumonitis
					•	•
	Pksy:		s probeset Ide			
60	ExAcon:			ber, Genbank accession number		
OU): Unigene m Tile: Unigene ge	44-4			
•	R1:	90th cerce	ntile of HP Als	divided by 90th percentile of IPF Als, where 15th percent	ie of normal tissue Als w	as subtracted from both the numerator and denominator.
		The minim	um value for ti	ie numerator and denominator was set to 50.		
65	R2:	90th perce	entile of HP Ala	divided by the median of IPF Als, where the minimum val	ue for the numerator and	denominator was set to 50.
03	Pkey	ExAccit	UnigenelD	Unigene Title	Rì	R2
	1. Wolf	Livezii	Girgore	OHE THE	,,,	,
	402550			Target Exon	4.03	4.70
70	421563	NM_006433			3.37	2.70
70	424326	NM_014479			3.31	2.42 1.51
	417967 411089	BE244373 AA456454	Hs.1119	nuclear receptor subfamily 4, group A, m cell division cycle 2-like 1 (PITSLRE pr	3.09 2.99	1.2B
	416350	AF188625	Hs.16950		2.71	1.43
	406654	M90586	Hs.73885	HLA-G histocompatibility antigen, class	2.70	1.53
75	459705	BE082764	Hs.27025	ESTs, Wealdy similar to androgen recepto	2.70	1.14
	412610	X90908	Hs.74126		2.69	2.99
	452194 447709	A1694413 1J97145	Hs,19317	olfactory receptor, family 2, subfamily GDNF family receptor alpha 2	2.63 2.63	2.67 1.52
	410910	AW810204	1 10, 100 } {	gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.59	1.00
80	454671	AW812929	Hs.33690	B ESTs	2,50	2.34
	441859	AW194364			2.45	1.90
	422398 403244	Al476149	Hs.33448		2.45 2.40	1.36 1.53
	443244			C2002870*:gi 82698 pir JIQ0985 hydroxypr	240	1.00
				407		

					• • •	4.00
	415462	R52692	Hs.12698	ESTs	2.40	1.00
	447028	A)973128	Hs.167257	brein link protein-1 gb:PM2-HN0008-170300-001-h09 HN0008 Homo	2.33 2.32	1.64 1.00
	41 <i>2</i> 394 450165	AW984150 AA007235	Ms.63931	ESTs	2.32	1.32
5	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.30	1.81
~	444090	569115	Hs.10306	natural killer cell group 7 sequence	2.28	1.69
	413682	BE156991	1,00,000	gb:RC3-HT0371-290100-013-e02 HT0371 Homo	2.27	1,59
	441320	AJ768724		Stoufin 1	2.27	1.87
	456766	R87310	Hs.7740	oxysterol binding protein-like 1	2.27	1.36
10	420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TiT3 com	2.26	1.98
	459721	A1299050	Hs.143835	gb:qn14d12x1 NCI_CGAP_Lu5 Homo seplens	2.25	1.62
	405452			Target Exon	2.25	1.29
	458079	Al796870	Hs,54277	DNA segment on chromosome X (unique) 992	2.25	5.80
15	401447			Target Exon	2.25	1.55
15	423066	Y18264	Hs. 123094	sal (Orosophila)-like 1	2.24	1,51
	441704 405097	A1458766	Hs.192125	ESTS	2.24 2.24	1.00 1.00
	405097 408544	AW293825		ENSP00000175238*:A disintegrin and metal	2.24	1.95
	413454	BE141162		gb:MR0-HT0076-021299-001-003 HT0076 Homo	2,20	2.26
20	444404	M31525		major histocompatibility complex, class	2.20	1.37
20	418460	M25315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.19	2.88
	436063	AK000028	110.002.00	ribosomal protein S24	2.19	1.42
	429212	NM_001504	Hs.198252	G protein-coupled receptor 9	2.18	1.22
_	400712			Target Exon	2.18	1.00
25	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.17	1.79
	403478			NM_022342:Homo saplens kinesin protein 9	2.17	1.80
	418747	AJ249977	Hs,88049	protein kinase, AMP-activated, gamma 3 n	2.17	1.76
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquinone oxldore	2,16	1.44
	451668	Z43948	Hs.326444	cartilage addic protein 1	2.16	212
30	414020	NM_002984	Hs.75703	small Inducible cytokine A4 (homologous	2.15	2.88
	456057	AA947457	Hs.135560	ESTs, Weekly similar to T43458 hypotheti	2.15	2.50
	444346	A1142274		ESTs	2.15	2.38
	418916	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.14	1.93
35	451318	AA029888	Hs.95071	ESTs	2.14 2.13	1.16 1.52
33	458935	Y16521 X60992	Hs.24812 Hs.81226	CDP-diacylglycerol synthese (phosphalida	2.13 2.13	2.61
	417105	X00992 BEQ61111		CD6 antigen gb:QV0-BT0041-011199-039-f02 BT0041 Homo	213	1,94
	408219 420137	AA306478	Hs.254211 Hs.95327	CD3D anligen, delta polypeptide (TiT3 co	211	2.66
	443711	N67861	Hs.49390	ESTs	2,10	1.00
40	423234	AA323534	Hs.296162	AD037 protein	2.10	1.52
-10	416975	NM_004131	Hs.1051	granzyma B (granzyma 2, cytotoxic T-lymp	2.09	3.74
	425280	U31519	Hs.1872	phosphoenolpyruvale carboxykinase 1 (sol	2.08	1.B4
	405827	20.0.0		Target Exon	2.08	1.00
	406909	1.20777	Hs.73885	gb:Human MHC class I HLA-G gane (HLA-A33	2.08	2.29
45	437295	AW779318	Hs.88417	ESTs	2.07	1,72
	424281	AA768243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo saptens	2.07	1.00
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.07	2.16
	423901	AA333006		gb:EST37064 Embryo, 8 week I Homo sapien	2.07	1.50
50	405075			Target Exon	2.07	1.15
50	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.07	2.67
	406267		41 6-140	Target Exon	2.07	1.30
	423365	AA324992	Hs.25716B	ESTs	2.05	1.70
	449970	Al678058	Hs.201227	ESTS	2.06 2.08	2.48 1.00
5 5	430733 446323	AW975920 Al288274	Hs.121036 Hs.345792	EST8 ESTs	206	1.00
33	402240	MZUUZIA	NS.340132	Target Exon	2.05	1.94
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypothes	2.05	1.44
	424463	AW195353	Hs.119903	ESTs	2.04	1.32
	400107	1111100000	115/110000	Eos Control	2.04	2.42
60	404811			NM_021096:Homo saplens calcium channel,	2.03	2.18
	403589			Target Exon	2.03	1.57
	404088			Target Exon	2.03	1.00
	414991	C17898		gb:C17698 Human placenta cDNA (TFt/iwara	2.03	2.04
~~	429073	AA446167	Hs.47385	ESTs	2.03	3.10
65	425274	D3B122	Hs.2007	tumor necrosis factor (ligand) superfami	2.02	1.92
	401897			C17001987:gtj7303380 gb]AAF5B43B.1 (AE0	2.02	1.55
	431094	AW972276	Hs.116195	ESTs	2.02	1.00
	424899	AL119387	Hs.119062	ESTs	2,01	241
70	419711	C02621	Hs.159282	ESTs	2.01 2.01	1.92 1.76
70	459019 405463	AA017156	Hs.40719	hypothetical protein KIAA1164 NM_005748*:Homo sapiens YY1-associated f	201	1.24
	402516			Target Exor.	2.01	1.00
	457365	AA577297	Hs.303249	EST	2.01	2.36
	407928	NM_002262		killer cell lectin-like receptor aubfami	2.01	2.62
75	436553	AW407157	Hs.8997	immunoglobulin lambda locus	2.00	1.64
	406266	101 101	11000000	Target Exon	2.00	2.46
	419409	AW297831	Hs.143792	hypothetical protein MGC2656	2.00	1.60
	435028	AW193035	Hs.187370	ESTs	2.00	1.55
00	404696			NM_013443:Homo saplens CMP-NevAC:(beta)-	2.00	1.21
80	403533			Target Exon	2.00	1.17
	411673			gb:RC1-BT0313-110300-015-706 BT0313 Homo	2.00	1.00
	42414B		Hs.1741	integrin, beta 7	1.99	3.66
	419833	AA251131	Hs.220697	ESTs .	1.99	1.69

	16.5	*14004=		L	1.99	1.84
				hypothetical protein FLJ11004 killer cell lectin-like receptor subfami	1.98	2.56
	426416 449317	AW612744 AW293413	Hs.169824 Hs.132906	19A24 protein	1.98	2.44
		W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	1.97	2.51
5	422109	S73265	Hs.1473	gastrin-releasing peptide	1.97	3.32
	424218	AF031824	Hs.143212	cystalin F (leukocystalin)	1,95 1.96	1.86 2.16
	406303 438676	AAB13745	Hs.123446	C16000922:gij7499103(pirj)T20903 hypothe ESTs	1.95	3.62
	404240	AAG10140	Па. 12.0940	NM_018950:Homo saplens major histocompat	1.95	2.06
10	404056			Target Exon	1.94	2.60
	425508	AA991551	Hs.97013	Homo septens, Similar to RIKEN cDNA 2310	1.93	3.24
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	1.93 1.92	2.35 2.24
	416941 446998	BE000150 N99013	Hs.48778 Hs.16762	niban protein Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.92	5.44
15	409153	W03754	Hs.50813	hypothetical protein FLJ20022	1.92	6.08
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cyloloxic T-lymp	1.90	5.52
	446608	N75217	Hs.257846	ESTs	1.90	4,63 1.50
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t monokine induced by gamma interferon	1.89 1.89	4.93
20	414812 422994	X72755 AW891802	Hs.77367 Hs.296276	ESTs	1.88	3.30
20	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1,88	2.17
	433671	AW138797	Hs.132906	19A24 protein	1,88	1.83
	412116	AW402166	Hs.784	Epsiein-Barr virus induced gene 2 (lymph	1.86 1.86	3.12 1.88
25	447656	NM_003726	Hs.19126 Hs.3003	arc kinase-associated phosphoprotein of CD3E antigen, epsilon polypaptide (TIT3	1.84	1.65
23	432468 419231	AW402155 AL046294	Hs.136245	ESTs. Weakly similar to T17227 hypotheti	1.83	2.46
	427527	A1809057	Hs.153261	immunoglobulin heavy constant mu	1.82	2.07
	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	1.82	2.63
20	436485	X59135	Hs.156110	immunoglobulin kappa constant	1,62 1,81	2,75 4.56
30	432606 421379	NM_002104 Y15221	Hs,3066 Hs.103982	granzyme K (serine protesse, granzyme 3; small inducible cytokine subfamily B (Cy	1.80	5.10
	448569	BE382857	Hs.21486	signal transducer and activator of trans	1.79	1.89
	429670	101087	Hs.211593	protein kinase C, theta	1.78	3.34
25	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.78 1.78	3.55 1.97
35	413869	NM_000878	Hs.75598	Interleukin 2 receptor, beta major histocompatibility complex, class	1.76	2.12
	406672 452203	M26041 X57522	Hs.198253	transporter 1, ATP-binding cassette, sub	1.75	1.55
	426451	AJ908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.73	2.04
	447131	NM_004585	Hs.17468	retingic acid receptor responder (tazaro	1.73	1.56
40	414512	AL044336	Hs.6831	golgi phosphoprotein 1	1.73 1.73	2.00 2.62
	426752 444793	X69490 U89281	Hs.172004 Hs.11958	titin oxidalive 3 alpha hydroxysteroid dehydro	1.72	2.30
	452334	D60471	Hs.13390	gb:HUM111B09B Clontech human fetal brain	1.72	2.12
	446227	AI281459	Hs_270114	ESTS	1.72	2.48
45	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterese)	1 <i>,7</i> 2 1.71	2.72 2.40
	423799	AW026300	Hs.132906	19A24 protein ESTs	1.70	3.71
	458332 408380	A1000341 AF123050	Hs.44532	diubiquitin	1.70	271
	437644	AA748575	Hs.136748	tectin-like NK cell receptor	1.70	2.58
50	402736			NM_024852:Homo sepiens hypothetical prot	1.69	2.10 1.39
	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2 neutrophil cytosolic factor 1 (47kD, Chr	1.69 1.68	2.02
	422846 426202	BE513934 BE266484	Hs.1583 Hs.82916	chaperonin containing TCP1, subunit 6A (1.68	214
	414546	AA353776	Hs.501	CD48 antigen (B-cell membrane protein)	1.68	3.30
55	420440	NM_002407		mammagloblit 2	1.67	2.42 1.49
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.67 1.65	216
	415823 421924	R81864 BE514514	Hs.205103 Hs.109606	ESTs coronia, actin-binding protein, 1A	1.65	1.58
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	1.63	1.94
60	444929	Al685841	Hs.161354	ESTs	1.63	2.16
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 8-cell gr	1.63 1.62	1.74 2.76
	418196 428227	A1745649 AA321649	Hs.26549 Hs.2248	KIAA1708 protein small inducible cylokine subfamily B (Cy	1.62	4.42
	438568	R98865	Hs.11135	major histocompatibility complex, class	1.62	1.74
65	430308	BE640865	Hs.238990	cyclin-dependent kinase Inhibitor 18 (p2	1.62	1.85
	433934	AW273261	Hs.216292	ESTS	1,62 1.61	2.00 2.00
	443559	AI076765	Hs.269899 Hs.10888	ESTs, Moderately similar to ALUS_HUMAN A hypothetical protein FLJ21709	1.81	1.46
	450000 415349	A)952797 A)766697	Hs.13231	ESTs	1.60	2.00
70	406656		Hs.89643	major histocompatibility complex, class	1.60	1.47
	456974		Hs.169401	apolipoprotein E	1.60	1.63 1.68
	416401		Hs.268916 Hs.159225	ESTs ESTs	1.59 1.69	2.04
	439372 434668		Hs.112259		1.59	4.08
75	417696		Hs.82401	CD69 antigen (p60, early T-cell activati	1.58	3.06
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemostiracta	1.58	2.37
	431903		Hs.272100	SMS3 protein solute carrier family 1 (glia) high affi	1.57 1.57	2.14 2.28
	413472 425762				1.56	1.46
80	412472				1.56	2.26
	451406	A1694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	1.56	2,38
	412568		Hs.74034	caveolin 1, caveolae protein, 22kD I ESTs	1,55 1,55	1.67 2.16
	44983	5 AW979300	D Hs.293813	Lois 40		